(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
31 March 2005 (31.03.2005)

PCT

(10) International Publication Number
WO 2005/028624 A2

(51) International Patent Classification[7]: C12N

(21) International Application Number:
PCT/US2004/030360

(22) International Filing Date:
15 September 2004 (15.09.2004)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/503,277 15 September 2003 (15.09.2003) US

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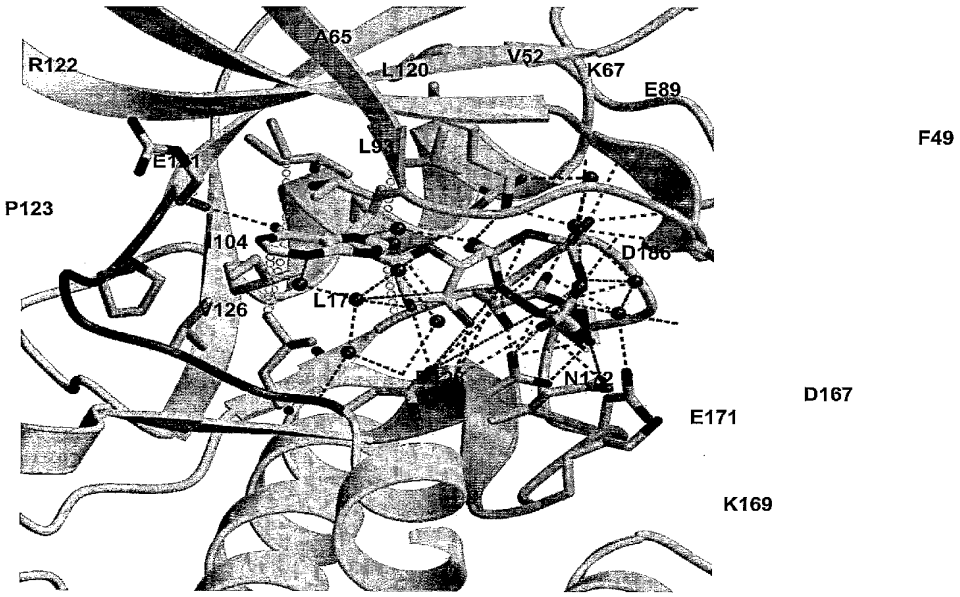
(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM),

[Continued on next page]

(54) Title: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT



(57) Abstract: Molecular scaffolds for compounds active on protein kinases are described, along with methods for using such scaffolds for kinase ligand development. The use of kinase structural information, exemplified with PIM-1 crystals and structural information can, for example, be used for identifying molecular scaffolds and for developing ligands that bind to and modulate particular kinases.

WO 2005/028624 A2

European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

— *without international search report and to be republished upon receipt of that report*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT

BACKGROUND OF THE INVENTION

[0001] This invention relates to the field of development of ligands for protein kinases.

[0002] Examples of protein kinases are the PIM kinases, including PIM-1, PIM-2, and PIM-3. The PIM-1 proto-oncogene was originally identified as a genetic locus frequently activated by the proviral insertion of Moloney murine leukemia virus into mouse T cell lymphomas (Cuypers, H. T., Selten, G., Quint, W., Zijlstra, M., Maandag, E. R., Boelens, W., van Wezenbeek, P., Melief, C., and Berns, A. (1984) Murine leukemia virus-induced T-cell lymphomagenesis: integration of proviruses in a distinct chromosomal region. *Cell* 37:141-150). The PIM-1 proto-oncogene has also been implicated in human hematopoietic malignancies with its overexpression frequently detected in human hematopoietic cell lines as well as in fresh tumor cells from patients with leukemia (Nagarajan L, Louie E, Tsujimoto Y, ar-Rushdi A, Huebner K, and Croce CM. (1986) Localization of the human PIM oncogene (PIM) to a region of chromosome 6 involved in translocations in acute leukemias. *Proc. Natl. Acad. Sci. USA* 83:2556-2560; Meeker TC, Nagarajan L, ar-Rushdi A, Rovera G, Huebner K, and Croce CM. (1987) Characterization of the human PIM-1 gene: a putative proto-oncogene coding for a tissue specific member of the protein kinase family. *Oncogene Res.*1: 87-101; Amson R, Sigaux F, Przedborski S, Flandrin G, Givol D, and Telerman A.(1989). The human proto-oncogene product p33PIM is expressed during fetal hematopoiesis and in diverse leukemias. *Proc. Natl. Acad. Sci. USA* 86: 8857-8861).

[0003] The PIM family of proto-oncogenes in human and mouse now consists of at least three members, that code for highly related serine/threonine specific protein kinases (Saris CJ, Domen J, and Berns A. (1991) The PIM-1 oncogene encodes two related protein-serine/threonine kinases by alternative initiation at AUG and CUG. *EMBO J.* 10: 655-664; Eichmann A, Yuan L, Breant C, Alitalo K, and Koskinen PJ. (2000) Developmental expression of PIM kinases suggests functions also outside of the hematopoietic system. *Oncogene* 19: 1215-1224). The function of these three kinases (PIM-1, PIM-2 and PIM-3) appear to complement each other in mice, as deletion of one of the PIM family protein genes did not result in any severe defects (Laird PW, van der Lugt NM, Clarke A, Domen J, Linders K, McWhir J, Berns A, Hooper M. (1993) In vivo analysis of PIM-1 deficiency.

Nucl. Acids Res. 21:4750-4755). During embryonal development PIM genes are expressed in partially overlapping fashion in cells in both immune and central nervous system as well as in epithelia (Eichmann A, Yuan L, Breant C, Alitalo K, and Koskinen PJ. (2000) Developmental expression of PIM kinases suggests functions also outside of the hematopoietic system. *Oncogene* 19: 1215-1224). PIM-1, the prototypical member of the PIM family is located both in the cytoplasm and nucleus, but its precise role in these two locations has not been fully elucidated.

[0004] Transgenic mice with PIM-1 driven by Emu enhancer sequences demonstrated that PIM-1 function as a weak oncogene because by itself it does not lead to tumor formation but does so after a second oncogenic gene become overexpressed. In 75% of the tumors over-expressing PIM-1, the second gene found to be over-expressed is c-myc (van der Houven van Oordt CW, Schouten TG, van Krieken JH, van Dierendonck JH, van der Eb AJ, Breuer ML.(1998) X-ray-induced lymphomagenesis in E mu-PIM-1 transgenic mice: an investigation of the co-operating molecular events. *Carcinogenesis* 19:847-853). In fact when crosses were made between Emu-PIM transgenic mice and Emu-myc transgenic mice, the combination of genes is so oncogenic that the offsprings die in utero due to pre B cell lymphomas (Verbeek S, van Lohuizen M, van der Valk M, Domen J, Kraal G, and Berns A. (1991) Mice bearing the Emu-myc and Emu-PIM-1 transgenes develop pre-B-cell leukemia prenatally. *Mol. Cell. Biol.*, 11: 1176-1179).

[0005] Mice deficient for PIM-1 show normal synaptic transmission and short-term plasticity but failed to consolidate enduring LTP even though PIM-2 and PIM-3 are expressed in the hippocampus (Konietzko U, Kauselmann G, Scafidi J, Staubli U, Mikkers H, Berns A, Schweizer M, Waltereit R, and Kuhl D.(1999) PIM kinase expression is induced by LTP stimulation and required for the consolidation of enduring LTP. *EMBO J.* 18: 3359-3369).

[0006] Various factors are known to enhance the transcription of PIM-1 kinase in mouse and human. PIM-1 closely cooperates with another oncoprotein, c-myc, in triggering intracellular signals leading to both transformation and apoptosis and the selective inhibition of apoptotic signaling pathways leading to Bcl-2 (van Lohuizen M, Verbeek S, Krimpenfort P, Domen J, Saris C, Radaszkiewicz T, and Berns A. (1989) Predisposition to lymphomagenesis in PIM-1 transgenic mice: cooperation with c-myc and N-myc in murine leukemia virus-induced tumors. *Cell* 56:673-682; Breuer ML, Cuypers HT, Berns A.

(1989). Evidence for the involvement of PIM-2, a new common proviral insertion site, in progression of lymphomas. *EMBO J.* 8:743-748.; Verbeek S, van Lohuizen M, van der Valk M, Domen J, Kraal G, and Berns A. (1991) Mice bearing the E mu-myc and E mu-PIM-1 transgenes develop pre-B-cell leukemia prenatally. *Mol. Cell. Biol.* 11: 1176-1179; Shirogane T, Fukada T, Muller JM, Shima DT, Hibi M, and Hirano T. (1999) Synergistic roles for PIM-1 and c-Myc in STAT3-mediated cell cycle progression and antiapoptosis. *Immunity*, 11: 709-719). PIM-1 kinase is induced by T cell antigen receptor cross linking by cytokines and growth factors and by mitogens including IL2, IL3, IL6, IL9, IL12, IL15, GM-CSF, G-CSF, IFNa, INFg, prolactin, ConA, PMA and anti-CD3 antibodies (Zhu N, Ramirez LM, Lee RL, Magnuson NS, Bishop GA, and Gold MR.(2002) CD40 signaling in B cells regulates the expression of the PIM-1 kinase via the NF-kappa B pathway. J *Immunol.* 168: 744-754). PIM-1 expression is rapidly induced after cytokine stimulation and the proliferative response to cytokines is impaired in cells from PIM-1 deficient mice (Domen J, van der Lugt NM, Acton D, Laird PW, Linders K, Berns A.(1993) PIM-1 levels determine the size of early B lymphoid compartments in bone marrow. *J. Exp. Med.* 178: 1665-1673).

[0007] Recently, it has been reported that PIM family of kinases interact with Socs-1 protein, a potent inhibitor of JAK activation thereby playing a major role in signaling down stream of cytokine receptors. The phosphorylation of Socs-1 by PIM family of kinases prolongs the half-life of Socs-1 protein, thus potentiating the inhibitory effect of Socs-1 on JAK-STAT activation (Chen XP, Losman JA, Cowan S, Donahue E, Fay S, Vuong BQ, Nawijn MC, Capece D, Cohan VL, Rothman P. (2002) PIM serine/threonine kinases regulate the stability of Socs-1 protein. *Proc. Natl. Acad. Sci. USA* 99:2175-2180.). PIM-1 is expressed during G1/S phase of the cell cycle suggesting that it is involved in cell cycle regulation (Liang H, Hittelman W, Nagarajan L., Ubiquitous expression and cell cycle regulation of the protein kinase PIM-1. (1996) *Arch Biochem Biophys.* 330:259-265).). PIM-1 kinase activity and the protein level is increased in CD 40 mediated B cell signaling and this increase in PIM-1 level is mediated through the activation of NF-kB (Zhu et al. 2002. *supra*). PIM-1 can physically interact with NFATc transcription factors enhancing NFATc dependant transactivation and IL2 production in Jurkat cells (Rainio EM, Sandholm J, Koskinen PJ. (2002) Cutting edge: Transcriptional activity of NFATc1 is enhanced by the PIM-1 kinase. *J. Immunol.* 168:1524-1527). This indicates a novel phosphorylation dependant regulatory mechanism targeting NFATc1 through which PIM-1 acts as down

stream effector of ras to facilitate IL2 dependant proliferation and survival of lymphoid cells (*Id.*).

[0008] PIM-1 is shown to interact with many other targets. Phosphorylation of Cdc25A phosphatase, a direct transcriptional target of c-myc, increase its phosphatase activity both *in-vivo* and *in-vitro* indicating that Cdc25A link PIM-1 and c-myc in cell transformation and apoptosis (Mochizuki T, Kitanaka C, Noguchi K, Muramatsu T, Asai A, and Kuchino Y. (1999) Physical and functional interactions between PIM-1 kinase and Cdc25A phosphatase. Implications for the PIM-1-mediated activation of the c-Myc signaling pathway; *J. Biol. Chem.* 274:18659-18666). PIM-1 also phosphorylate PTP-U2S, a tyrosine phosphatase associated with differentiation and apoptosis in myeloid cells, decreasing its phosphatase activity and hence preventing premature onset of apoptosis following PMA-induced differentiation (Wang et al. (2001) Pim-1 negatively regulates the activity of PTP-U2S phosphatase and influences terminal differentiation and apoptosis of monoblastoid leukemia cells. *Arch. Biochem. Biophys.* 390:9-18). The phosphorylation of p100, a co-activator of c-myb (Weston, 1999, Reassessing the role of C-MYB in tumorigenesis. *Oncogene* 18:3034-3038), by PIM-1 is involved in Ras-dependent regulation of transcription (Leverson JD, Koskinen PJ, Orrico FC, Rainio EM, Jalkanen KJ, Dash AB, Eisenman RN, and Ness SA. (1998) PIM-1 kinase and p100 cooperate to enhance c-Myb activity. *Mol. Cell.* 2: 417-425). The phosphorylation of another PIM-1 target, heterochromatin protein 1(HP1) has been shown to be involved in transcription repression (Koike N, Maita H, Taira T, Ariga H, Iguchi-Ariga SM. (2000) Identification of heterochromatin protein 1 (HP1) as a phosphorylation target by PIM-1 kinase and the effect of phosphorylation on the transcriptional repression function of HP-1 (1). *FEBS Lett.* 467: 17-21).

[0009] The information provided above is intended solely to assist the understanding of the reader. None of the information provided or references cited is admitted to be prior art to the present invention.

SUMMARY OF THE INVENTION

[0010] The present invention concerns molecular scaffolds that can be used to identify and develop ligands active on one or more kinases, for example, the PIM kinases, (*e.g.*, PIM-1, PIM-2, and PIM-3). Compounds representing the present molecular scaffolds have

been co-crystallized with PIM-1, and the co-crystal structures have been determined to confirm the orientation of the compound within the binding site. In addition, such compounds also bind to other kinases, such that the scaffolds can be used for ligand development for other kinases also. In the description herein, PIM-1 and the use of molecular scaffolds and ligands with PIM-1 are described as examples, but the invention is not limited to PIM-1.

[0011] In a first aspect, the invention provides a kinase scaffold library comprising at least one set of compounds of a chemical structure selected from the group consisting of Formula I, II, III, IV, V, VI, and VII as described herein, Formula I, II, and III as described in U.S. Appl. 10/664,421 and corresponding PCT/US03/29415, and Formula I as described in U.S. Appl. 10/789,818 and corresponding PCT/US2004/005904, all of which are incorporated herein by reference in their entireties. (Unless specifically indicated to the contrary, reference to any of Formulas I-VII means the Formulas I-VII described with a generic structure herein.). In certain embodiments, the scaffold library contains at least one set of compounds having chemical structures of Formula I, II, III, IV, V, VI, or VII.

[0012] Libraries with large numbers of compounds can be highly useful. In particular embodiments, a library includes at least 50, 100, 200, 300, 400, 500, 600, 800, 1000 1400, or even more different compounds of the particular chemical structure; a library can include a plurality of such sets of compounds of different chemical structures selected from the indicated Formulas; a plurality of sets of compounds of different chemical structure can include any combination of the specified chemical structures, e.g., Formulas I and II, Formulas I and III, Formulas II and III, Formulas I, II, and III (including each individual combination of the 11 Formulas listed above, taken 2, 3, 4, 5,6, 7, 8, 9, 10, or 11 at a time); a plurality of sets is 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11, or more such sets; a majority of compounds in a set or sets have been demonstrated to bind to one or more kinases; one or more kinases are selected from the kinases including PIM-1, Pyk2, c-Abl, Her2, cMet, VEGFR, EGFR, cKit, Pkcβ, p38, Cdk2, Akt, Gsk3β, or other kinase listed in Table 5; the kinase domain of the kinase has at least 30%, 35%, 40% or more sequence identity to PIM-1 kinase domain.

[0013] As used herein in connection with the present compounds, the term "scaffold library" refers to a defined set of compounds in a format suitable for testing as biochemical or biological activity modulators. For example, such compounds can be in solution or dry

in wells of a plate such as a microtiter plate (or a plurality of such plates). Such a library is distinguished from conventional compound libraries and commercially available compound libraries by being selected such that at least 50, 60, 70, 80, 90, 95, 98, or 100% of the compounds in the library are derivatives of the chemical structures that have been described herein as kinase binding compounds or molecular scaffolds. Such libraries can also include compounds that are derivatives of other kinase binding compounds.

[0014] Because initial ligand identification can be carried out by fitting electronic representations of compounds in binding sites of target molecules, in another aspect the invention provides a system for fitting compounds in binding sites of one or more protein kinases. Such a system includes an electronic kinase scaffold library that includes at least one set of electronic representations of compounds of a chemical structure selected from the group consisting of Formula I, II, III, IV, V, VI, and VII as described herein, Formula I, II, and III as described in U.S. Appl. 10/664,421 and corresponding PCT/US03/29415, and Formula I as described in U.S. Appl. 10/789,818 and corresponding PCT/US2004/005904, where the kinase scaffold library is embedded in a computer memory device, the electronic representations of the compounds can be selectively retrieved and functionally connected with computer software adapted to fit electronic representations of compounds in an electronic representation of a binding site of a kinase. The system can also include at least one electronic representation of a kinase binding site (e.g., an electronic representation of a crystal structure of a kinase, kinase domain, or kinase binding site) embedded in computer memory such that the electronic representation of a kinase binding site can be functionally connected with the computer software. The system can include one or more electronic representations of binding sites of kinases selected from PIM-1, Pyk2, c-Abl, Her2, cMet, VEGFR, EGFR, cKit, Pkcβ, p38, Cdk2, Akt, Gsk3β, or another kinase from Table 5., e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more such kinases.

[0015] In a related aspect, the invention provides a method for obtaining improved ligands binding to a kinase (*e.g.*, PIM-1, Pyk2, c-Abl, Her2, cMet, VEGFR, EGFR, cKit, Pkcβ, p38, Cdk2, Akt, Gsk3β, or other kinase from Table 5), where the method involves determining whether a derivative of a compound of any of Formulas I, II, III, IV, V, VI, or VII that binds to the kinase, binds to the kinase with greater affinity or greater specificity or both than the parent binding compound. Binding with greater affinity or greater specificity or both than the parent compound indicates that the derivative is an improved ligand. This process can also be carried out in successive rounds of selection and derivatization and/or with multiple

parent compounds to provide a compound or compounds with improved ligand characteristics. Likewise, the derivative compounds can be tested and selected to give high selectivity for the kinase, or to give cross-reactivity to a particular set of kinase targets.

[0016] In the context of the present invention, the terms "kinase" and "protein kinase" refers to an enzyme that phosphorylates other proteins. These enzymes are often grouped according to the amino acid that is phosphorylated, into tyrosine kinases, serine/threonine kinases, and histidine kinases.

[0017] The term "PIM kinase" or "PIM family kinase" means a protein kinase with greater than 45% amino acid sequence identity to PIM-1 from the same species, and includes PIM-1, PIM-2, and PIM-3. Unless clearly indicated to the contrary, use of the term "PIM kinase" constitutes a reference to any of the group of PIM kinases, specifically including individual reference to each of PIM-1, PIM-2, and PIM-3.

[0018] As used herein, the terms "ligand" and "modulator" refer to a compound that modulates the activity of a target biomolecule, *e.g.*, an enzyme such as a kinase. Generally a ligand or modulator will be a small molecule, where "small molecule refers to a compound with a molecular weight of 1500 daltons or less, or preferably 1000 daltons or less, 800 daltons or less, or 600 daltons or less. Thus, an "improved ligand" is one that possesses better pharmacological and/or pharmacokinetic properties than a reference compound, where "better" can be defined by a person for a particular biological system or therapeutic use.

[0019] In the context of binding compounds, molecular scaffolds, and ligands, the term "derivative" or "derivative compound" refers to a compound having a chemical structure that contains a common core chemical structure as a parent or reference compound, but differs by having at least one structural difference, *e.g.*, by having one or more substituents added and/or removed and/or substituted, and/or by having one or more atoms substituted with different atoms. Unless clearly indicated to the contrary, the term "derivative" does not mean that the derivative is synthesized using the parent compound as a starting material or as an intermediate, although in some cases, the derivative may be synthesized from the parent.

[0020] Thus, the term "parent compound" refers to a reference compound for another compound, having structural features continued in the derivative compound. Often but not always, a parent compound has a simple chemical structure than the derivative.

[0021] By "chemical structure" or "chemical substructure" is meant any definable atom or group of atoms that constitute a part of a molecule. Normally, chemical substructures of a scaffold or ligand can have a role in binding of the scaffold or ligand to a target molecule, or can influence the three-dimensional shape, electrostatic charge, and/or conformational properties of the scaffold or ligand.

[0022] The term "binds" in connection with the interaction between a target and a potential binding compound indicates that the potential binding compound associates with the target to a statistically significant degree as compared to association with proteins generally (*i.e.*, non-specific binding). Thus, the term "binding compound" refers to a compound that has a statistically significant association with a target molecule. Preferably a binding compound interacts with a specified target with a dissociation constant (k_d) of 1 mM or less. A binding compound can bind with "low affinity", "very low affinity", "extremely low affinity", "moderate affinity", "moderately high affinity", or "high affinity" as described herein.

[0023] In the context of compounds binding to a target, the term "greater affinity" indicates that the compound binds more tightly than a reference compound, or than the same compound in a reference condition, *i.e.*, with a lower dissociation constant. In particular embodiments, the greater affinity is at least 2, 3, 4, 5, 8, 10, 50, 100, 200, 400, 500, 1000, or 10,000-fold greater affinity.

[0024] Also in the context of compounds binding to a biomolecular target, the term "greater specificity" indicates that a compound binds to a specified target to a greater extent than to another biomolecule or biomolecules that may be present under relevant binding conditions, where binding to such other biomolecules produces a different biological activity than binding to the specified target. Typically, the specificity is with reference to a limited set of other biomolecules, *e.g.*, other kinases or even other type of enzymes. In particular embodiments, the greater specificity is at least 2, 3, 4, 5, 8, 10, 50, 100, 200, 400, 500, or 1000-fold greater specificity.

[0025] As used in connection with binding of a compound with a particular kinase, the term "interact" indicates that the distance from a bound compound to a particular amino acid residue will be 5.0 angstroms or less, or 6 angstroms or less with one water molecule coordinated between the compound and the residue, or 9 angstroms or less with two water molecules coordinated between the compound and the residue. In particular embodiments, the distance from the compound to the particular amino acid residue is 4.5 angstroms or less, 4.0 angstroms or less, or 3.5 angstroms or less. Such distances can be determined, for example, using co-crystallography, or estimated using computer fitting of a compound in the kinase active site.

[0026] Reference to particular amino acid residues in PIM-1 polypeptide residue number is defined by the numbering provided in Meeker, T. C., Nagarajan, L., ar-Rushdi, A., Rovera, G., Huebner, K., Corce, C. M.; (1987) Characterization of the human PIM-1 gene: a putative proto-oncogene coding for a tissue specific member of the protein kinase family. *Oncogene Res.* 1:87-101, in accordance with the sequence provided in SEQ ID NO: 1. PIM-2 is as described in Baytel et al. (1998) The human Pim-2 proto-oncogene and its testicular expression, *Biochim. Biophys. Acta* 1442,274-285. PIM-3 from rat is described in Feldman, et al. (1998) KID-1, a protein kinase induced by depolarization in brain, *J. Biol. Chem.* 273, 16535-16543; and Kinietzko et al. (1999) Pim kinase expression is induced by LTP stimulation and required for the consolidation of enduring LTP, *EMBO J.* 18, 3359-3369. (KID-1 is the same as PIM-3.) Human PIM-3 nucleic acid and amino acid sequences are provided herein.

[0027] In a related aspect, the invention provides a method for developing ligands specific for a kinase, such as a PIM kinase, *e.g.*, PIM-1, where the method involves determining whether a derivative of a compound that binds to a plurality of kinases has greater specificity for the particular kinase than the parent compound.

[0028] As used herein in connection with binding compounds or ligands, the term "specific for a kinase", "specific for PIM-1" and terms of like import mean that a particular compound binds to the particular kinase to a statistically greater extent than to other kinases that may be present in a particular organism. Also, where biological activity other than binding is indicated, the term "specific for a kinase" indicates that a particular compound has greater biological activity associated with binding to the particular kinase than to other kinases. Preferably, the specificity is also with respect to other biomolecules (not limited to

kinases) that may be present from an organism. A particular compound may also be selected that is specific for kinase sub-group (e.g., tyrosine kinases, serine/threonine kinases, histidine kinases), indicating that it binds to and/or has a greater biological activity associated with binding to a plurality of kinases in that sub-group than to other kinases.

[0029] In another aspect, the invention concerns a method for developing ligands binding to a particular kinase, *e.g.*, PIM-1, where the method includes determining the orientation of at least one molecular scaffold of Formula I, II, III, IV, V, VI, or VII in co-crystals with the kinase; identifying chemical structures of one or more of the molecular scaffolds, that, when modified, alter the binding affinity or binding specificity or both between the molecular scaffold and the kinase; and synthesizing a ligand in which one or more of the chemical structures of the molecular scaffold is modified to provide a ligand that binds to the kinase with altered binding affinity or binding specificity or both. Due to the significant of sequence identity between various kinases, e.g., PIM-1 and the other PIM kinases, PIM-1 can also be used as a surrogate or in a homology model for orientation determination and to allow identification of chemical structures that can be modified to provide improved ligands.

[0030] By "molecular scaffold" is meant a core molecule to which one or more additional chemical moieties can be covalently attached, modified, or eliminated to form a plurality of molecules with common structural elements. The moieties can include, but are not limited to, a halogen atom, a hydroxyl group, a methyl group, a nitro group, a carboxyl group, or any other type of molecular group including, but not limited to, those recited in this application. Molecular scaffolds bind to at least one target molecule, and the target molecule can preferably be a protein or enzyme. Preferred characteristics of a scaffold can include binding at a target molecule binding site such that one or more substituents on the scaffold are situated in binding pockets in the target molecule binding site; having chemically tractable structures that can be chemically modified, particularly by synthetic reactions, so that a combinatorial library can be easily constructed; having chemical positions where moieties can be attached that do not interfere with binding of the scaffold to a protein binding site, such that the scaffold or library members can be modified to achieve additional desirable characteristics, e.g., enabling the ligand to be actively transported into cells and/or to specific organs, or enabling the ligand to be attached to a chromatography column for additional analysis.

[0031] By "binding site" is meant an area of a target molecule to which a ligand can bind non-covalently. Binding sites embody particular shapes and often contain multiple binding pockets present within the binding site. The particular shapes are often conserved within a class of molecules, such as a molecular family. Binding sites within a class also can contain conserved structures such as, for example, chemical moieties, the presence of a binding pocket, and/or an electrostatic charge at the binding site or some portion of the binding site, all of which can influence the shape of the binding site.

[0032] By "binding pocket" is meant a specific volume within a binding site. A binding pocket can often be a particular shape, indentation, or cavity in the binding site. Binding pockets can contain particular chemical groups or structures that are important in the non-covalent binding of another molecule such as, for example, groups that contribute to ionic, hydrogen bonding, or van der Waals interactions between the molecules.

[0033] By "orientation", in reference to a binding compound bound to a target molecule is meant the spatial relationship of the binding compound and at least some of its constituent atoms to the binding pocket and/or atoms of the target molecule at least partially defining the binding pocket.

[0034] By "co-crystals" is meant a complex of the compound, molecular scaffold, or ligand bound non-covalently to the target molecule and present in a crystal form appropriate for analysis by X-ray or protein crystallography. In preferred embodiments the target molecule-ligand complex can be a protein-ligand complex.

[0035] The phrase "alter the binding affinity or binding specificity" refers to changing the binding constant of a first compound for another, or changing the level of binding of a first compound for a second compound as compared to the level of binding of the first compound for third compounds, respectively. For example, the binding specificity of a compound for a particular protein is increased if the relative level of binding to that particular protein is increased as compared to binding of the compound to unrelated proteins.

[0036] As used herein in connection with test compounds, binding compounds, and modulators (ligands), the term "synthesizing" and like terms means chemical synthesis from one or more precursor materials.

[0037] The phrase "chemical structure of the molecular scaffold is modified" means that a derivative molecule has a chemical structure that differs from that of the molecular scaffold but still contains common core chemical structural features. The phrase does not necessarily mean that the molecular scaffold is used as a precursor in the synthesis of the derivative.

[0038] By "assaying" is meant the creation of experimental conditions and the gathering of data regarding a particular result of the experimental conditions. For example, enzymes can be assayed based on their ability to act upon a detectable substrate. A compound or ligand can be assayed based on its ability to bind to a particular target molecule or molecules.

[0039] Certain compounds have been identified as molecular scaffolds and binding compounds for protein kinases, as exemplified by PIM-1. Thus, in another aspect, the invention provides a method for identifying a ligand binding to specific kinase, that includes determining whether a derivative compound that includes a core structure selected from the group consisting of the core structures of Formula I, Formula II, Formula III, Formula IV, Formula V, Formula VI, and Formula VII, as described herein binds to the kinase with altered binding affinity or specificity or both as compared to a parent compound.

[0040] In reference to compounds of any of Formula I, II, III, IV, V, VI, and VII, the term "core structure" refers to the structures shown diagramatically as part of the description of compounds of each of Formulas I-VII, but excluding non-ring variable substituents. More generally, the term "core structure" refers to a characteristic chemical structure common to a set of compounds, especially a chemical structure that carries variable substituents in the compound set.

[0041] By a "set" of compounds is meant a collection of compounds. The compounds may or may not be structurally related.

[0042] The invention further concerns co-crystals of a particular kinase and a kinase binding compound of Formula I, II, III, IV, V, VI, or VII. Advantageously, such co-crystals are of sufficient size and quality to allow structural determination to at least 3 Angstroms, 2.5 Angstroms, or 2.0 Angstroms. The co-crystals can, for example, be in a crystallography plate, be mounted for X-ray crystallography and/or in an X-ray beam. Such co-crystals are beneficial, for example, for obtaining structural information concerning interaction between the kinase and kinase binding compounds.

[0043] Kinase binding compounds can include compounds that interact with at least one of PIM-1 residues 49, 52, 65, 67, 121, 128, and 186, or any 2, 3, 4, 5, 6, or 7 of those residues. Exemplary compounds that bind to PIM-1 include compounds of any of Formulas I-VII.

[0044] Likewise, in additional aspects, methods for obtaining PIM-1 co-crystals with compounds of Formula I, II, III, IV, V, VI, and VII are provided. The method involves subjecting PIM-1 protein at 5-20 mg/ml to crystallization conditions substantially equivalent to Hampton Screen 1 conditions 2, 7, 14, 17, 23, 25, 29, 36, 44, or 49, in the presence of binding compound for a time sufficient for crystal development. The binding compound may be added at various concentrations depending on the nature of the compound, *e.g.*, final concentration of 0.5 to 1.0 mM. In many cases, the binding compound will be in an organic solvent such as dimethyl sulfoxide solution. Exemplary co-crystallization conditions include 0.4-0.9 M sodium acetate trihydrate pH 6.5, 0.1 M imidazole; or 0.2-0.7 M. sodium potassium tartrate, 00.1 M MES buffer pH 6.5.

[0045] In another aspect, provision of compounds active on a variety of different kinases (e.g., PIM-1) also provides a method for modulating kinase activity by contacting the kinase with a compound of any of Formulas I, II, III, IV, V, VI, and VII that binds to the kinase. The compound is preferably provided at a level sufficient to modulate the activity of PIM-1 by at least 10%, more preferably at least 20%, 30%, 40%, or 50%. In many embodiments, the compound will be at a concentration of about 1 μM, 100 μM, or 1 mM, or in a range of 1-100 nM, 100-500 nM, 500-1000 nM, 1-100 μM, 100-500 μM, or 500-1000 μM. The compound can be one that interacts with one more of PIM-1 residues 49, 52, 65, 67, 121, 128, and 186.

[0046] As used herein, the term "modulating" or "modulate" refers to an effect of altering a biological activity, especially a biological activity associated with a particular biomolecule such as PIM-1. For example, an agonist or antagonist of a particular biomolecule modulates the activity of that biomolecule, *e.g.*, an enzyme.

[0047] The term "PIM-1 activity" refers to a biochemical activity of PIM-1, particularly including kinase activity.

[0048] In the context of the use, testing, or screening of compounds that are or may be modulators, the term "contacting" means that the compound(s) are caused to be in sufficient

proximity to a particular molecule, complex, cell, tissue, organism, or other specified material that potential binding interactions and/or chemical reaction (e.g., modulating enzymatic action) between the compound and other specified material can occur.

[0049] In a related aspect, the invention provides a method for treating a patient suffering from or at risk of a kinase-mediated disease or condition or a disease or condition in which kinase modulation provides a therapeutic benefit, such as a disease or condition characterized by abnormal kinase activity, *e.g.*, PIM-1 activity, where the method involves administering to the patient a compound of Formula I, II, III, IV, V, VI, or VII. The compound can, for example, be one that interacts with one or more of PIM-1 residues 49, 52, 65, 67, 121, 128, and 186.

[0050] In certain embodiments, the disease or condition is a proliferative disease or neoplasia, such as benign or malignant tumors, psoriasis, leukemias (such as myeloblastic leukemia), lymphoma, prostate cancer, liver cancer, breast cancer, sarcoma, neuroblastoma, Wilm's tumor, bladder cancer, thyroid cancer, neoplasias of the epithelial origin such as mammacarcinoma, or a chronic inflammatory disease or condition, resulting, for example, from a persistent infection (*e.g.*, tuberculosis, syphilis, fungal infection), from prolonged exposure to endogenous (*e.g.*, elevated plasma lipids) or exogenous (*e.g.*, silica, asbestos, cigarette tar, surgical sutures) toxins, and from autoimmune reactions (*e.g.*, rheumatoid arthritis, systemic lupus erythrymatosis, multiple sclerosis, psoriasis). Thus, chronic inflammatory diseases include many common medical conditions, such as rheumatoid arthritis, restenosis, psoriasis, multiple sclerosis, surgical adhesions, tuberculosis, and chronic inflammatory lung and airway diseases, such as asthma pheumoconiosis, chronic obstructive pulmonary disease, nasal polyps, and pulmonary fibrosis. Kinase modulators may also be useful in inhibiting development of hematomous plaque and restinosis, in controlling restinosis, as anti-metastatic agents, in treating diabetic complications, as immunosuppressants, and in control of angiogenesis to the extent the kinase is involved in a particular disease or condition.

[0051] In certain embodiments, the disease or condition is one listed in Table 5; the disease or condition is one listed in Table 5. In certain embodiments, the therapeutic or prophylactic effect of the compound is due to modulation of a kinase from Table 5; the therapeutic or prophylactic effect of the compound is due to modulation of a kinase from Table 5 and the disease or condition is one that corresponds thereto in Table 5.

[0052] As used herein, the term "kinase-mediated" disease or condition and like terms refer to a disease or condition in which the biological function of a kinase affects the development and/or course of the disease or condition, and/or in which modulation of a kinase alters the development, course, and/or symptoms of the disease or condition. Similarly, the phrase "kinase modulation provides a therapeutic benefit" indicates that modulation of the level of activity of a kinase in a subject indicates that such modulation reduces the severity and/or duration of the disease, reduces the likelihood or delays the onset of the disease or condition, and/or causes an improvement in one or more symptoms of the disease or condtion. Parallel terms apply to each of the kinases indicated herein.

[0053] Because molecular scaffolds are described, a large number of different kinases can be used in connection with the described scaffolds and compounds. A list of such kinases (not intended to be comprehensive) is provided in Table 6. Exemplary kinases and a major indication for which modulation of the kinase is useful include the following:

Table 6

Tyrosine Kinases	Indication
c-abl	CML (chronic myeloid leukemia)
her2	breast cancer
c-met	cancer
VEGFR	angiogenesis
c-kit	cancer
Serine Kinases	
pkcβ	retinopathy
p38	inflammation/RA
cdk2	cancer
akt	cancer/apoptosis
gsk3β	diabetes

[0054] As crystals of PIM-1 and other kinases have been developed and analyzed, another aspect concerns an electronic representation of the kinase with an electronic representation of a kinase binding compound or a test compound in the binding site, where the compound has a chemical structure of Formula I, Formula II, Formula III, Formula IV, Formula V, Formula VI, or Formula VII.

[0055] Likewise, in a related aspect, the invention concerns an electronic representation of a portion of a kinase binding site, *e.g.*, PIM-1, (which can be an active site), which includes a representation of Formula I, II, III, IV, V, VI, or VII. A binding site can be represented in various ways, e.g., as representations of atomic coordinates of residues around the binding

site and/or as a binding site surface contour, and can include representations of the binding character of particular residues at the binding site, e.g., conserved residues.

[0056] In another aspect, the invention provides a method for identifying potential kinase, *e.g.*, PIM-1 or other kinase listed herein, binding compounds by fitting at least one electronic representation of a compound of Formula I, II, III, IV, V, VI, or VII in an electronic representation of a kinase, *e.g.*, PIM-1, binding site. The representation of the binding site may be part of an electronic representation of a larger portion(s) (e.g., kinase domain) or all of a PIM molecule or may be a representation of only the binding site. The electronic representation may be as described above or otherwise described herein.

[0057] In particular embodiments, the method involves fitting a computer representation of a compound from a computer database with a computer representation of the active site of a kinase, *e.g.*, PIM-1; and involves removing a computer representation of a compound complexed with the kinase molecule and identifying compounds that best fit the active site based on favorable geometric fit and energetically favorable complementary interactions as potential binding compounds.

[0058] In other embodiments, the method involves modifying a computer representation of a compound complexed with a kinase molecule, *e.g.*, PIM-1, by the deletion or addition or both of one or more chemical groups; fitting a computer representation of a compound from a computer database with a computer representation of the active site of the kinase molecule; and identifying compounds that best fit the active site based on favorable geometric fit and energetically favorable complementary interactions as potential binding compounds.

[0059] In still other embodiments, the method involves removing a computer representation of a compound complexed with a kinase, such as PIM-1, and searching a database for compounds having structural similarity to the complexed compound using a compound searching computer program or replacing portions of the complexed compound with similar chemical structures using a compound construction computer program.

[0060] Fitting a compound can include determining whether a compound will interact with one or more of PIM-1 residues 49, 52, 65, 67, 121, 128, and 186.

[0061] In another aspect, the invention concerns a method for attaching a kinase binding compound of Formula I, II, III, IV, V, VI, or VII (*e.g.*, a PIM-1 binding compound) to an

attachment component, as well as a method for identifying attachment sites on such kinase binding compound. The method involves identifying energetically allowed sites for attachment of an attachment component; and attaching the compound or a derivative thereof to the attachment component at the energetically allowed site. In certain embodiments, the kinase is a kinase listed herein; the kinase has at least 25% amino acid sequence identity or 30% sequence similarity to wild type PIM-1, and/or includes conserved residues matching at least one of PIM-1 residues 49, 52, 65, 67, 121, 128, and 186 (i.e., matching any one, any 2, 3, 4, 5, 6, or 7 of those residues).

[0062] Attachment components can include, for example, linkers (including traceless linkers) for attachment to a solid phase or to another molecule or other moiety. Such attachment can be formed by synthesizing the compound or derivative on the linker attached to a solid phase medium e.g., in a combinatorial synthesis in a plurality of compound. Likewise, the attachment to a solid phase medium can provide an affinity medium (e.g., for affinity chromatography).

[0063] The attachment component can also include a label, which can be a directly detectable label such as a fluorophore, or an indirectly detectable such as a member of a specific binding pair, e.g., biotin.

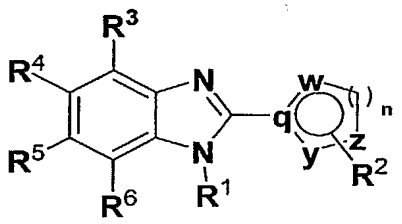
[0064] The ability to identify energetically allowed sites on a kinase binding compound of Formula I, II, III, IV, V, VI, and VII, e.g., a PIM-1 binding compound also, in a related aspect, provides modified binding compounds that have linkers attached, for example, compounds of Formula I-VII, preferably at an energetically allowed site for binding of the modified compound to a kinase. The linker can be attached to an attachment component as described above.

[0065] Still another aspect of the invention concerns a method for developing a ligand for a kinase that includes conserved residues matching any one, 2, 3, 4, 5, 6, or 7 of PIM-1 residues 49, 52, 65, 67, 121, 128, and 186, by determining whether a compound of Formula I, II, III, IV, V, VI, or VII binds to the kinase. The method can also include determining whether the compound modulates the activity of the kinase. In certain embodiments, the kinase has at least 25% sequence identity or at least 30% sequence similarity to PIM-1, or PIM-1 kinase domain.

[0066] In particular embodiments, the determining includes computer fitting the compound in a binding site of the kinase and/or the method includes forming a co-crystal of the kinase and the compound. Such co-crystals can be used for determining the binding orientation of the compound with the kinase and/or provide structural information on the kinase, e.g., on the binding site and interacting amino acid residues. Such binding orientation and/or other structural information can be accomplished using X-ray crystallography.

[0067] The invention also provides compounds of Formula I, II, III, IV, V, VI, and VII that bind to and/or modulate (*e.g.*, inhibit) kinase activity for a particular kinase, *e.g.*, PIM-1. Accordingly, in aspects and embodiments involving kinase binding compounds, molecular scaffolds, and ligands or modulators, the compound is a weak binding compound; a moderate binding compound; a strong binding compound; a compound that binds at a level identified herein; the compound interacts with one or more of PIM-1 residues 49, 52, 65, 67, 121, 128, and 186; the compound is a small molecule; the compound binds to a plurality of different kinases (*e.g.*, at least 5, 10, 15, 20 different kinases). In particular embodiments, the invention concerns compounds of Formula I, Formula II, Formula III, Formula IV, Formula V, Formula VI, and Formula VII as described below.

[0068] In certain embodiments, the invention concerns compounds of Formula I:



Formula I

where, with reference to Formula I:

[0069] R^1 is hydrogen, optionally substituted lower alkyl, optionally substituted lower alkenyl, optionally substituted lower alkynyl, optionally substituted cycloalkyl, optionally substituted heterocyclyoalkyl, optionally substituted aryl, optionally substituted aralkyl, optionally substituted heteroaryl, optionally substituted heteroaralkyl, $-C(X)R^{20}$, $-C(X)NR^{16}R^{17}$, $-S(O)_2R^{21}$, or $-S(O)_2NR^{16}R^{17}$.

[0070] R^2 is hydrogen, halo, optionally substituted lower alkyl (e.g., trifluoromethyl), optionally substituted lower alkenyl, optionally substituted lower alkynyl, optionally substituted cycloalkyl, optionally substituted heterocycloalkyl, optionally substituted aryl, optionally substituted aralkyl, optionally substituted heteroaryl, optionally substituted heteroaralkyl, $-C(X)NR^{16}R^{17}$, $-NR^{22}R^{23}$, or $-S(O)_2R^{21}$, or $-S(O)_2NR^{16}R^{17}$, with the proviso that if R^2 is attached to nitrogen, it is not $-NR^{22}R^{23}$.

[0071] R^3, R^4, R^5 and R^6 are independently hydrogen, halo, hydroxy, optionally substituted alkoxyl, optionally substituted thioalkoxy, optionally substituted amine, optionally substituted lower alkyl (e.g., trifluoromethyl), optionally substituted lower alkenyl, optionally substituted lower alkynyl, optionally substituted cycloalkyl, optionally substituted heterocycloalkyl, optionally substituted aryl, optionally substituted aralkyl, optionally substituted heteroaryl, or optionally substituted heteroaralkyl, $-C(X)R^{20}$, $C(X)NR^{16}R^{17}$, $S(O)_2NR^{16}R^{17}$, $-NR^{22}R^{23}$, or $-S(O)_2R^{21}$;

[0072] R^{16} and R^{17} are independently hydrogen, optionally substituted lower alkyl, optionally substituted lower alkenyl, optionally substituted lower alkynyl, optionally substituted cycloalkyl, optionally substituted heterocycloalkyl, optionally substituted aryl, optionally substituted aralkyl, optionally substituted heteroaryl, optionally substituted heteroaralkyl, or R^{16} and R^{17} together form a 5-7 membered carbocyclic or heterocyclic ring;

[0073] R^{20} is hydroxyl, optionally substituted lower alkoxy, optionally substituted amine, optionally substituted lower alkyl, optionally substituted lower alkenyl, optionally substituted lower alkynyl, optionally substituted cycloalkyl, optionally substituted heterocycloalkyl, optionally substituted aryl, optionally substituted aralkyl, optionally substituted heteroaryl, or optionally substituted heteroaralkyl;

[0074] R^{21} is optionally substituted lower alkoxy, optionally substituted lower alkyl, optionally substituted lower alkenyl, optionally substituted lower alkynyl, optionally substituted cycloalkyl, optionally substituted heterocycloalkyl, optionally substituted aryl, optionally substituted aralkyl, optionally substituted heteroaryl, or optionally substituted heteroaralkyl;

[0075] R^{22} and R^{23} are independently hydrogen, optionally substituted lower alkyl, optionally substituted lower alkenyl, optionally substituted lower alkynyl, optionally substituted cycloalkyl, optionally substituted heterocycloalkyl, optionally substituted aryl, optionally substituted aralkyl, optionally substituted heteroaryl, optionally substituted heteroaralkyl, $-C(X)R^{20}$, $C(X)NR^{16}R^{17}$, or $-S(O)_2R^{21}$;

[0076] w, y, and z are independently O, S, N, or CR^2;

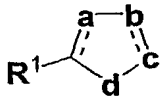
[0077] q is N or C;

[0078] X = O or S; and

[0079] n = 1 or 2.

[0080] In particular embodiments of compounds of Formula I, with reference to Formula I, one or more of R^1, R^2, R^3, R^4, R^5, R^6 is H; any two of R^1, R^2, R^3, R^4, R^5, R^6 are H; any 3 of R^1, R^2, R^3, R^4, R^5, R^6 are H; any 4 of R^1, R^2, R^3, R^4, R^5, R^6 are H; any 5 of R^1, R^2, R^3, R^4, R^5, R^6 are H. Specification of the preceding subgroups is intended to expressly include each possible combination of the specified substituent groups. For example, in particular embodiments, R^3, R^4, R^5, and R^6 are H.

[0081] Likewise, in certain embodiments the invention concerns compounds of Formula II.



Formula II

Where, with reference to Formula II:

[0082] R^1 is hydrogen, halo, hydroxy, optionally substituted alkoxyl, optionally substituted thioalkoxy, optionally substituted amine, optionally substituted lower alkyl (e.g., trifluoromethyl), optionally substituted lower alkenyl, optionally substituted lower alkynyl, optionally substituted cycloalkyl, optionally substituted heterocycloalkyl, optionally substituted aryl, optionally substituted aralkyl, optionally substituted heteroaryl, or

optionally substituted heteroaralkyl, -C(X)R^2, C(X)NR^3R^4, $S(O)_2NR^3R^4$, –NR^3R^4, or -$S(O)_2R^5$;

[0083] a, b, c, and d are independently O, S, NR^3, or CR^{11} with the proviso that two of them are N (and not more than 2) and one (and not more than one) of them is either O or S, and the remaining one is CR^{11};

[0084] R^2 is hydroxyl, optionally substituted lower alkoxy, optionally substituted amine, optionally substituted lower alkyl, optionally substituted lower alkenyl, optionally substituted lower alkynyl, optionally substituted cycloalkyl, optionally substituted heterocycloalkyl, optionally substituted aryl, optionally substituted aralkyl, optionally substituted heteroaryl, or optionally substituted heteroaralkyl;

[0085] R^3 and R^4 are independently hydrogen, optionally substituted lower alkyl, optionally substituted lower alkenyl, optionally substituted lower alkynyl, optionally substituted cycloalkyl, optionally substituted heterocycloalkyl, optionally substituted aryl, optionally substituted aralkyl, optionally substituted heteroaryl, or optionally substituted heteroaralkyl;

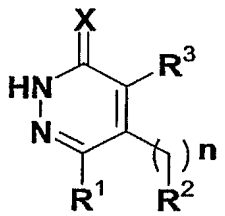
[0086] R^5 is optionally substituted lower alkoxy, optionally substituted amine, optionally substituted lower-alkyl, optionally substituted lower alkenyl, optionally substituted lower alkynyl, optionally substituted cycloalkyl, optionally substituted heterocycloalkyl, optionally substituted aryl, optionally substituted aralkyl, optionally substituted heteroaryl, or optionally substituted heteroaralkyl;

[0087] R^{11} is hydroxy, optionally substituted alkoxyl, optionally substituted thioalkoxy, optionally substituted amine, optionally substituted lower alkyl (e.g., trifluoromethyl), optionally substituted lower alkenyl, optionally substituted lower alkynyl, optionally substituted cycloalkyl, optionally substituted heterocycloalkyl, optionally substituted aryl, optionally substituted aralkyl, optionally substituted heteroaryl, or optionally substituted heteroaralkyl, -C(X)R^2, C(X)NR^3R^4, $S(O)_2NR^3R^4$, –NR^3R^4, or -$S(O)_2R^5$;

[0088] In particular embodiments of compounds of Formula II, with reference to Formula II, a & b, a & c, a& d, b & c, b & d, or c & d are N. In embodiments where a & b are N, c is S or O, or d is S or O; where a & c are N, b is S or O, or d is S or O; where a & d are N, b is S or O, or c is S or O; where b & c are N, a is S or O, or d is S or O; where b & d are N, a is S or O, or c is S or O, where c & d are N, a is S or O, or b is S or O. In particular

embodiments of each of the preceding designations of a, b, c, and d, R^{11} is optionally substituted hydrogen or halo; R^{11} is trifluoromethyl, hydroxy, optionally substituted alkoxyl, optionally substituted thioalkoxy; R^{11} is optionally substituted amine; R^{11} is optionally substituted lower alkyl, optionally substituted lower alkenyl, optionally substituted lower alkynyl; R^{11} is optionally substituted cycloalkyl, optionally substituted heterocycloalkyl, optionally substituted aryl, optionally substituted aralkyl, optionally substituted heteroaryl, or optionally substituted heteroaralkyl; R^{11} is $-C(X)R^2$, $C(X)NR^3R^4$, $S(O)_2NR^3R^4$, $-NR^3R^4$, or $-S(O)_2R^5$.

[0089] In other embodiments, the invention concerns compounds of Formula III.



Formula III

where, with reference to Formula III:

[0090] R^1, R^2, and R^3 are independently hydrogen, halo, hydroxy, optionally substituted alkoxyl, optionally substituted thioalkoxy, optionally substituted amine, optionally substituted lower alkyl (e.g., trifluoromethyl), optionally substituted lower alkenyl, optionally substituted lower alkynyl, optionally substituted cycloalkyl, optionally substituted heterocycloalkyl, optionally substituted aryl, optionally substituted aralkyl, optionally substituted heteroaryl, or optionally substituted heteroaralkyl, $-C(X)R^4$, $-C(X)NR^5R^6$, $-S(O)_2NR^5R^6$, $-NR^5R^6$, or $-S(O)_2R^7$;

[0091] R^4 is hydroxyl, optionally substituted lower alkoxy, optionally substituted amine, optionally substituted lower alkyl, optionally substituted lower alkenyl, optionally substituted lower alkynyl, optionally substituted cycloalkyl, optionally substituted heterocycloalkyl, optionally substituted aryl, optionally substituted aralkyl, optionally substituted heteroaryl, or optionally substituted heteroaralkyl;

[0092] R^5 and R^6 are independently hydrogen, optionally substituted lower alkyl, optionally substituted lower alkenyl, optionally substituted lower alkynyl, optionally substituted cycloalkyl, optionally substituted heterocycloalkyl, optionally substituted aryl,

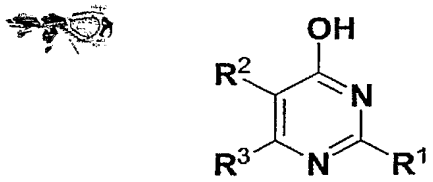
optionally substituted aralkyl, optionally substituted heteroaryl, optionally substituted heteroaralkyl, or R^5 and R^6 together for a 5-7 membered carbocyclic or heterocyclic ring;

[0093] R^7 is optionally substituted lower alkoxy, optionally substituted amine, optionally substituted lower alkyl, optionally substituted lower alkenyl, optionally substituted lower alkynyl, optionally substituted cycloalkyl, optionally substituted heterocycloalkyl, optionally substituted aryl, optionally substituted aralkyl, optionally substituted heteroaryl, or optionally substituted heteroaralkyl;

[0094] X = O or S; and n = 0 or 1.

[0095] In particular embodiments of compounds of Formula III, with reference to Formula III, X is O; X is S. In particular embodiments for each selection of X, R^1 is H; R^2 is H; R^3 is H; R^1 and R^2 are H; R^2 and R^3 are H. In particular embodiments for each selection of X with each selection where one of R^1, R^2, and R^3 is H, the other two of R^1, R^2 and R^3 are independently halo, trifluoromethyl; the other two of R^1, R^2 and R^3 are independently hydroxy, optionally substituted alkoxyl, optionally substituted thioalkoxy; the other two of R^1, R^2 and R^3 are independently optionally substituted amine; the other two of R^1, R^2 and R^3 are independently optionally substituted lower alkyl, optionally substituted lower alkenyl, optionally substituted lower alkynyl, optionally substituted cycloalkyl, optionally substituted heterocycloalkyl, optionally substituted aryl, optionally substituted aralkyl, optionally substituted heteroaryl, or optionally substituted heteroaralkyl; the other two of R^1, R^2 and R^3 are independently $-C(X)R^4$, $-C(X)NR^5R^6$, $-S(O)_2NR^5R^6$, $-NR^5R^6$, or $-S(O)_2R^7$. In particular embodiments, one of R^1, R^2, and R^3 is halo, trifluoromethyl; one of R^1, R^2, and R^3 is hydroxy, optionally substituted alkoxyl, optionally substituted thioalkoxy; one of R^1, R^2, and R^3 is optionally substituted amine; one of R^1, R^2, and R^3 is optionally substituted lower alkyl, optionally substituted lower alkenyl, optionally substituted lower alkynyl, optionally substituted cycloalkyl, optionally substituted heterocycloalkyl, optionally substituted aryl, optionally substituted aralkyl, optionally substituted heteroaryl, or optionally substituted heteroaralkyl one of R^1, R^2, and R^3 is $-C(X)R^4$, $-C(X)NR^5R^6$, $-S(O)_2NR^5R^6$, $-NR^5R^6$, or $-S(O)_2R^7$.

[0096] In other embodiments, the invention concerns compounds of Formula IV.



Formula IV

where, with reference to Formula IV:

[0097] R^1 is optionally substituted lower alkyl, optionally substituted lower alkenyl, optionally substituted lower alkynyl, optionally substituted cycloalkyl, optionally substituted heterocycloalkyl, optionally substituted aryl, optionally substituted aralkyl, optionally substituted heteroaryl, optionally substituted heteroaralkyl, $-NR^{16}R^{17}$, $-OR^{21}$, or $-SR^{21}$;

[0098] R^2 and R^3 are independently hydrogen, optionally substituted lower alkyl, optionally substituted lower alkenyl, optionally substituted lower alkynyl, optionally substituted cycloalkyl, optionally substituted heterocycloalkyl, optionally substituted aryl, optionally substituted aralkyl, optionally substituted heteroaryl, optionally substituted heteroaralkyl, optionally substituted heteroaralkyl, $-C(X)R^{20}$, $-C(X)NR^{16}R^{17}$, $-C(X)R^{20}$, or $-C(X)NR^{16}R^{17}$;

[0099] R^{16} and R^{17} are independently hydrogen, optionally substituted lower alkyl, optionally substituted lower alkenyl, optionally substituted lower alkynyl, optionally substituted cycloalkyl, optionally substituted heterocycloalkyl, optionally substituted aryl, optionally substituted aralkyl, optionally substituted heteroaryl, optionally substituted heteroaralkyl, or R^{16} and R^{17} together form a carbocyclic or heterocyclic ring;

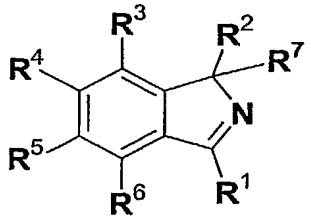
[0100] R^{20} is hydroxyl, optionally substituted lower alkoxy, optionally substituted amine, optionally substituted lower alkyl, optionally substituted lower alkenyl, optionally substituted lower alkynyl, optionally substituted cycloalkyl, optionally substituted heterocycloalkyl, optionally substituted aryl, optionally substituted aralkyl, optionally substituted heteroaryl, or optionally substituted heteroaralkyl; and

[0101] R^{21} is optionally substituted lower alkyl, optionally substituted lower alkenyl, optionally substituted lower alkynyl, optionally substituted cycloalkyl, optionally

substituted heterocycloalkyl, optionally substituted aryl, optionally substituted aralkyl, optionally substituted heteroaryl, or optionally substituted heteroaralkyl.

[0102] In particular embodiments of compounds of Formula IV, with reference to Formula IV, R^1 is optionally substituted lower alkyl; R^1 is optionally substituted lower alkenyl; R^1 is optionally substituted lower alkynyl, optionally substituted cycloalkyl; R^1 is optionally substituted heterocycloalkyl; R^1 is optionally substituted aryl, optionally substituted aralkyl; R^1 is optionally substituted heteroaryl, optionally substituted heteroaralkyl; R^1 is $-NR^{16}R^{17}$, $-OR^{21}$, $-SR^{21}$, $-C(X)R^{20}$, or $-C(X)NR^{16}R^{17}$. In particular embodiments, R^2 or R^3 (but not both) is hydrogen; R^2 or R^3 (but not the other) is optionally substituted lower alkyl, optionally substituted lower alkenyl, optionally substituted lower alkynyl, optionally substituted cycloalkyl; R^2 or R^3 (but not the other) is optionally substituted heterocycloalkyl; R^2 or R^3 (but not the other) is optionally substituted aryl, optionally substituted aralkyl; R^2 or R^3 (but not the other) is optionally substituted heteroaryl, optionally substituted heteroaralkyl, or optionally substituted heteroaralkyl; R^2 or R^3 (but not both) is $-C(X)R^{20}$, or $-C(X)NR^{16}R^{17}$. In particular embodiments, R^2 is H; R^3 is H; R^2 and R^3 are H.

[0103] The invention also concerns compounds of Formula V.



Formula V

where, with reference to Formula V:

[0104] R^1 and R^7 are independently hydrogen, hydroxyl, optionally substituted alkoxyl, optionally substituted thioalkoxy, optionally substituted lower alkyl, optionally substituted lower alkenyl, optionally substituted lower alkynyl, optionally substituted cycloalkyl, optionally substituted heterocycloalkyl, optionally substituted aryl, optionally substituted aralkyl, optionally substituted heteroaryl, optionally substituted heteroaralkyl, $-NR^{16}R^{17}$, $-C(X)R^{20}$, $C(X)NR^{16}R^{17}$, $-S(O)_2NR^{16}R^{17}$, $-S(O)_2R^{21}$, or R^1 and R^7, when one of them is $-NR^{16}R^{17}$, hydroxyl, alkoxyl, thioalkoxyl, aralkyl or heteroaralkyl and the other one is

hydrogen can combine to form $=NR^{16}$, =O, =S, or =Caryl/heteroaryl, with the proviso that R^1 and R^7 both cannot be hydroxyl, alkoxyl, thioalkoxyl or $-NR^{16}R^{17}$ at the same time;

[0105] R^2 is hydrogen, halo, optionally substituted lower alkyl, optionally substituted lower alkenyl, optionally substituted lower alkynyl, optionally substituted cycloalkyl, optionally substituted heterocycloalkyl, optionally substituted aryl, optionally substituted aralkyl, optionally substituted heteroaryl, optionally substituted heteroaralkyl, optionally substituted heteroaralkyl, $-C(X)R^{20}$, or $C(X)NR^{16}R^{17}$;

[0106] R^3, R^4, R^5, and R^6 are independently hydrogen, halo, hydroxyl, optionally substituted alkoxyl, optionally substituted thioalkoxy, optionally substituted amine, optionally substituted lower alkyl (e.g., trifluoromethyl), optionally substituted lower alkenyl, optionally substituted lower alkynyl, optionally substituted cycloalkyl, optionally substituted heterocycloalkyl, optionally substituted aryl, optionally substituted aralkyl, optionally substituted heteroaryl, optionally substituted heteroaralkyl, $-C(X)R^{20}$, $-C(X)NR^{16}R^{17}$, $-S(O)_2NR^{16}R^{17}$,or $-S(O)_2R^{21}$;

[0107] R^{16} and R^{17} are independently hydrogen, optionally substituted lower alkyl, optionally substituted lower alkenyl, optionally substituted lower alkynyl, optionally substituted cycloalkyl, optionally substituted heterocycloalkyl, optionally substituted aryl, optionally substituted aralkyl, optionally substituted heteroaryl, optionally substituted heteroaralkyl, or R^{16} and R^{17} together form a carbocyclic or heterocyclic ring;

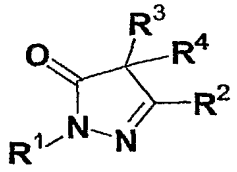
[0108] R^{20} is hydroxyl, optionally substituted lower alkoxy, optionally substituted amine, optionally substituted lower alkyl, optionally substituted lower alkenyl, optionally substituted lower alkynyl, optionally substituted cycloalkyl, optionally substituted heterocycloalkyl, optionally substituted aryl, optionally substituted aralkyl, optionally substituted heteroaryl, or optionally substituted heteroaralkyl; and

[0109] R^{21} is optionally substituted amine, optionally substituted lower alkyl, optionally substituted lower alkenyl, optionally substituted lower alkynyl, optionally substituted cycloalkyl, optionally substituted heterocycloalkyl, optionally substituted aryl, optionally substituted aralkyl, optionally substituted heteroaryl, or optionally substituted heteroaralkyl.

[0110] In particular embodiments of compounds of Formula V, with reference to Formula V, R^1 is H; R^2 is H; R^3 is H; R^4 is H; R^5 is H; R^6 is H; each combination of two of R^1, R^2, R^3, R^4, R^5, and R^6 are H and the others; each combination of three of R^1, R^2, R^3, R^4, R^5, and

R^6 are H; each combination of 4 of R^1, R^2, R^3, R^4, R^5, and R^6 are H; each combination of 5 of R^1, R^2, R^3, R^4, R^5, and R^6 are H.

[0111] Likewise, the invention concerns compounds of Formula VI.



Formula VI

where, with reference to Formula VI:

[0112] R^1 is hydrogen, optionally substituted lower alkyl, optionally substituted lower alkenyl, optionally substituted lower alkynyl, optionally substituted cycloalkyl, optionally substituted heterocycloalkyl, optionally substituted aryl, optionally substituted aralkyl, optionally substituted heteroaryl, optionally substituted heteroaralkyl, $-C(X)R^{20}$, $-C(X)NR^{16}R^{17}$, $-S(O)_2NR^{16}R^{17}$, or $-S(O)_2R^{21}$;

[0113] R^2 is hydrogen, halo, optionally substituted lower alkyl, optionally substituted lower alkenyl, optionally substituted lower alkynyl, optionally substituted cycloalkyl, optionally substituted heterocycloalkyl, optionally substituted aryl, optionally substituted aralkyl, optionally substituted heteroaryl, optionally substituted heteroaralkyl, optionally substituted heteroaralkyl, $-C(X)R^{20}$, $-C(X)NR^{16}R^{17}$, $-S(O)_2NR^{16}R^{17}$, or $-S(O)_2R^{21}$;

[0114] R^3 and R^4 are independently hydrogen, halo, hydroxyl, optionally substituted alkoxyl, optionally substituted thioalkoxy, optionally substituted amine, optionally substituted lower alkyl (e.g., trifluoromethyl), optionally substituted lower alkenyl, optionally substituted lower alkynyl, optionally substituted cycloalkyl, optionally substituted heterocycloalkyl, optionally substituted aryl, optionally substituted aralkyl, optionally substituted heteroaryl, optionally substituted heteroaralkyl, $-NR^{16}R^{17}$, $-C(X)R^{20}$, $-C(X)NR^{16}R^{17}$, $-S(O)_2NR^{16}R^{17}$,or $-S(O)_2R^{21}$ or R^3 and R^4, when one of them is $-NR^{16}R^{17}$, hydroxyl, alkoxyl, thioalkoxyl, aralkyl or heteroaralkyl and the other one is hydrogen can combine to form $=NR^{16}$, =O, =S, or =Caryl/heteroaryl, with the proviso that R^1 and R^7 both cannot be hydroxyl, alkoxyl, thioalkoxyl or $-NR^{16}R^{17}$ at the same time;

[0115] R^{16} and R^{17} are independently hydrogen, optionally substituted lower alkyl, optionally substituted lower alkenyl, optionally substituted lower alkynyl, optionally

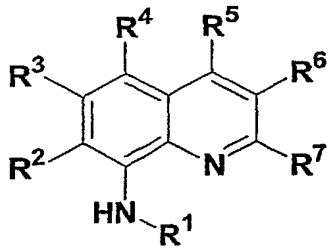
substituted cycloalkyl, optionally substituted heterocycloalkyl, optionally substituted aryl, optionally substituted aralkyl, optionally substituted heteroaryl, optionally substituted heteroaralkyl, or R^{16} and R^{17} together form a carbocyclic or heterocyclic ring;

[0116] R^{20} is hydroxyl, optionally substituted lower alkoxy, optionally substituted amine, optionally substituted lower alkyl, optionally substituted lower alkenyl, optionally substituted lower alkynyl, optionally substituted cycloalkyl, optionally substituted heterocycloalkyl, optionally substituted aryl, optionally substituted aralkyl, optionally substituted heteroaryl, or optionally substituted heteroaralkyl; and

[0117] R^{21} is optionally substituted lower alkoxy, optionally substituted amine, optionally substituted lower alkyl, optionally substituted lower alkenyl, optionally substituted lower alkynyl, optionally substituted cycloalkyl, optionally substituted heterocycloalkyl, optionally substituted aryl, optionally substituted aralkyl, optionally substituted heteroaryl, or optionally substituted heteroaralkyl.

[0118] In particular embodiments of compounds of Formula VI, with reference to Formula VI, R^1 is H; R^2 is H; R^3 is H; R^1 and R^2 are H; R^2 and R^3 are H; R^1 is optionally substituted lower alkyl, optionally substituted lower alkenyl, optionally substituted lower alkynyl; R^1 is optionally substituted cycloalkyl, optionally substituted heterocycloalkyl; R^1 is optionally substituted aryl, optionally substituted aralkyl, optionally substituted heteroaryl, optionally substituted heteroaralkyl; R^1 is $-C(X)R^{20}$, $-C(X)NR^{16}R^{17}$, $-S(O)_2NR^{16}R^{17}$, or $-S(O)_2R^{21}$; R^2 is halo; R^2 is optionally substituted lower alkyl, optionally substituted lower alkenyl, optionally substituted lower alkynyl; R^2 is optionally substituted cycloalkyl, optionally substituted heterocycloalkyl; R^2 is optionally substituted aryl, optionally substituted aralkyl, optionally substituted heteroaryl, optionally substituted heteroaralkyl, or optionally substituted heteroaralkyl; R^2 is $-C(X)R^{20}$, $-C(X)NR^{16}R^{17}$, $-S(O)_2NR^{16}R^{17}$, or $-S(O)_2R^{21}$; R^3 is halo; R^3 is trifluoromethyl; R^3 is optionally substituted alkoxyl, optionally substituted thioalkoxy; R^3 is optionally substituted amine; R^3 is optionally substituted lower alkyl, optionally substituted lower alkenyl, optionally substituted lower alkynyl; R^3 is optionally substituted cycloalkyl, optionally substituted heterocycloalkyl; R^3 is optionally substituted aryl, optionally substituted aralkyl, optionally substituted heteroaryl, or optionally substituted heteroaralkyl; R^3 is $-C(X)R^{20}$, $-C(X)NR^{16}R^{17}$, $-S(O)_2NR^{16}R^{17}$,or $-S(O)_2R^{21}$.

[0119] In yet other embodiments, the invention concerns compounds of Formula VII.



Formula VII

where, with reference to Formula VII:

[0120] R^1 is hydrogen, optionally substituted lower alkyl, optionally substituted lower alkenyl, optionally substituted lower alkynyl, optionally substituted cycloalkyl, optionally substituted heteralkyl ,optionally substituted heterocycloalkyl, optionally substituted aryl, optionally substituted aralkyl, optionally substituted heteroaryl, optionally substituted heteroaralkyl, $-C(X)R^{20}$, $-C(X)NR^{16}R^{17}$, $-S(O)_2NR^{16}R^{17}$,or $-S(O)_2R^{21}$;

[0121] R^2, R^3, R^4, R^5, R^6, and R^7 are independently hydrogen, halo, optionally substituted amine, optionally substituted alkoxy, optionally substituted thioether, optionally substituted lower alkyl, optionally substituted lower alkenyl, optionally substituted lower alkynyl, optionally substituted cycloalkyl, optionally substituted heterocycloalkyl, optionally substituted aryl, optionally substituted aralkyl, optionally substituted heteroaryl, optionally substituted heteroaralkyl, optionally substituted heteroaralkyl, $-C(X)R^{20}$, $-C(X)NR^{16}R^{17}$, $-S(O)_2NR^{16}R^{17}$, or $-S(O)_2R^{21}$;

[0122] R^{16} and R^{17} are independently hydrogen, optionally substituted lower alkyl, optionally substituted lower alkenyl, optionally substituted lower alkynyl, optionally substituted cycloalkyl, optionally substituted heteroalkyl, optionally substituted heterocycloalkyl, optionally substituted aryl, optionally substituted aralkyl, optionally substituted heteroaryl, optionally substituted heteroaralkyl, or R^{16} and R^{17} together form a carbocyclic or heterocyclic ring;

[0123] R^{20} is hydroxyl, optionally substituted lower alkoxy, optionally substituted lower alkyl, optionally substituted lower alkenyl, optionally substituted lower alkynyl, optionally substituted cycloalkyl, optionally substituted heteroalkyl, optionally substituted

heterocycloalkyl, optionally substituted aryl, optionally substituted aralkyl, optionally substituted heteroaryl, or optionally substituted heteroaralkyl; and

[0124] R^{21} is optionally substituted lower alkoxy, optionally substituted lower alkyl, optionally substituted lower alkenyl, optionally substituted lower alkynyl, optionally substituted cycloalkyl, optionally substituted heteroalkyl, optionally substituted heterocycloalkyl, optionally substituted aryl, optionally substituted aralkyl, optionally substituted heteroaryl, or optionally substituted heteroaralkyl.

[0125] In particular embodiments of compounds of Formula VII, with reference to Formula VII, R^1 is H; R^2 is H; R^3 is H; R^4 is H; R^5 is H; R^6 is H; R^7 is H; each combination of two of R^1, R^2, R^3, R^4, R^5, R^6, and R^7 are H; each combination of three of R^1, R^2, R^3, R^4, R^5, R^6, and R^7 are H; each combination of 4 of R^1, R^2, R^3, R^4, R^5, R^6, and R^7 are H; each combination of 5 of R^1, R^2, R^3, R^4, R^5, R^6, and R^7 are H; each combination of six of R^1, R^2, R^3, R^4, R^5, R^6, and R^7 are H (e.g., all except for R^1 and R^6).

[0126] As used in connection with the present invention, unless indicated clearly to the contrary, the description of compounds and the use of such compounds, e.g., compounds of any of Formula I-VII, includes pharmaceutically acceptable salts and solvates of such compounds.

[0127] In connection with the compounds of Formulas I-VII, the following definitions apply.

[0128] "Halo" or "Halogen" - alone or in combination means all halogens, that is, chloro (Cl), fluoro (F), bromo (Br), iodo (I).

[0129] "Hydroxyl" refers to the group -OH.

[0130] "Thiol" or "mercapto" refers to the group -SH.

[0131] "Alkyl" - alone or in combination means an alkane-derived radical containing from 1 to 20, preferably 1 to 15, carbon atoms (unless specifically defined). It is a straight chain alkyl, branched alkyl or cycloalkyl. Preferably, straight or branched alkyl groups containing from 1-15, more preferably 1 to 8, even more preferably 1-6, yet more preferably 1-4 and most preferably 1-2, carbon atoms, such as methyl, ethyl, propyl, isopropyl, butyl, t-butyl and the like. The term "lower alkyl" is used herein to describe the straight chain alkyl groups of 1-6, 1-4, or 1-2 carbon atoms. Preferably, cycloalkyl groups are monocyclic.

bicyclic or tricyclic ring systems of 3-8, more preferably 3-6, ring members per ring, such as cyclopropyl, cyclopentyl, cyclohexyl, and the like, but can also include larger ring structures such as adamantyl. Alkyl also includes a straight chain or branched alkyl group that contains or is interrupted by a cycloalkyl portion. The straight chain or branched alkyl group is attached at any available point to produce a stable compound. Examples of this include, but are not limited to, 4-(isopropyl)-cyclohexylethyl or 2-methyl-cyclopropylpentyl. A substituted alkyl is a straight chain alkyl, branched alkyl, or cycloalkyl group defined previously, independently substituted with 1 to 3 groups or substituents of halo, hydroxy, alkoxy, alkylthio, alkylsulfinyl, alkylsulfonyl, acyloxy, aryloxy, heteroaryloxy, amino optionally mono- or di-substituted with alkyl, aryl or heteroaryl groups, amidino, urea optionally substituted with alkyl, aryl, heteroaryl or heterocyclyl groups, aminosulfonyl optionally N-mono- or N,N-di-substituted with alkyl, aryl or heteroaryl groups, alkylsulfonylamino, arylsulfonylamino, heteroarylsulfonylamino, alkylcarbonylamino, arylcarbonylamino, heteroarylcarbonylamino, or the like.

[0132] "Alkenyl" - alone or in combination means a straight, branched, or cyclic hydrocarbon containing 2-20, preferably 2-17, more preferably 2-10, even more preferably 2-8, most preferably 2-4, carbon atoms and at least one, preferably 1-3, more preferably 1-2, most preferably one, carbon to carbon double bond. In the case of a cycloalkyl group, conjugation of more than one carbon to carbon double bond is not such as to confer aromaticity to the ring. Carbon to carbon double bonds may be either contained within a cycloalkyl portion, with the exception of cyclopropyl, or within a straight chain or branched portion. Examples of alkenyl groups include ethenyl, propenyl, isopropenyl, butenyl, cyclohexenyl, cyclohexenylalkyl and the like. A substituted alkenyl is the straight chain alkenyl, branched alkenyl or cycloalkenyl group defined previously, independently substituted with 1 to 3 groups or substituents of halo, hydroxy, alkoxy, alkylthio, alkylsulfinyl, alkylsulfonyl, acyloxy, aryloxy, heteroaryloxy, amino optionally mono- or di-substituted with alkyl, aryl or heteroaryl groups, amidino, urea optionally substituted with alkyl, aryl, heteroaryl or heterocyclyl groups, aminosulfonyl optionally N-mono- or N,N-di-substituted with alkyl, aryl or heteroaryl groups, alkylsulfonylamino, arylsulfonylamino, heteroarylsulfonylamino, alkylcarbonylamino, arylcarbonylamino, heteroarylcarbonylamino, carboxy, alkoxycarbonyl, aryloxycarbonyl, heteroaryloxycarbonyl, or the like attached at any available point to produce a stable compound.

[0133] "Alkynyl" - alone or in combination means a straight or branched hydrocarbon containing 2-20, preferably 2-17, more preferably 2-10, even more preferably 2-8, most preferably 2-4, carbon atoms containing at least one, preferably one, carbon to carbon triple bond. Examples of alkynyl groups include ethynyl, propynyl, butynyl and the like. A substituted alkynyl refers to a straight chain alkynyl or branched alkynyl, independently substituted with 1 to 3 groups or substituents of halo, hydroxy, alkoxy, alkylthio, alkylsulfinyl, alkylsulfonyl, acyloxy, aryloxy, heteroaryloxy, amino optionally mono- or di-substituted with alkyl, aryl or heteroaryl groups, amidino, urea optionally substituted with alkyl, aryl, heteroaryl or heterocyclyl groups, aminosulfonyl optionally N-mono- or N,N-di-substituted with alkyl, aryl or heteroaryl groups, alkylsulfonylamino, arylsulfonylamino, heteroarylsulfonylamino, alkylcarbonylamino, arylcarbonylamino, heteroarylcarbonylamino, or the like attached at any available point to produce a stable compound.

[0134] "Alkyl alkenyl" refers to a group -R-CR'=CR''' R'''', where R is lower alkylene, or substituted lower alkylene, R', R''', R'''' may independently be hydrogen, halogen, lower alkyl, substituted lower alkyl, acyl, aryl, substituted aryl, heteroaryl, or substituted heteroaryl as defined below.

[0135] "Alkyl alkynyl" refers to a groups -RCCR' where R is lower alkylene or substituted lower alkylene, R' is hydrogen, lower alkyl, substituted lower alkyl, acyl, aryl, substituted aryl, heteroaryl, or substituted heteroaryl as defined below.

[0136] "Alkoxy" denotes the group -OR, where R is lower alkyl, substituted lower alkyl, acyl, aryl, substituted aryl, aralkyl, substituted aralkyl, heteroalkyl, heteroarylalkyl, cycloalkyl, substituted cycloalkyl, cycloheteroalkyl, or substituted cycloheteroalkyl as defined.

[0137] "Alkylthio" or "thioalkoxy" denotes the group -SR, $-S(O)_{n=1-2}-R$, where R is lower alkyl, substituted lower alkyl, aryl, substituted aryl, aralkyl or substituted aralkyl as defined herein.

[0138] "Acyl" denotes groups -C(O)R, where R is hydrogen, lower alkyl substituted lower alkyl, aryl, substituted aryl and the like as defined herein.

[0139] "Aryloxy" denotes groups -OAr, where Ar is an aryl, substituted aryl, heteroaryl, or substituted heteroaryl group as defined herein.

[0140] "Amino" or substituted amine denotes the group NRR', where R and R' may independently by hydrogen, lower alkyl, substituted lower alkyl, aryl, substituted aryl, heteroaryl, or substituted heteroaryl as defined herein, acyl or sulfonyl.

[0141] "Amido" denotes the group -C(O)NRR', where R and R' may independently by hydrogen, lower alkyl, substituted lower alkyl, aryl, substituted aryl, heteroaryl, substituted heteroaryl as defined herein.

[0142] "Carboxyl" denotes the group -C(O)OR, where R is hydrogen, lower alkyl, substituted lower alkyl, aryl, substituted aryl, heteroaryl, and substituted heteroaryl as defined herein.

[0143] "Carbocyclic" refers to a saturated, unsaturated, or aromatic group having a single ring (e.g., phenyl) or multiple condensed rings where all ring atoms are carbon atoms, which can optionally be unsubstituted or substituted with, e.g., halogen, lower alkyl, lower alkoxy, alkylthio, acetylene, amino, amido, carboxyl, hydroxyl, aryl, aryloxy, heterocycle, heteroaryl, substituted heteroaryl, nitro, cyano, thiol, sulfamido and the like.

[0144] "Aryl" - alone or in combination means phenyl or naphthyl optionally carbocyclic fused with a cycloalkyl of preferably 5-7, more preferably 5-6, ring members and/or optionally substituted with 1 to 3 groups or substituents of halo, hydroxy, alkoxy, alkylthio, alkylsulfinyl, alkylsulfonyl, acyloxy, aryloxy, heteroaryloxy, amino optionally mono- or di-substituted with alkyl, aryl or heteroaryl groups, amidino, urea optionally substituted with alkyl, aryl, heteroaryl or heterocyclyl groups, aminosulfonyl optionally N-mono- or N,N-di-substituted with alkyl, aryl or heteroaryl groups, alkylsulfonylamino, arylsulfonylamino, heteroarylsulfonylamino, alkylcarbonylamino, arylcarbonylamino, heteroarylcarbonylamino, or the like.

[0145] "Substituted aryl" refers to aryl optionally substituted with one or more functional groups, e.g., halogen, lower alkyl, lower alkoxy, alkylthio, acetylene, amino, amido, carboxyl, hydroxyl, aryl, aryloxy, heterocycle, heteroaryl, substituted heteroaryl, nitro, cyano, thiol, sulfamido and the like.

[0146] "Heteroaryl" - alone or in combination means a monocyclic aromatic ring structure containing 5 or 6 ring atoms, or a bicyclic aromatic group having 8 to 10 atoms, containing one or more, preferably 1-4, more preferably 1-3, even more preferably 1-2, heteroatoms independently selected from the group O, S, and N, and optionally substituted

with 1 to 3 groups or substituents of halo, hydroxy, alkoxy, alkylthio, alkylsulfinyl, alkylsulfonyl, acyloxy, aryloxy, heteroaryloxy, amino optionally mono- or di-substituted with alkyl, aryl or heteroaryl groups, amidino, urea optionally substituted with alkyl, aryl, heteroaryl or heterocyclyl groups, aminosulfonyl optionally N-mono- or N,N-di-substituted with alkyl, aryl or heteroaryl groups, alkylsulfonylamino, arylsulfonylamino, heteroarylsulfonylamino, alkylcarbonylamino, arylcarbonylamino, heteroarylcarbonylamino, or the like. Heteroaryl is also intended to include oxidized S or N, such as sulfinyl, sulfonyl and N-oxide of a tertiary ring nitrogen. A carbon or nitrogen atom is the point of attachment of the heteroaryl ring structure such that a stable aromatic ring is retained. Examples of heteroaryl groups are pyridinyl, pyridazinyl, pyrazinyl, quinazolinyl, purinyl, indolyl, quinolinyl, pyrimidinyl, pyrrolyl, oxazolyl, thiazolyl, thienyl, isoxazolyl, oxathiadiazolyl, isothiazolyl, tetrazolyl, imidazolyl, triazinyl, furanyl, benzofuryl, indolyl and the like. A substituted heteroaryl contains a substituent attached at an available carbon or nitrogen to produce a stable compound.

[0147] "Heterocyclyl" - alone or in combination means a non-aromatic cycloalkyl group having from 5 to 10 atoms in which from 1 to 3 carbon atoms in the ring are replaced by heteroatoms of O, S or N, and are optionally benzo fused or fused heteroaryl of 5-6 ring members and/or are optionally substituted as in the case of cycloalkyl. Heterocycyl is also intended to include oxidized S or N, such as sulfinyl, sulfonyl and N-oxide of a tertiary ring nitrogen. The point of attachment is at a carbon or nitrogen atom. Examples of heterocyclyl groups are tetrahydrofuranyl, dihydropyridinyl, piperidinyl, pyrrolidinyl, piperazinyl, dihydrobenzofuryl, dihydroindolyl, and the like. A substituted hetercyclyl contains a substituent nitrogen attached at an available carbon or nitrogen to produce a stable compound.

[0148] "Heterocycle" refers to a saturated, unsaturated, or aromatic carbocyclic group having a single ring (e.g., morpholino, pyridyl or furyl) or multiple condensed rings (e.g., naphthpyridyl, quinoxalyl, quinolinyl, indolizinyl or benzo[b]thienyl) and having at least one hetero atom, such as N, O or S, within the ring, which can optionally be unsubstituted or substituted with, e.g., halogen, lower alkyl, lower alkoxy, alkylthio, acetylene, amino, amido, carboxyl, hydroxyl, aryl, aryloxy, heterocycle, heteroaryl, substituted heteroaryl, nitro, cyano, thiol, sulfamido and the like.

[0149] "Substituted heteroaryl" refers to a heterocycle optionally mono or poly substituted with one or more functional groups, e.g., halogen, lower alkyl, lower alkoxy, alkylthio, acetylene, amino, amido, carboxyl, hydroxyl, aryl, aryloxy, heterocycle, substituted heterocycle, heteroaryl, substituted heteroaryl, nitro, cyano, thiol, sulfamido and the like.

[0150] "Aralkyl" refers to the group -R-Ar where Ar is an aryl group and R is lower alkyl or substituted lower alkyl group. Aryl groups can optionally be unsubstituted or substituted with, e.g., halogen, lower alkyl, alkoxy, alkylthio, acetylene, amino, amido, carboxyl, hydroxyl, aryl, aryloxy, heterocycle, substituted heterocycle, heteroaryl, substituted heteroaryl, nitro, cyano, thiol, sulfamido and the like.

[0151] "Heteroalkyl" refers to the group -R-Het where Het is a heterocycle group and R is a lower alkyl group. Heteroalkyl groups can optionally be unsubstituted or substituted with e.g., halogen, lower alkyl, lower alkoxy, alkylthio, acetylene, amino, amido, carboxyl, aryl, aryloxy, heterocycle, substituted heterocycle, heteroaryl, substituted heteroaryl, nitro, cyano, thiol, sulfamido and the like.

[0152] "Heteroarylalkyl" refers to the group -R-HetAr where HetAr is an heteroaryl group and R lower alkyl or substituted lower alkyl. Heteroarylalkyl groups can optionally be unsubstituted or substituted with, e.g., halogen, lower alkyl, substituted lower alkyl, alkoxy, alkylthio, acetylene, aryl, aryloxy, heterocycle, substituted heterocycle, heteroaryl, substituted heteroaryl, nitro, cyano, thiol, sulfamido and the like.

[0153] "Cycloalkyl" refers to a cyclic or polycyclic alkyl group containing 3 to 15 carbon atoms.

[0154] "Substituted cycloalkyl" refers to a cycloalkyl group comprising one or more substituents with, e.g., halogen, lower alkyl, substituted lower alkyl, alkoxy, alkylthio, acetylene, aryl, aryloxy, heterocycle, substituted heterocycle, heteroaryl, substituted heteroaryl, nitro, cyano, thiol, sulfamido and the like.

[0155] "Cycloheteroalkyl" refers to a cycloalkyl group wherein one or more of the ring carbon atoms is replaced with a heteroatom (e.g., N, O, S or P).

[0156] "Substituted cycloheteroalkyl" refers to a cycloheteroalkyl group as herein defined which contains one or more substituents, such as halogen, lower alkyl, lower alkoxy,

alkylthio, acetylene, amino, amido, carboxyl, hydroxyl, aryl, aryloxy, heterocycle, substituted heterocycle, heteroaryl, substituted heteroaryl, nitro, cyano, thiol, sulfamido and the like.

[0157] "Alkyl cycloalkyl" denotes the group -R-cycloalkyl where cycloalkyl is a cycloalkyl group and R is a lower alkyl or substituted lower alkyl. Cycloalkyl groups can optionally be unsubstituted or substituted with e.g. halogen, lower alkyl, lower alkoxy, alkylthio, acetylene, amino, amido, carboxyl, hydroxyl, aryl, aryloxy, heterocycle, substituted heterocycle, heteroaryl, substituted heteroaryl, nitro, cyano, thiol, sulfamido and the like.

[0158] "Alkyl cycloheteroalkyl" denotes the group -R-cycloheteroalkyl where R is a lower alkyl or substituted lower alkyl. Cycloheteroalkyl groups can optionally be unsubstituted or substituted with e.g. halogen, lower alkyl, lower alkoxy, alkylthio, amino, amido, carboxyl, acetylene, hydroxyl, aryl, aryloxy, heterocycle, substituted heterocycle, heteroaryl, substituted heteroaryl, nitro, cyano, thiol, sulfamido and the like.

[0159] An additional aspect of this invention relates to pharmaceutical formulations or compositions, that include a therapeutically effective amount of a compound of Formula I, II, III, IV, V, VI, or VII, (or a compound within a sub-group of compounds within any of those generic formulas) and at least one pharmaceutically acceptable carrier or excipient. The composition can include a plurality of different pharmacalogically active compounds.

[0160] As used herein, the term "pharmaceutical composition" refers to a preparation that includes a therapeutically significant quantity of an active agent, that is prepared in a form adapted for administration to a subject. Thus, the preparation does not include any component or components in such quantity that a reasonably prudent medical practitioner would find the preparation unsuitable for administration to a normal subject. In many cases, such a pharmaceutical composition is a sterile preparation.

[0161] In a related aspect, the invention provides kits that include a pharmaceutical composition as described herein. In particular embodiments, the pharmaceutical composition is packaged, e.g., in a vial, bottle, flask, which may be further packaged, e.g., within a box, envelope, or bag; the pharmaceutical composition is approved by the U.S. Food and Drug Administration or similar regulatory agency for administration to a mammal,e.g., a human; the pharmaceutical composition is approved for administration to a

mammal, e.g., a human for a kinase-mediated disease or condition; the kit includes written instructions or other indication that the composition is suitable or approved for administration to a mammal, e.g., a human, for a kinase-mediated disease or condition; the pharmaceutical composition is packaged in unit does or single dose form, e.g., single dose pills, capsules, or the like.

[0162] In another related aspect, compounds of any of Formulas I-VII can be used in the preparation of a medicament for the treatment of a kinase-mediated disease or condition or a disease or condition in which modulation of a kinase provides a therapeutic benefit.

[0163] In the present context, the term "therapeutically effective" indicates that the materials or amount of material is effective to prevent, alleviate, or ameliorate one or more symptoms of a disease or medical condition, and/or to prolong the survival of the subject being treated.

[0164] The term "pharmaceutically acceptable" indicates that the indicated material does not have properties that would cause a reasonably prudent medical practitioner to avoid administration of the material to a patient, taking into consideration the disease or conditions to be treated and the respective route of administration. For example, it is commonly required that such a material be essentially sterile, e.g., for injectibles.

[0165] "A pharmaceutically acceptable salt" is intended to mean a salt that retains the biological effectiveness of the free acids and bases of the specified compound and that is not biologically or otherwise unacceptable. A compound of the invention may possess a sufficiently acidic, a sufficiently basic, or both functional groups, and accordingly react with any of a number of inorganic or organic bases, and inorganic and organic acids, to form a pharmaceutically acceptable salt. Exemplary pharmaceutically acceptable salts include those salts prepared by reaction of the compounds of the present invention with a mineral or organic acid or an inorganic base, such as salts including sodium, chloride, sulfates, pyrosulfates, bisulfates, sulfites, bisulfites, phosphates, monohydrogenphosphates, dihydrogenphosphates, metaphosphates, pyrophosphates, chlorides, bromides, iodides, acetates, propionates, decanoates, caprylates, acrylates, formates, isobutyrates, caproates, heptanoates, propiolates, oxalates, malonates, succinates, suberates, sebacates, fumarates, maleates, butyne-1,4 dioates, hexyne-1,6-dioates, benzoates, chlorobenzoates, methylbenzoates, dinitrobenzoates, hydroxybenzoates, methoxybenzoates, phthalates, sulfonates, xylenesulfonates, phenylacetates, phenylpropionates, phenylbutyrates, citrates,

lactates, .gamma.-hydroxybutyrates, glycollates, tartrates, methane-sulfonates, propanesulfonates, naphthalene-1-sulfonates, naphthalene-2-sulfonates, and mandelates.

[0166] The term "pharmaceutically acceptable metabolite" refers to a pharmacologically acceptable product, which may be an active product, produced through metabolism of a specified compound (or salt thereof) in the body of a subject or patient. Metabolites of a compound may be identified using routine techniques known in the art, and their activities determined using tests such as those described herein. For example, in some compounds, one or more alkoxy groups can be metabolized to hydroxyl groups while retaining pharmacologic activity and/or carboxyl groups can be esterified, e.g., glucuronidation. In some cases, there can be more than one metabolite, where an intermediate metabolite(s) is further metabolized to provide an active metabolite. For example, in some cases a derivative compound resulting from metabolic glucuronidation may be inactive or of low activity, and can be further metabolized to provide an active metabolite.

[0167] Additional aspects and embodiments will be apparent from the following Detailed Description and from the claims.

BRIEF DESCRIPTION OF THE DRAWINGS

[0168] FIGURE 1 shows a schematic representation of AMP-PNP in the binding site of PIM-1, showing conserved interacting residues.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

[0169] The Tables will first be briefly described.

[0170] Table 1 provides atomic coordinates for human PIM-1. In this table and in Table 4, the various columns have the following content, beginning with the left-most column:
ATOM: Refers to the relevant moiety for the table row.
Atom number: Refers to the arbitrary atom number designation within the coordinate table.
Atom Name: Identifier for the atom present at the particular coordinates.
Chain ID: Chain ID refers to one monomer of the protein in the crystal, *e.g.*, chain "A", or to other compound present in the crystal, e.g., HOH for water, and L for a ligand or binding compound. Multiple copies of the protein monomers will have different chain Ids.
Residue Number: The amino acid residue number in the chain.

X, Y, Z: Respectively are the X, Y, and Z coordinate values.
Occupancy: Describes the fraction of time the atom is observed in the crystal. For example, occupancy = 1 means that the atom is present all the time; occupancy = o.5 indicates that the atom is present in the location 50% of the time.
B-factor: A measure of the thermal motion of the atom.
Element: Identifier for the element.

[0171] Table 2 provides an alignment of catalytic domains of several PIM kinases, including human PIM-1, PIM-2, and PIM-3 as well as PIM kinases from other species.

[0172] Table 2 provides an alignment of catalytic domains of several PIM kinases, including human PIM-1, PIM-2, and PIM-3 as well as PIM kinases from other species. Sequences from the following species are included in the alignment: Hs, Homo sapiens; Mm, Mus musculus; Dr, Danio rerio; Xl, Xenopus laevis; Cc, Coturnix coturnix; and Ce, Caenorhabditis elegans. Residues with >90% and >75% conservations are in red and yellow background, respectively. Phosphate binding sites are indicated by purple circles. Residues that are invariably involved in ligand binding are indicated by filled uparrows, whereas residues that can be involved in ligand binding are indicated by open uparrows. The backbone atoms of two residues (indicated by leftarrows) in the hinge region have been shown to make hydrogen bonds to ligands in many known kinase/ligand complex structures. Note that PIM family kinases all have Pro as the second residue, resulting in theloss of a hydrogen bond donor.

[0173] Table 4 provides atomic coordinates for PIM-1 with AMP-PNP in the binding site.

[0174] Table 5 provides a list of kinases which have been correlated with diseases (or pathological condition).

I. Introduction

[0175] The present invention concerns the use of certain molecular scaffolds in the development of kinase modulators, e.g., kinase inhibitors. Such development can utilize kinase structures, for example, PIM kinase structures, structural information, and related compositions for identifying compounds that modulate kinase activity and for determining structures of other kinases. The following description utilizes PIM-1 for illustrative purposes. However, the invention is not limited to PIM-1; other protein kinases can also be utilized for modulation by the present compounds, and for developing additional modulators

based on the present molecular scaffolds. The use of molecular scaffolds in connection with PIM kinases and Pyk2 is described in U.S. Appl. 10/664,421 and corresponding PCT/US03/29415, and Formula I as described in U.S. Appl. 10/789,818 and corresponding PCT/US2004/005904 respectively. Both of those applications are incorporated herein by reference in their entireties, including drawings.

[0176] Kinases, e.g., PIM-1, are involved in a variety of disease conditions, and a number have been utilized as therapeutic targets.

Exemplary Diseases Associated with Kinases

[0177] As indicated above, the present invention is exemplified in connection with PIM-1. As indicated in the Background above, PIM-1 functions as a weak oncogene. In transgenic mice with PIM-1 driven by Emu enhancer sequences, overexpression of PIM-1 by itself it does not lead to tumor formation, but does so in conjunction with overexpression of a second oncogenic gene. In 75% of tumors over-expressing PIM-1, the second gene found to be overexpressed was c-myc (van der Houven van Oordt CW, Schouten TG, van Krieken JH, van Dierendonck J H, van der Eb AJ, Breuer ML.(1998) X-ray-induced lymphomagenesis in Eμ-*PIM-1* transgenic mice: an investigation of the co-operating molecular events. *Carcinogenesis* 19:847-853). Other PIM kinases are also involved, as the functions of the various PIM kinases appears to be at least partially complementary.

[0178] Since PIM-1 is a protooncogene and it closely cooperates with other protooncogenes like c-myc in triggering intracellular signals leading to cell transformation, PIM-1 inhibitors have therapeutic applications in the treatment of various cancers, as wells as other disease states. Some examples are described below.

Prostate cancer

[0179] A significant inter-relationship between PIM-1 and a disease state was reported in prostate cancer (Dhanasekaran et al. (2001) Delineation of prognostic biomarkers in prostate cancer. *Nature* 412: 822-826.) Using microarrays of complementary DNA, the gene expression profiles of approximately 10,000 genes from more than 50 normal and neoplastic prostate cancer specimens and three common prostate cancer cell lines were examined. Two of these genes, hepsin, a transmembrane serine protease, and PIM-1, a serine/threonine kinase are upregulated to several-fold. The PIM-1 kinase is strongly expressed in the cytoplasm of prostate cancer tissues while the normal tissues showed no or weak staining

with anti-PIM-1 antibody (*Id.*) indicating PIM-1 is an appropriate target for drug development.

Leukemia

[0180] PIM-1 has been mapped to the 6p21 chromosomal region in humans. Nagarajan et al. (Nagarajan et al. (1986) Localization of the human pim oncogene (PIM) to a region of chromosome 6 involved in translocations in acute leukemias. *Proc. Natl. Acad. Sci. USA* 83:2556-2560) reported increased expression of PIM-1 in K562 erythroleukemia cell lines which contain cytogenetically demonstrable rearrangement in the 6p21 region. A characteristic chromosome anomaly, a reciprocal translocation t(6;9)(p21;q33), has been described in myeloid leukemias that may be due to involvement of PIM-1. Amson et al. (1989) also observed overexpression in 30 % of myeloid and lymphoid acute leukemia. These studies also indicate a role for PIM-1 protooncogene during development and in deregulation in various leukemias.

Kaposi Sarcoma

[0181] Analysis of gene expression profiles by microarrays in human hematopoietic cells after *in vitro* infection with human Herpes virus (HHV 8), also known as Kaposi Sarcoma associated virus (KSHV), resulted in differential expression of 400 genes out of about 10,000 analyzed. Of these four hundred genes, PIM-2 is upregulated more than 3.5 fold indicating PIM-2 as a potential target for therapeutic intervention. Thus, inhibitors selective to PIM-2 are of great therapeutic value in treating disease states mediated by HHV8 (Mikovits et al. (2001) Potential cellular signatures of viral infections in human hematopoietic cells. *Dis. Markers* 17:173-178.)

Asthma and Allergy.

[0182] The increase in eosinophils at the site of antigen challenge has been used as evidence that eosinophils play a role in pathophysiology of asthma. Aberrant production of several different cytokines has been shown to result in eosinophilia. The cytokine IL-5 for example influences the development and maturation of eosinophils in a number of ways. Using microarray techniques, a role for PIM-1 in IL-5 signaling pathway in eosinophils was indicated. (Temple et al. (2001) Microarray analysis of eosinophils reveals a number of candidate survival and apoptosis genes. *Am. J. Respir. Cell Mol. Biol.* 25: 425-433.) Thus, inhibitors of PIM-1 can have therapeutic value in treatment of asthma and allergies.

Inflammation

[0183] PIM-1 and/or the compounds described herein can also be useful for treatment of inflammation, either chronic or acute. Chronic inflammation is regarded as prolonged inflammation (weeks or months), involving simultaneous active inflammation, tissue destruction, and attempts at healing. (R.S. Cotran, V. Kumar, and S.L. Robbins, Saunders Co., (1989) Robbins Pathological Basis of Disease, p.75.) Although chronic inflammation can follow an acute inflammatory episode, it can also begin as a process that progresses over time, *e.g.*, as a result of a chronic infection such as tuberculosis, syphilis, fungal infection which causes a delayed hypersensitivity reaction, prolonged exposure to endogenous or exogenous toxins, or autoimmune reactions (*e.g.*, rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis, psoriasis). Chronic inflammatory disease thus include many common medical conditions such as autoimmune disorders such as those listed above, chronic infections, surgical adhesions, chronic inflammatory lung and airway diseases (*e.g.*, asthma, pneumoconiosis, chronic obstructive pulmonary disease, nasal polyps, and pulmonary fibrosis). For skin and airway inflammatory disease, topical or inhaled forms of drug administration can be used respectively.

[0184] While kinase-related diseases and conditions are exemplified in connection with PIM-1, numerous other kinases have been correlated with particular disease and conditions, and are identified as target in a number of current treatments. Compounds derived from the present scaffolds can be developed to target such additional kinases for treating associated diseases and conditions.

II. Crystalline Kinases

[0185] In development of kinase modulators based on molecular scaffolds, crystalline kinases (e.g., human PIM-1) include native crystals, derivative crystals and co-crystals are useful. Native crystals generally comprise substantially pure polypeptides corresponding to the kinase in crystalline form. Crystal structures for a number of different kinases (or kinase domains) have been determined and are available for use in the present methods.

[0186] It is to be understood that the crystalline kinases are not limited to naturally occurring or native kinase. Indeed, the crystals of the invention include crystals of mutants of native kinases. Mutants of native kinases are obtained by replacing at least one amino acid residue in a native kinase with a different amino acid residue, or by adding or deleting

amino acid residues within the native polypeptide or at the N- or C-terminus of the native polypeptide, and have substantially the same three-dimensional structure as the native kinase from which the mutant is derived.

[0187] By having substantially the same three-dimensional structure is meant having a set of atomic structure coordinates that have a root-mean-square deviation of less than or equal to about 2Å when superimposed with the atomic structure coordinates of the native kinase from which the mutant is derived when at least about 50% to 100% of the Cα atoms of the native kinase domain are included in the superposition.

[0188] Amino acid substitutions, deletions and additions which do not significantly interfere with the three-dimensional structure of the kinase will depend, in part, on the region of the kinase where the substitution, addition or deletion occurs. In highly variable regions of the molecule, non-conservative substitutions as well as conservative substitutions may be tolerated without significantly disrupting the three-dimensional, structure of the molecule. In highly conserved regions, or regions containing significant secondary structure, conservative amino acid substitutions are preferred. Such conserved and variable regions can be identified by sequence alignment of a particular kinase (e.g., PIM-1) with other kinases). Such alignment of some kinases is provided in Table 3.

[0189] Conservative amino acid substitutions are well known in the art, and include substitutions made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the amino acid residues involved. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; amino acids with uncharged polar head groups having similar hydrophilicity values include the following: leucine, isoleucine, valine; glycine, alanine; asparagine, glutamine; serine, threonine; phenylalanine, tyrosine. Other conservative amino acid substitutions are well known in the art.

[0190] For kinases obtained in whole or in part by chemical synthesis, the selection of amino acids available for substitution or addition is not limited to the genetically encoded amino acids. Indeed, the mutants described herein may contain non-genetically encoded amino acids. Conservative amino acid substitutions for many of the commonly known non-genetically encoded amino acids are well known in the art. Conservative substitutions for other amino acids can be determined based on their physical properties as compared to the properties of the genetically encoded amino acids.

[0191] In some instances, it may be particularly advantageous or convenient to substitute, delete and/or add amino acid residues to a native kinase in order to provide convenient cloning sites in cDNA encoding the polypeptide, to aid in purification of the polypeptide, and for crystallization of the polypeptide. Such substitutions, deletions and/or additions which do not substantially alter the three dimensional structure of the native kinase domain will be apparent to those of ordinary skill in the art.

[0192] It should be noted that the mutants contemplated herein need not all exhibit kinase activity. Indeed, amino acid substitutions, additions or deletions that interfere with the kinase activity but which do not significantly alter the three-dimensional structure of the domain are specifically contemplated by the invention. Such crystalline polypeptides, or the atomic structure coordinates obtained therefrom, can be used to identify compounds that bind to the native domain. These compounds can affect the activity of the native domain.

[0193] The derivative crystals of the invention can comprise a crystalline kinase polypeptide in covalent association with one or more heavy metal atoms. The polypeptide may correspond to a native or a mutated kinase. Heavy metal atoms useful for providing derivative crystals include, by way of example and not limitation, gold, mercury, selenium, etc.

[0194] The co-crystals of the invention generally comprise a crystalline kinase domain polypeptide in association with one or more compounds. The association may be covalent or non-covalent. Such compounds include, but are not limited to, cofactors, substrates, substrate analogues, inhibitors, allosteric effectors, etc.

[0195] Exemplary mutations for PIM family kinases include the substitution or of the proline at the site corresponding to residue 123 in human PIM-1. One useful substitution is a proline to methionine substitution at residue 123 (P123M). Such substitution is useful, for example, to assist in using PIM family kinases to model other kinases that do not have proline at that site. Additional exemplary mutations include substitution or deletion of one or more of PIM-1 residues 124-128 or a residue from another PIM aligning with PIM-1 residues 124-128. For example, a PIM residue aligning with PIM-1 residue 128 can be deleted. Mutations at other sites can likewise be carried out, *e.g.*, to make a mutated PIM family kinase more similar to another kinase for structure modeling and/or compound fitting purposes.

III. Three Dimensional Structure Determination Using X-ray Crystallography

[0196] X-ray crystallography is a method of solving the three dimensional structures of molecules. The structure of a molecule is calculated from X-ray diffraction patterns using a crystal as a diffraction grating. Three dimensional structures of protein molecules arise from crystals grown from a concentrated aqueous solution of that protein. The process of X-ray crystallography can include the following steps:

(a) synthesizing and isolating (or otherwise obtaining) a polypeptide;

(b) growing a crystal from an aqueous solution comprising the polypeptide with or without a modulator; and

(c) collecting X-ray diffraction patterns from the crystals, determining unit cell dimensions and symmetry, determining electron density, fitting the amino acid sequence of the polypeptide to the electron density, and refining the structure.

Production of Polypeptides

[0197] The native and mutated kinase polypeptides described herein may be chemically synthesized in whole or part using techniques that are well-known in the art (*see, e.g.*, Creighton (1983) Biopolymers 22(1):49-58).

[0198] Alternatively, methods which are well known to those skilled in the art can be used to construct expression vectors containing the native or mutated kinase polypeptide coding sequence and appropriate transcriptional/translational control signals. These methods include *in vitro* recombinant DNA techniques, synthetic techniques and *in vivo* recombination/genetic recombination. See, for example, the techniques described in Maniatis, T (1989). Molecular cloning: A laboratory Manual. Cold Spring Harbor Laboratory, New York. Cold Spring Harbor Laboratory Press; and Ausubel, F.M. et al. (1994) Current Protocols in Molecular Biology. John Wiley & Sons, Secaucus, N.J.

[0199] A variety of host-expression vector systems may be utilized to express the kinase coding sequence. These include but are not limited to microorganisms such as bacteria transformed with recombinant bacteriophage DNA, plasmid DNA or cosmid DNA expression vectors containing the kinase domain coding sequence; yeast transformed with recombinant yeast expression vectors containing the kinase domain coding sequence; insect cell systems infected with recombinant virus expression vectors (*e.g.*, baculovirus)

containing the kinase domain coding sequence; plant cell systems infected with recombinant virus expression vectors (*e.g.*, cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or transformed with recombinant plasmid expression vectors (*e.g.*, Ti plasmid) containing the kinase domain coding sequence; or animal cell systems. The expression elements of these systems vary in their strength and specificities.

[0200] Depending on the host/vector system utilized, any of a number of suitable transcription and translation elements, including constitutive and inducible promoters, may be used in the expression vector. For example, when cloning in bacterial systems, inducible promoters such as pL of bacteriophage λ, plac, ptrp, ptac (ptrp-lac hybrid promoter) and the like may be used; when cloning in insect cell systems, promoters such as the baculovirus polyhedrin promoter may be used; when cloning in plant cell systems, promoters derived from the genome of plant cells (*e.g.*, heat shock promoters; the promoter for the small subunit of RUBISCO; the promoter for the chlorophyll a/b binding protein) or from plant viruses (*e.g.*, the 35S RNA promoter of CaMV; the coat protein promoter of TMV) may be used; when cloning in mammalian cell systems, promoters derived from the genome of mammalian cells (*e.g.*, metallothionein promoter) or from mammalian viruses (*e.g.*, the adenovirus late promoter; the vaccinia virus 7.5K promoter) may be used; when generating cell lines that contain multiple copies of the kinase domain DNA, SV4O-, BPV- and EBV-based vectors may be used with an appropriate selectable marker.

[0201] Exemplary methods describing methods of DNA manipulation, vectors, various types of cells used, methods of incorporating the vectors into the cells, expression techniques, protein purification and isolation methods, and protein concentration methods are disclosed in detail in PCT publication WO 96/18738. This publication is incorporated herein by reference in its entirety, including any drawings. Those skilled in the art will appreciate that such descriptions are applicable to the present invention and can be easily adapted to it.

Crystal Growth

[0202] Crystals are grown from an aqueous solution containing the purified and concentrated polypeptide by a variety of techniques. These techniques include batch, liquid, bridge, dialysis, vapor diffusion, and hanging drop methods. McPherson (1982) John Wiley, New York; McPherson (1990) *Eur. J. Biochem.* 189:1-23; Webber (1991) *Adv. Protein*

Chem. 41:1-36, incorporated by reference herein in their entireties, including all figures, tables, and drawings.

[0203] The native crystals of the invention are, in general, grown by adding precipitants to the concentrated solution of the polypeptide. The precipitants are added at a concentration just below that necessary to precipitate the protein. Water is removed by controlled evaporation to produce precipitating conditions, which are maintained until crystal growth ceases.

[0204] For crystals of the invention, exemplary crystallization conditions are described in the Examples. Those of ordinary skill in the art will recognize that the exemplary crystallization conditions can be varied. Such variations may be used alone or in combination. In addition, other crystallizations may be found, *e.g.*, by using crystallization screening plates to identify such other conditions.

[0205] Derivative crystals of the invention can be obtained by soaking native crystals in mother liquor containing salts of heavy metal atoms. It has been found that soaking a native crystal in a solution containing about 0.1 mM to about 5 mM thimerosal, 4-chloromeruribenzoic acid or $KAu(CN)_2$ for about 2 hr to about 72 hr provides derivative crystals suitable for use as isomorphous replacements in determining the X-ray crystal structure of PIM-1.

[0206] Co-crystals of the invention can be obtained by soaking a native crystal in mother liquor containing compound that binds the kinase, or can be obtained by co-crystallizing the kinase polypeptide in the presence of a binding compound.

[0207] Generally, co-crystallization of kinase and binding compound can be accomplished using conditions identified for crystallizing the corresponding kinase without binding compound. It is advantageous if a plurality of different crystallization conditions have been identified for the kinase, and these can be tested to determine which condition gives the best co-crystals. It may also be beneficial to optimize the conditions for co-crystallization. Exemplary co-crystallization conditions are provided in the Examples.

Determining Unit Cell Dimensions and the Three Dimensional Structure of a Polypeptide or Polypeptide Complex

[0208] Once the crystal is grown, it can be placed in a glass capillary tube or other mounting device and mounted onto a holding device connected to an X-ray generator and an X-ray detection device. Collection of X-ray diffraction patterns are well documented by those in the art. See, *e.g.*, Ducruix and Geige, (1992), IRL Press, Oxford, England, and references cited therein. A beam of X-rays enters the crystal and then diffracts from the crystal. An X-ray detection device can be utilized to record the diffraction patterns emanating from the crystal. Although the X-ray detection device on older models of these instruments is a piece of film, modern instruments digitally record X-ray diffraction scattering. X-ray sources can be of various types, but advantageously, a high intensity source is used, *e.g.*, a synchrotron beam source.

[0209] Methods for obtaining the three dimensional structure of the crystalline form of a peptide molecule or molecule complex are well known in the art. See, *e.g.*, Ducruix and Geige, (1992), IRL Press, Oxford, England, and references cited therein. The following are steps in the process of determining the three dimensional structure of a molecule or complex from X-ray diffraction data.

[0210] After the X-ray diffraction patterns are collected from the crystal, the unit cell dimensions and orientation in the crystal can be determined. They can be determined from the spacing between the diffraction emissions as well as the patterns made from these emissions. The unit cell dimensions are characterized in three dimensions in units of Angstroms (one Å= 10^{-10} meters) and by angles at each vertices. The symmetry of the unit cell in the crystals is also characterized at this stage. The symmetry of the unit cell in the crystal simplifies the complexity of the collected data by identifying repeating patterns. Application of the symmetry and dimensions of the unit cell is described below.

[0211] Each diffraction pattern emission is characterized as a vector and the data collected at this stage of the method determines the amplitude of each vector. The phases of the vectors can be determined using multiple techniques. In one method, heavy atoms can be soaked into a crystal, a method called isomorphous replacement, and the phases of the vectors can be determined by using these heavy atoms as reference points in the X-ray analysis. (Otwinowski, (1991), Daresbury, United Kingdom, 80-86). The isomorphous replacement method usually utilizes more than one heavy atom derivative. In another method, the amplitudes and phases of vectors from a crystalline polypeptide with an already determined structure can be applied to the amplitudes of the vectors from a crystalline

polypeptide of unknown structure and consequently determine the phases of these vectors. This second method is known as molecular replacement and the protein structure which is used as a reference must have a closely related structure to the protein of interest. (Naraza (1994) *Proteins* 11:281-296). Thus, the vector information from a kinase of known structure, such as those reported herein, are useful for the molecular replacement analysis of another kinase with unknown structure.

[0212] Once the phases of the vectors describing the unit cell of a crystal are determined, the vector amplitudes and phases, unit cell dimensions, and unit cell symmetry can be used as terms in a Fourier transform function. The Fourier transform function calculates the electron density in the unit cell from these measurements. The electron density that describes one of the molecules or one of the molecule complexes in the unit cell can be referred to as an electron density map. The amino acid structures of the sequence or the molecular structures of compounds complexed with the crystalline polypeptide may then be fitted to the electron density using a variety of computer programs. This step of the process is sometimes referred to as model building and can be accomplished by using computer programs such as Turbo/FRODO or "O". (Jones (1985) *Methods in Enzymology* 115:157-171).

[0213] A theoretical electron density map can then be calculated from the amino acid structures fit to the experimentally determined electron density. The theoretical and experimental electron density maps can be compared to one another and the agreement between these two maps can be described by a parameter called an R-factor. A low value for an R-factor describes a high degree of overlapping electron density between a theoretical and experimental electron density map.

[0214] The R-factor is then minimized by using computer programs that refine the theoretical electron density map. A computer program such as X-PLOR can be used for model refinement by those skilled in the art. Brünger (1992) *Nature 355:472-475.* Refinement may be achieved in an iterative process. A first step can entail altering the conformation of atoms defined in an electron density map. The conformations of the atoms can be altered by simulating a rise in temperature, which will increase the vibrational frequency of the bonds and modify positions of atoms in the structure. At a particular point in the atomic perturbation process, a force field, which typically defines interactions between atoms in terms of allowed bond angles and bond lengths, Van der Waals

interactions, hydrogen bonds, ionic interactions, and hydrophobic interactions, can be applied to the system of atoms. Favorable interactions may be described in terms of free energy and the atoms can be moved over many iterations until a free energy minimum is achieved. The refinement process can be iterated until the R-factor reaches a minimum value.

[0215] The three dimensional structure of the molecule or molecule complex is described by atoms that fit the theoretical electron density characterized by a minimum R-value. A file can then be created for the three dimensional structure that defines each atom by coordinates in three dimensions. An example of such a structural coordinate file is shown in Table 1.

IV. Structures of an Exemplary Kinase Domain: human PIM-1

[0216] As an example of kinase structure, high-resolution three-dimensional structures and atomic structure coordinates of crystalline PIM-1 and PIM-1 co-complexed with exemplary binding compounds as determined by X-ray crystallography are provided. The specific methods used to obtain the structure coordinates are provided in the examples. The atomic structure coordinates of crystalline PIM-1 are listed in Table 1, and atomic coordinates for PIM-1 co-crystallized with AMP-PMP are provided in Table 4. Co-crystal coordinates can be used in the same way, *e.g.*, in the various aspects described herein, as coordinates for the protein by itself.

[0217] Those having skill in the art will recognize that atomic structure coordinates as determined by X-ray crystallography are not without error. Thus, it is to be understood that any set of structure coordinates obtained for crystals of PIM-1, whether native crystals, derivative crystals or co-crystals, that have a root mean square deviation ("r.m.s.d.") of less than or equal to about 1.5 Å when superimposed, using backbone atoms (N, C_α, C and 0), on the structure coordinates listed in Table 1 (or Table 4) are considered to be identical with the structure coordinates listed in the Table 1 (or Table 4) when at least about 50% to 100% of the backbone atoms of PIM-1 are included in the superposition.

[0218] In addition to the PIM-1 structures provided herein, additional protein kinase structures are available and can be used, for example, publicly available structures deposited in the Protein Data Bank (PDB) (available for example, over the Internet). Higher quality structures are preferred (e.g., at least 2.5, 2.2, 2.0, 1.8, 1.7, 1.6, 1.5, 1.4, 1.3, or 1.2Å

resolution, as they provide more or more precise information for compound fitting and selection or design of derivatives.

V. Uses of the Crystals and Atomic Structure Coordinates

[0219] Kinase crystals, and particularly the atomic structure coordinates obtained therefrom, have a wide variety of uses. For example, the kinase crystals such as those described herein can be used as a starting point in any of the methods of use for kinases known in the art or later developed. Such methods of use include, for example, identifying molecules that bind to the native or mutated catalytic domain of kinases. The crystals and structure coordinates are particularly useful for identifying ligands that modulate kinase activity as an approach towards developing new therapeutic agents. In particular, the crystals and structural information are useful in methods for ligand development utilizing molecular scaffolds.

[0220] The structure coordinates described herein can be used as phasing models for determining the crystal structures of additional kinases, as well as the structures of co-crystals of such kinases with ligands such as inhibitors, agonists, antagonists, and other molecules. The structure coordinates, as well as models of the three-dimensional structures obtained therefrom, can also be used to aid the elucidation of solution-based structures of native or mutated kinases, such as those obtained via NMR.

VI. Electronic Representations of Kinase Structures

[0221] Structural information of kinases or portions of kinases (*e.g.*, kinase active sites) can be represented in many different ways. Particularly useful are electronic representations, as such representations allow rapid and convenient data manipulations and structural modifications. Electronic representations can be embedded in many different storage or memory media, frequently computer readable media. Examples include without limitations, computer random access memory (RAM), floppy disk, magnetic hard drive, magnetic tape (analog or digital), compact disk (CD), optical disk, CD-ROM, memory card, digital video disk (DVD), and others. The storage medium can be separate or part of a computer system. Such a computer system may be a dedicated, special purpose, or embedded system, such as a computer system that forms part of an X-ray crystallography system, or may be a general purpose computer (which may have data connection with other equipment such as a sensor device in an X-ray crystallographic system. In many cases, the

information provided by such electronic representations can also be represented physically or visually in two or three dimensions, *e.g.*, on paper, as a visual display (*e.g.*, on a computer monitor as a two dimensional or pseudo-three dimensional image) or as a three dimensional physical model. Such physical representations can also be used, alone or in connection with electronic representations. Exemplary useful representations include, but are not limited to, the following:

Atomic Coordinate Representation

[0222] One type of representation is a list or table of atomic coordinates representing positions of particular atoms in a molecular structure, portions of a structure, or complex (*e.g.*, a co-crystal). Such a representation may also include additional information, for example, information about occupancy of particular coordinates.

Energy Surface or Surface of Interaction Representation

[0223] Another representation is an energy surface representation, *e.g.*, of an active site or other binding site, representing an energy surface for electronic and steric interactions. Such a representation may also include other features. An example is the inclusion of representation of a particular amino acid residue(s) or group(s) on a particular amino acid residue(s), *e.g.*, a residue or group that can participate in H-bonding or ionic interaction.

Structural Representation

[0224] Still another representation is a structural representation, *i.e.*, a physical representation or an electronic representation of such a physical representation. Such a structural representation includes representations of relative positions of particular features of a molecule or complex, often with linkage between structural features. For example, a structure can be represented in which all atoms are linked; atoms other than hydrogen are linked; backbone atoms, with or without representation of side chain atoms that could participate in significant electronic interaction, are linked; among others. However, not all features need to be linked. For example, for structural representations of portions of a molecule or complex, structural features significant for that feature may be represented (*e.g.*, atoms of amino acid residues that can have significant binding interaction with a ligand at a binding site. Those amino acid residues may not be linked with each other.

[0225] A structural representation can also be a schematic representation. For example, a schematic representation can represent secondary and/or tertiary structure in a schematic

manner. Within such a schematic representation of a polypeptide, a particular amino acid residue(s) or group(s) on a residue(s) can be included, *e.g.*, conserved residues in a binding site, and/or residue(s) or group(s) that may interact with binding compounds.

VII. Structure Determination for Kinases with Unknown Structure Using Structural Coordinates

[0226] Structural coordinates, such as those set forth in Table 1, can be used to determine the three dimensional structures of kinases with unknown structure. The methods described below can apply structural coordinates of a polypeptide with known structure to another data set, such as an amino acid sequence, X-ray crystallographic diffraction data, or nuclear magnetic resonance (NMR) data. Preferred embodiments of the invention relate to determining the three dimensional structures of other PIM kinases, other serine/threonine kinases, and related polypeptides.

Structures Using Amino Acid Homology

[0227] Homology modeling is a method of applying structural coordinates of a polypeptide of known structure to the amino acid sequence of a polypeptide of unknown structure. This method is accomplished using a computer representation of the three dimensional structure of a polypeptide or polypeptide complex, the computer representation of amino acid sequences of the polypeptides with known and unknown structures, and standard computer representations of the structures of amino acids. Homology modeling generally involves (a) aligning the amino acid sequences of the polypeptides with and without known structure; (b) transferring the coordinates of the conserved amino acids in the known structure to the corresponding amino acids of the polypeptide of unknown structure; refining the subsequent three dimensional structure; and (d) constructing structures of the rest of the polypeptide. One skilled in the art recognizes that conserved amino acids between two proteins can be determined from the sequence alignment step in step (a).

[0228] The above method is well known to those skilled in the art. (Greer (1985) *Science* 228:1055; Blundell et *al.* A(1988) *Eur. J. Biochemi.* 172:513. An exemplary computer program that can be utilized for homology modeling by those skilled in the art is the Homology module in the Insight II modeling package distributed by Accelerys Inc.

[0229] Alignment of the amino acid sequence is accomplished by first placing the computer representation of the amino acid sequence of a polypeptide with known structure

above the amino acid sequence of the polypeptide of unknown structure. Amino acids in the sequences are then compared and groups of amino acids that are homologous (e.g., amino acid side chains that are similar in chemical nature - aliphatic, aromatic, polar, or charged) are grouped together. This method will detect conserved regions of the polypeptides and account for amino acid insertions or deletions.

[0230] Once the amino acid sequences of the polypeptides with known and unknown structures are aligned, the structures of the conserved amino acids in the computer representation of the polypeptide with known structure are transferred to the corresponding amino acids of the polypeptide whose structure is unknown. For example, a tyrosine in the amino acid sequence of known structure may be replaced by a phenylalanine, the corresponding homologous amino acid in the amino acid sequence of unknown structure.

[0231] The structures of amino acids located in non-conserved regions are to be assigned manually by either using standard peptide geometries or molecular simulation techniques, such as molecular dynamics. The final step in the process is accomplished by refining the entire structure using molecular dynamics and/or energy minimization. The homology modeling method is well known to those skilled in the art and has been practiced using different protein molecules. For example, the three dimensional structure of the polypeptide corresponding to the catalytic domain of a serine/threonine protein kinase, myosin light chain protein kinase, was homology modeled from the cAMP-dependent protein kinase catalytic subunit. (Knighton et *al.* (1992) *Science* 258:130-135.)

Structures Using Molecular Replacement

[0232] Molecular replacement is a method of applying the X-ray diffraction data of a polypeptide of known structure to the X-ray diffraction data of a polypeptide of unknown sequence. This method can be utilized to define the phases describing the X-ray diffraction data of a polypeptide of unknown structure when only the amplitudes are known. X-PLOR is a commonly utilized computer software package used for molecular replacement. Brünger (1992) *Nature* 355:472-475. AMORE is another program used for molecular replacement. Navaza (1994) *Acta Crystallogr.* A50:157-163. Preferably, the resulting structure does not exhibit a root-mean-square deviation of more than 3Å.

[0233] A goal of molecular replacement is to align the positions of atoms in the unit cell by matching electron diffraction data from two crystals. A program such as X-PLOR can involve four steps. A first step can be to determine the number of molecules in the unit cell

and define the angles between them. A second step can involve rotating the diffraction data to define the orientation of the molecules in the unit cell. A third step can be to translate the electron density in three dimensions to correctly position the molecules in the unit cell. Once the amplitudes and phases of the X-ray diffraction data is determined, an R-factor can be calculated by comparing electron diffraction maps calculated experimentally from the reference data set and calculated from the new data set. An R-factor between 30-50% indicates that the orientations of the atoms in the unit cell are reasonably determined by this method. A fourth step in the process can be to decrease the R-factor to roughly 20% by refining the new electron density map using iterative refinement techniques described herein and known to those or ordinary skill in the art.

Structures Using NMR Data

[0234] Structural coordinates of a polypeptide or polypeptide complex derived from X-ray crystallographic techniques can be applied towards the elucidation of three dimensional structures of polypeptides from nuclear magnetic resonance (NMR) data. This method is used by those skilled in the art. (Wuthrich, (1986), John Wiley and Sons, New York:176-199; Pflugrath et *al.* (1986) *J. Mol. Biol.* 189:383-386; Kline *et al.* (1986) *J. Mol. Biol.* 189:377-382). While the secondary structure of a polypeptide is often readily determined by utilizing two-dimensional NMR data, the spatial connections between individual pieces of secondary structure are not as readily determinable. The coordinates defining a three-dimensional structure of a polypeptide derived from X-ray crystallographic techniques can guide the NMR spectroscopist to an understanding of these spatial interactions between secondary structural elements in a polypeptide of related structure.

[0235] The knowledge of spatial interactions between secondary structural elements can greatly simplify Nuclear Overhauser Effect (NOE) data from two-dimensional NMR experiments. Additionally, applying the crystallographic coordinates after the determination of secondary structure by NMR techniques only simplifies the assignment of NOEs relating to particular amino acids in the polypeptide sequence and does not greatly bias the NMR analysis of polypeptide structure. Conversely, using the crystallographic coordinates to simplify NOE data while determining secondary structure of the polypeptide would bias the NMR analysis of protein structure.

VIII. Structure-Based Design of Modulators of Kinase Function Utilizing Structural Coordinates

[0236] Structure-based modulator design and identification methods are powerful techniques that can involve searches of computer databases containing a wide variety of potential modulators and chemical functional groups. The computerized design and identification of modulators is useful as the computer databases contain more compounds than the chemical libraries, often by an order of magnitude. For reviews of structure-based drug design and identification (*see* Kuntz et *al.* (1994), *Acc. Chem. Res.* 27:117; Guida (1994) *Current Opinion in Struc. Biol.* 4: 777; Colman (1994) *Current Opinion in Struc. Biol.* 4: 868).

[0237] The three dimensional structure of a polypeptide defined by structural coordinates can be utilized by these design methods, for example, the structural coordinates of Table 1. In addition, the three dimensional structures of kinases determined by the homology, molecular replacement, and NMR techniques described herein can also be applied to modulator design and identification methods.

[0238] For identifying modulators, structural information for a native kinase, in particular, structural information for the active site of the kinase, can be used. However, it may be advantageous to utilize structural information from one or more co-crystals of the kinase with one or more binding compounds. It can also be advantageous if the binding compound has a structural core in common with test compounds.

Design by Searching Molecular Data Bases

[0239] One method of rational design searches for modulators by docking the computer representations of compounds from a database of molecules. Publicly available databases include, for example:

a) ACD from Molecular Designs Limited
b) NCI from National Cancer Institute
c) CCDC from Cambridge Crystallographic Data Center
d) CAST from Chemical Abstract Service
e) Derwent from Derwent Information Limited
f) Maybridge from Maybridge Chemical Company LTD
g) Aldrich from Aldrich Chemical Company
h) Directory of Natural Products from Chapman & Hall

[0240] One such data base (ACD distributed by Molecular Designs Limited Information Systems) contains compounds that are synthetically derived or are natural products.

Methods available to those skilled in the art can convert a data set represented in two dimensions to one represented in three dimensions. These methods are enabled by such computer programs as CONCORD from Tripos Associates or DE-Converter from Molecular Simulations Limited.

[0241] Multiple methods of structure-based modulator design are known to those in the art. (Kuntz et *al.*, (1982), *J. Mol. Biol. 162:* 269; Kuntz et al., (1994), *Acc. Chem. Res. 27:* 117; Meng *et al.*, (1992), *J. Compt. Chem. 13:* 505; Bohm, (1994), *J. Comp. Aided Molec. Design 8:* 623).

[0242] A computer program widely utilized by those skilled in the art of rational modulator design is DOCK from the University of California in San Francisco. The general methods utilized by this computer program and programs like it are described in three applications below. More detailed information regarding some of these techniques can be found in the Accelerys User Guide, 1995. A typical computer program used for this purpose can comprise the following steps:

(a) remove the existing compound from the protein;

(b) dock the structure of another compound into the active-site using the computer program (such as DOCK) or by interactively moving the compound into the active-site;

(c) characterize the space between the compound and the active-site atoms;

(d) search libraries for molecular fragments which (i) can fit into the empty space between the compound and the active-site, and (ii) can be linked to the compound; and

(e) link the fragments found above to the compound and evaluate the new modified compound.

[0243] Part (c) refers to characterizing the geometry and the complementary interactions formed between the atoms of the active site and the compounds. A favorable geometric fit is attained when a significant surface area is shared between the compound and active-site atoms without forming unfavorable steric interactions. One skilled in the art would note that the method can be performed by skipping parts (d) and (e) and screening a database of many compounds.

[0244] Structure-based design and identification of modulators of kinase function can be used in conjunction with assay screening. As large computer databases of compounds

(around 10,000 compounds) can be searched in a matter of hours, the computer-based method can narrow the compounds tested as potential modulators of kinase function in biochemical or cellular assays.

[0245] The above descriptions of structure-based modulator design are not all encompassing and other methods are reported in the literature:

(1) CAVEAT: Bartlett *et* al.,(1989), in Chemical and Biological Problems in Molecular Recognition, Roberts, S.M.; Ley, S.V.; Campbell, M.M. eds.; *Royal Society of Chemistry*: Cambridge, ppl82-l96.

(2) FLOG: Miller et al., (1994), *J. Comp. Aided Molec. Design* 8:153.

(3) PRO Modulator: Clark *et al.,* (1995), *J. Comp. Aided Molec. Design* 9:13.

(4) MCSS: Miranker and Karplus, (1991), *Proteins: Structure, Function, and Genetics 11:29.*

(5) AUTODOCK: Goodsell and Olson, (1990), *Proteins: Structure, Function, and Genetics 8:195.*

(6) GRID: Goodford, (1985), *J. Med. Chem.* 28:849.

Design by Modifying Compounds in Complex with a Kinase

[0246] Another way of identifying compounds as potential modulators is to modify an existing modulator in the polypeptide active site. For example, the computer representation of modulators can be modified within the computer representation of a PIM-1 or other PIM kinase active site. Detailed instructions for this technique can be found in the Accelerys User Manual, 1995 in LUDI. The computer representation of the modulator is typically modified by the deletion of a chemical group or groups or by the addition of a chemical group or groups.

[0247] Upon each modification to the compound, the atoms of the modified compound and active site can be shifted in conformation and the distance between the modulator and the active-site atoms may be scored along with any complementary interactions formed between the two molecules. Scoring can be complete when a favorable geometric fit and favorable complementary interactions are attained. Compounds that have favorable scores are potential modulators.

Design by Modifying the Structure of Compounds that Bind a Kinase

[0248] A third method of structure-based modulator design is to screen compounds designed by a modulator building or modulator searching computer program. Examples of these types of programs can be found in the Molecular Simulations Package, Catalyst. Descriptions for using this program are documented in the Molecular Simulations User Guide (1995). Other computer programs used in this application are ISIS/HOST, ISIS/BASE, ISIS/DRAW) from Molecular Designs Limited and UNITY from Tripos Associates.

[0249] These programs can be operated on the structure of a compound that has been removed from the active site of the three dimensional structure of a compound-kinase complex. Operating the program on such a compound is preferable since it is in a biologically active conformation.

[0250] A modulator construction computer program is a computer program that may be used to replace computer representations of chemical groups in a compound complexed with a kinase or other biomolecule with groups from a computer data base. A modulator searching computer program is a computer program that may be used to search computer representations of compounds from a computer data base that have similar three dimensional structures and similar chemical groups as compound bound to a particular biomolecule.

[0251] A typical program can operate by using the following general steps:

(a) map the compounds by chemical features such as by hydrogen bond donors or acceptors, hydrophobic/lipophilic sites, positively ionizable sites, or negatively ionizable sites;

(b) add geometric constraints to the mapped features; and

(c) search databases with the model generated in (b).

[0252] Those skilled in the art also recognize that not all of the possible chemical features of the compound need be present in the model of (b). One can use any subset of the model to generate different models for data base searches.

Modulator Design Using Molecular Scaffolds

[0253] The present invention can also advantageously utilize methods for designing compounds, designated as molecular scaffolds, that can act broadly across families of molecules and for using the molecular scaffold to design ligands that target individual or multiple members of those families. In preferred embodiments, the molecules can be proteins and a set of chemical compounds can be assembled that have properties such that they are 1) chemically designed to act on certain protein families and/or 2) behave more like molecular scaffolds, meaning that they have chemical substructures that make them specific for binding to one or more proteins in a family of interest. Alternatively, molecular scaffolds can be designed that are preferentially active on an individual target molecule.

[0254] Useful chemical properties of molecular scaffolds can include one or more of the following characteristics, but are not limited thereto: an average molecular weight below about 350 daltons, or between from about 150 to about 350 daltons, or from about 150 to about 300 daltons; having a clogP below 3; a number of rotatable bonds of less than 4; a number of hydrogen bond donors and acceptors below 5 or below 4; a polar surface area of less than 50 $Å^2$; binding at protein binding sites in an orientation so that chemical substituents from a combinatorial library that are attached to the scaffold can be projected into pockets in the protein binding site; and possessing chemically tractable structures at its substituent attachment points that can be modified, thereby enabling rapid library construction.

[0255] By "clog P" is meant the calculated log P of a compound, "P" referring to the partition coefficient between octanol and water.

[0256] The term "Molecular Polar Surface Area (PSA)" refers to the sum of surface contributions of polar atoms (usually oxygens, nitrogens and attached hydrogens) in a molecule. The polar surface area has been shown to correlate well with drug transport properties, such as intestinal absorption, or blood-brain barrier penetration.

[0257] Additional useful chemical properties of distinct compounds for inclusion in a combinatorial library include the ability to attach chemical moieties to the compound that will not interfere with binding of the compound to at least one protein of interest, and that will impart desirable properties to the library members, for example, causing the library members to be actively transported to cells and/or organs of interest, or the ability to attach

to a device such as a chromatography column (e.g., a streptavidin column through a molecule such as biotin) for uses such as tissue and proteomics profiling purposes.

[0258] A person of ordinary skill in the art will realize other properties that can be desirable for the scaffold or library members to have depending on the particular requirements of the use, and that compounds with these properties can also be sought and identified in like manner. Methods of selecting compounds for assay are known to those of ordinary skill in the art, for example, methods and compounds described in U.S. Patent No. 6,288,234, 6,090,912, 5,840,485, each of which is hereby incorporated by reference in its entirety, including all charts and drawings.

[0259] In various embodiments, the present invention provides methods of designing ligands that bind to a plurality of members of a molecular family, where the ligands contain a common molecular scaffold. Thus, a compound set can be assayed for binding to a plurality of members of a molecular family, e.g., a protein family. One or more compounds that bind to a plurality of family members can be identified as molecular scaffolds. When the orientation of the scaffold at the binding site of the target molecules has been determined and chemically tractable structures have been identified, a set of ligands can be synthesized starting with one or a few molecular scaffolds to arrive at a plurality of ligands, wherein each ligand binds to a separate target molecule of the molecular family with altered or changed binding affinity or binding specificity relative to the scaffold. Thus, a plurality of drug lead molecules can be designed to preferentially target individual members of a molecular family based on the same molecular scaffold, and act on them in a specific manner.

Binding Assays

[0260] The methods of the present invention can involve assays that are able to detect the binding of compounds to a target molecule at a signal of at least about three times the standard deviation of the background signal, or at least about four times the standard deviation of the background signal. The assays of the present invention can also include assaying compounds for low affinity binding to the target molecule. A large variety of assays indicative of binding are known for different target types and can be used for this invention. Compounds that act broadly across protein families are not likely to have a high affinity against individual targets, due to the broad nature of their binding. Thus, assays described herein allow for the identification of compounds that bind with low affinity, very

low affinity, and extremely low affinity. Therefore, potency (or binding affinity) is not the primary, nor even the most important, indicia of identification of a potentially useful binding compound. Rather, even those compounds that bind with low affinity, very low affinity, or extremely low affinity can be considered as molecular scaffolds that can continue to the next phase of the ligand design process.

[0261] By binding with "low affinity" is meant binding to the target molecule with a dissociation constant (k_d) of greater than 1 μM under standard conditions. By binding with "very low affinity" is meant binding with a k_d of above about 100 μM under standard conditions. By binding with "extremely low affinity" is meant binding at a k_d of above about 1 mM under standard conditions. By "moderate affinity" is meant binding with a k_d of from about 200 nM to about 1 μM under standard conditions. By "moderately high affinity" is meant binding at a k_d of from about 1 nM to about 200 nM. By binding at "high affinity" is meant binding at a k_d of below about 1 nM under standard conditions. For example, low affinity binding can occur because of a poorer fit into the binding site of the target molecule or because of a smaller number of non-covalent bonds, or weaker covalent bonds present to cause binding of the scaffold or ligand to the binding site of the target molecule relative to instances where higher affinity binding occurs. The standard conditions for binding are at pH 7.2 at 37°C for one hour. For example, 100 μl/well can be used in HEPES 50 mM buffer at pH 7.2, NaCl 15 mM, ATP 2 μM, and bovine serum albumin 1 ug/well, 37°C for one hour.

[0262] Binding compounds can also be characterized by their effect on the activity of the target molecule. Thus, a "low activity" compound has an inhibitory concentration (IC_{50}) or excitation concentration (EC_{50}) of greater than 1 μM under standard conditions. By "very low activity" is meant an IC_{50} or EC_{50} of above 100 μM under standard conditions. By "extremely low activity" is meant an IC_{50} or EC_{50} of above 1 mM under standard conditions. By "moderate activity" is meant an IC_{50} or EC_{50} of 200 nM to 1 μM under standard conditions. By "moderately high activity" is meant an IC_{50} or EC_{50} of 1 nM to 200 nM. By "high activity" is meant an IC_{50} or EC_{50} of below 1 nM under standard conditions. The IC_{50} (or EC_{50}) is defined as the concentration of compound at which 50% of the activity of the target molecule (e.g., enzyme or other protein) activity being measured is lost (or gained) relative to activity when no compound is present. Activity can be measured using methods known to those of ordinary skill in the art, *e.g.*, by measuring any detectable

product or signal produced by occurrence of an enzymatic reaction, or other activity by a protein being measured.

[0263] By "background signal" in reference to a binding assay is meant the signal that is recorded under standard conditions for the particular assay in the absence of a test compound, molecular scaffold, or ligand that binds to the target molecule. Persons of ordinary skill in the art will realize that accepted methods exist and are widely available for determining background signal.

[0264] By "standard deviation" is meant the square root of the variance. The variance is a measure of how spread out a distribution is. It is computed as the average squared deviation of each number from its mean. For example, for the numbers 1, 2, and 3, the mean is 2 and the variance is:

$$\sigma^2 = \frac{(1-2)^2 + (2-2)^2 + (3-2)^2}{3} = 0.667$$

[0265] To design or discover scaffolds that act broadly across protein families, proteins of interest can be assayed against a compound collection or set. The assays can preferably be enzymatic or binding assays. In some embodiments it may be desirable to enhance the solubility of the compounds being screened and then analyze all compounds that show activity in the assay, including those that bind with low affinity or produce a signal with greater than about three times the standard deviation of the background signal. The assays can be any suitable assay such as, for example, binding assays that measure the binding affinity between two binding partners. Various types of screening assays that can be useful in the practice of the present invention are known in the art, such as those described in U.S. Patent Nos. 5,763,198, 5,747,276, 5,877,007, 6,243,980, 6,294,330, and 6,294,330, each of which is hereby incorporated by reference in its entirety, including all charts and drawings.

[0266] In various embodiments of the assays at least one compound, at least about 5%, at least about 10%, at least about 15%, at least about 20%, or at least about 25% of the compounds can bind with low affinity. In general, up to about 20% of the compounds can show activity in the screening assay and these compounds can then be analyzed directly with high-throughput co-crystallography, computational analysis to group the compounds into classes with common structural properties (e.g., structural core and/or shape and polarity characteristics), and the identification of common chemical structures between compounds that show activity.

[0267] The person of ordinary skill in the art will realize that decisions can be based on criteria that are appropriate for the needs of the particular situation, and that the decisions can be made by computer software programs. Classes can be created containing almost any number of scaffolds, and the criteria selected can be based on increasingly exacting criteria until an arbitrary number of scaffolds is arrived at for each class that is deemed to be advantageous.

Surface Plasmon Resonance

[0268] Binding parameters can be measured using surface plasmon resonance, for example, with a BIAcore® chip (Biacore, Japan) coated with immobilized binding components. Surface plasmon resonance is used to characterize the microscopic association and dissociation constants of reaction between an sFv or other ligand directed against target molecules. Such methods are generally described in the following references which are incorporated herein by reference. Vely F. et al., (2000) BIAcore® analysis to test phosphopeptide-SH2 domain interactions, *Methods in Molecular Biology*. 121:313-21; Liparoto et al., (1999) Biosensor analysis of the interleukin-2 receptor complex, *Journal of Molecular Recognition*. 12:316-21; Lipschultz et al., (2000) Experimental design for analysis of complex kinetics using surface plasmon resonance, *Methods*. 20(3):310-8; Malmqvist., (1999) BIACORE: an affinity biosensor system for characterization of biomolecular interactions, Biochemical Society Transactions 27:335-40; Alfthan, (1998) Surface plasmon resonance biosensors as a tool in antibody engineering, *Biosensors & Bioelectronics*. 13:653-63; Fivash et al., (1998) BIAcore for macromolecular interaction, Current Opinion in Biotechnology. 9:97-101; Price et al.; (1998) Summary report on the ISOBM TD-4 Workshop: analysis of 56 monoclonal antibodies against the MUC1 mucin. *Tumour Biology* 19 Suppl 1:1-20; Malmqvist et al, (1997) Biomolecular interaction analysis: affinity biosensor technologies for functional analysis of proteins, *Current Opinion in Chemical Biology*. 1:378-83; O'Shannessy et al., (1996) Interpretation of deviations from pseudo-first-order kinetic behavior in the characterization of ligand binding by biosensor technology, *Analytical Biochemistry*. 236:275-83; Malmborg et al., (1995) BIAcore as a tool in antibody engineering, *Journal of Immunological Methods*. 183:7-13; Van Regenmortel, (1994) Use of biosensors to characterize recombinant proteins, *Developments in Biological Standardization*. 83:143-51; and O'Shannessy, (1994) Determination of kinetic rate and equilibrium binding constants for macromolecular

interactions: a critique of the surface plasmon resonance literature, *Current Opinions in Biotechnology*. 5:65-71.

[0269] BIAcore® uses the optical properties of surface plasmon resonance (SPR) to detect alterations in protein concentration bound to a dextran matrix lying on the surface of a gold/glass sensor chip interface, a dextran biosensor matrix. In brief, proteins are covalently bound to the dextran matrix at a known concentration and a ligand for the protein is injected through the dextran matrix. Near infrared light, directed onto the opposite side of the sensor chip surface is reflected and also induces an evanescent wave in the gold film, which in turn, causes an intensity dip in the reflected light at a particular angle known as the resonance angle. If the refractive index of the sensor chip surface is altered (e.g., by ligand binding to the bound protein) a shift occurs in the resonance angle. This angle shift can be measured and is expressed as resonance units (RUs) such that 1000 RUs is equivalent to a change in surface protein concentration of 1 ng/mm^2. These changes are displayed with respect to time along the y-axis of a sensorgram, which depicts the association and dissociation of any biological reaction.

High Throughput Screening (HTS) Assays

[0270] HTS typically uses automated assays to search through large numbers of compounds for a desired activity. Typically HTS assays are used to find new drugs by screening for chemicals that act on a particular enzyme or molecule. For example, if a chemical inactivates an enzyme it might prove to be effective in preventing a process in a cell which causes a disease. High throughput methods enable researchers to assay thousands of different chemicals against each target molecule very quickly using robotic handling systems and automated analysis of results.

[0271] As used herein, "high throughput screening" or "HTS" refers to the rapid in vitro screening of large numbers of compounds (libraries); generally tens to hundreds of thousands of compounds, using robotic screening assays. Ultra high-throughput Screening (uHTS) generally refers to the high-throughput screening accelerated to greater than 100,000 tests per day.

[0272] To achieve high-throughput screening, it is advantageous to house samples on a multicontainer carrier or platform. A multicontainer carrier facilitates measuring reactions of a plurality of candidate compounds simultaneously. Multi-well microplates may be used

as the carrier. Such multi-well microplates, and methods for their use in numerous assays, are both known in the art and commercially available.

[0273] Screening assays may include controls for purposes of calibration and confirmation of proper manipulation of the components of the assay. Blank wells that contain all of the reactants but no member of the chemical library are usually included. As another example, a known inhibitor (or activator) of an enzyme for which modulators are sought, can be incubated with one sample of the assay, and the resulting decrease (or increase) in the enzyme activity used as a comparator or control. It will be appreciated that modulators can also be combined with the enzyme activators or inhibitors to find modulators which inhibit the enzyme activation or repression that is otherwise caused by the presence of the known the enzyme modulator. Similarly, when ligands to a sphingolipid target are sought, known ligands of the target can be present in control/calibration assay wells.

Measuring Enzymatic and Binding Reactions During Screening Assays

[0274] Techniques for measuring the progression of enzymatic and binding reactions, e.g., in multicontainer carriers, are known in the art and include, but are not limited to, the following.

[0275] Spectrophotometric and spectrofluorometric assays are well known in the art. Examples of such assays include the use of colorimetric assays for the detection of peroxides, as disclosed in Example 1(b) and Gordon, A. J. and Ford, R. A., (1972) The Chemist's Companion: A Handbook Of Practical Data, Techniques, And References, John Wiley and Sons, N.Y., Page 437.

[0276] Fluorescence spectrometry may be used to monitor the generation of reaction products. Fluorescence methodology is generally more sensitive than the absorption methodology. The use of fluorescent probes is well known to those skilled in the art. For reviews, see Bashford et al., (1987) Spectrophotometry and Spectrofluorometry: A Practical Approach, pp. 91-114, IRL Press Ltd.; and Bell, (1981) Spectroscopy In Biochemistry, Vol. I, pp. 155-194, CRC Press.

[0277] In spectrofluorometric methods, enzymes are exposed to substrates that change their intrinsic fluorescence when processed by the target enzyme. Typically, the substrate is nonfluorescent and is converted to a fluorophore through one or more reactions. As a non-

limiting example, SMase activity can be detected using the Amplex® Red reagent (Molecular Probes, Eugene, OR). In order to measure sphingomyelinase activity using Amplex® Red, the following reactions occur. First, SMase hydrolyzes sphingomyelin to yield ceramide and phosphorylcholine. Second, alkaline phosphatase hydrolyzes phosphorylcholine to yield choline. Third, choline is oxidized by choline oxidase to betaine. Finally, H_2O_2, in the presence of horseradish peroxidase, reacts with Amplex® Red to produce the fluorescent product, Resorufin, and the signal therefrom is detected using spectrofluorometry.

[0278] Fluorescence polarization (FP) is based on a decrease in the speed of molecular rotation of a fluorophore that occurs upon binding to a larger molecule, such as a receptor protein, allowing for polarized fluorescent emission by the bound ligand. FP is empirically determined by measuring the vertical and horizontal components of fluorophore emission following excitation with plane polarized light. Polarized emission is increased when the molecular rotation of a fluorophore is reduced. A fluorophore produces a larger polarized signal when it is bound to a larger molecule (i.e. a receptor), slowing molecular rotation of the fluorophore. The magnitude of the polarized signal relates quantitatively to the extent of fluorescent ligand binding. Accordingly, polarization of the "bound" signal depends on maintenance of high affinity binding.

[0279] FP is a homogeneous technology and reactions are very rapid, taking seconds to minutes to reach equilibrium. The reagents are stable, and large batches may be prepared, resulting in high reproducibility. Because of these properties, FP has proven to be highly automatable, often performed with a single incubation with a single, premixed, tracer-receptor reagent. For a review, see Owickiet al., (1997), Application of Fluorescence Polarization Assays in High-Throughput Screening, *Genetic Engineering News*, 17:27.

[0280] FP is particularly desirable since its readout is independent of the emission intensity (Checovich, W. J., et al., (1995) *Nature* 375:254-256; Dandliker, W. B., et al., (1981) *Methods in Enzymology* 74:3-28) and is thus insensitive to the presence of colored compounds that quench fluorescence emission. FP and FRET (see below) are well-suited for identifying compounds that block interactions between sphingolipid receptors and their ligands. See, for example, Parker et al., (2000) Development of high throughput screening assays using fluorescence polarization: nuclear receptor-ligand-binding and kinase/phosphatase assays, *J Biomol Screen* 5:77-88.

[0281] Fluorophores derived from sphingolipids that may be used in FP assays are commercially available. For example, Molecular Probes (Eugene, OR) currently sells sphingomyelin and one ceramide fluorophores. These are, respectively, N-(4,4-difluoro-5,7-dimethyl-4-bora-3a,4a-diaza-s-indacene- 3-pentanoyl)sphingosyl phosphocholine (BODIPY® FL C5-sphingomyelin); N-(4,4-difluoro-5,7-dimethyl-4-bora-3a,4a-diaza-s-indacene- 3-dodecanoyl)sphingosyl phosphocholine (BODIPY® FL C12-sphingomyelin); and N-(4,4-difluoro-5,7-dimethyl-4-bora-3a,4a-diaza-s-indacene- 3-pentanoyl)sphingosine (BODIPY® FL C5-ceramide). U.S. Patent No. 4,150,949, (Immunoassay for gentamicin), discloses fluorescein-labelled gentamicins, including fluoresceinthiocarbanyl gentamicin. Additional fluorophores may be prepared using methods well known to the skilled artisan.

[0282] Exemplary normal-and-polarized fluorescence readers include the POLARION® fluorescence polarization system (Tecan AG, Hombrechtikon, Switzerland). General multiwell plate readers for other assays are available, such as the VERSAMAX® reader and the SPECTRAMAX® multiwell plate spectrophotometer (both from Molecular Devices).

[0283] Fluorescence resonance energy transfer (FRET) is another useful assay for detecting interaction and has been described. See, e.g., Heim et al., (1996) *Curr. Biol.* 6:178-182; Mitra et al., (1996) *Gene* 173:13-17; and Selvin et al., (1995) *Meth. Enzymol.* 246:300-345. FRET detects the transfer of energy between two fluorescent substances in close proximity, having known excitation and emission wavelengths. As an example, a protein can be expressed as a fusion protein with green fluorescent protein (GFP). When two fluorescent proteins are in proximity, such as when a protein specifically interacts with a target molecule, the resonance energy can be transferred from one excited molecule to the other. As a result, the emission spectrum of the sample shifts, which can be measured by a fluorometer, such as a fMAX multiwell fluorometer (Molecular Devices, Sunnyvale Calif.).

[0284] Scintillation proximity assay (SPA) is a particularly useful assay for detecting an interaction with the target molecule. SPA is widely used in the pharmaceutical industry and has been described (Hanselman et al., (1997) *J. Lipid Res.* 38:2365-2373; Kahl et al., (1996) *Anal. Biochem.* 243:282-283; Undenfriend et al., (1987) *Anal. Biochem.* 161:494-500). See also U.S. Patent Nos. 4,626,513 and 4,568,649, and European Patent No. 0,154,734. One commercially available system uses FLASHPLATE® scintillant-coated plates (NEN Life Science Products, Boston, MA).

[0285] The target molecule can be bound to the scintillator plates by a variety of well known means. Scintillant plates are available that are derivatized to bind to fusion proteins such as GST, His6 or Flag fusion proteins. Where the target molecule is a protein complex or a multimer, one protein or subunit can be attached to the plate first, then the other components of the complex added later under binding conditions, resulting in a bound complex.

[0286] In a typical SPA assay, the gene products in the expression pool will have been radiolabeled and added to the wells, and allowed to interact with the solid phase, which is the immobilized target molecule and scintillant coating in the wells. The assay can be measured immediately or allowed to reach equilibrium. Either way, when a radiolabel becomes sufficiently close to the scintillant coating, it produces a signal detectable by a device such as a TOPCOUNT NXT® microplate scintillation counter (Packard BioScience Co., Meriden Conn.). If a radiolabeled expression product binds to the target molecule, the radiolabel remains in proximity to the scintillant long enough to produce a detectable signal.

[0287] In contrast, the labeled proteins that do not bind to the target molecule, or bind only briefly, will not remain near the scintillant long enough to produce a signal above background. Any time spent near the scintillant caused by random Brownian motion will also not result in a significant amount of signal. Likewise, residual unincorporated radiolabel used during the expression step may be present, but will not generate significant signal because it will be in solution rather than interacting with the target molecule. These non-binding interactions will therefore cause a certain level of background signal that can be mathematically removed. If too many signals are obtained, salt or other modifiers can be added directly to the assay plates until the desired specificity is obtained (Nichols et al., (1998) *Anal. Biochem.* 257:112-119).

Assay Compounds and Molecular Scaffolds

[0288] Preferred characteristics of a scaffold include being of low molecular weight (e.g., less than 350 Da, or from about 100 to about 350 daltons, or from about 150 to about 300 daltons). Preferably clog P of a scaffold is from –1 to 8, more preferably less than 6, 5, or 4, most preferably less than 3. In particular embodiments the clogP is in a range –1 to an upper limit of 2, 3, 4, 5, 6, or 8; or is in a range of 0 to an upper limit of 2,3, 4, 5, 6, or 8. Preferably the number of rotatable bonds is less than 5, more preferably less than 4. Preferably the number of hydrogen bond donors and acceptors is below 6, more preferably

below 5. An additional criterion that can be useful is a polar surface area of less than 5. Guidance that can be useful in identifying criteria for a particular application can be found in Lipinski et al., (1997) *Advanced Drug Delivery Reviews* 23 3-25, which is hereby incorporated by reference in its entirety.

[0289] A scaffold may preferably bind to a given protein binding site in a configuration that causes substituent moieties of the scaffold to be situated in pockets of the protein binding site. Also, possessing chemically tractable groups that can be chemically modified, particularly through synthetic reactions, to easily create a combinatorial library can be a preferred characteristic of the scaffold. Also preferred can be having positions on the scaffold to which other moieties can be attached, which do not interfere with binding of the scaffold to the protein(s) of interest but do cause the scaffold to achieve a desirable property, for example, active transport of the scaffold to cells and/or organs, enabling the scaffold to be attached to a chromatographic column to facilitate analysis, or another desirable property. A molecular scaffold can bind to a target molecule with any affinity, such as binding with an affinity measurable as about three times the standard deviation of the background signal, or at high affinity, moderate affinity, low affinity, very low affinity, or extremely low affinity.

[0290] Thus, the above criteria can be utilized to select many compounds for testing that have the desired attributes. Many compounds having the criteria described are available in the commercial market, and may be selected for assaying depending on the specific needs to which the methods are to be applied.

[0291] A "compound library" or "library" is a collection of different compounds having different chemical structures. A compound library is screenable, that is, the compound library members therein may be subject to screening assays. In preferred embodiments, the library members can have a molecular weight of from about 100 to about 350 daltons, or from about 150 to about 350 daltons. Examples of libraries are provided above.

[0292] Libraries of the present invention can contain at least one compound than binds to the target molecule at low affinity. Libraries of candidate compounds can be assayed by many different assays, such as those described above, e.g., a fluorescence polarization assay. Libraries may consist of chemically synthesized peptides, peptidomimetics, or arrays of combinatorial chemicals that are large or small, focused or nonfocused. By "focused" it

is meant that the collection of compounds is prepared using the structure of previously characterized compounds and/or pharmacophores.

[0293] Compound libraries may contain molecules isolated from natural sources, artificially synthesized molecules, or molecules synthesized, isolated, or otherwise prepared in such a manner so as to have one or more moieties variable, e.g., moieties that are independently isolated or randomly synthesized. Types of molecules in compound libraries include but are not limited to organic compounds, polypeptides and nucleic acids as those terms are used herein, and derivatives, conjugates and mixtures thereof.

[0294] Compound libraries of the invention may be purchased on the commercial market or prepared or obtained by any means including, but not limited to, combinatorial chemistry techniques, fermentation methods, plant and cellular extraction procedures and the like (see, e.g., Cwirla et al., (1990) *Biochemistry*, 87, 6378-6382; Houghten et al., (1991) *Nature*, 354, 84-86; Lam et al., (1991) *Nature*, 354, 82-84; Brenner et al., (1992) *Proc. Natl. Acad. Sci. USA*, 89, 5381-5383; R. A. Houghten, (1993) *Trends Genet.*, 9, 235-239; E. R. Felder, (1994) *Chimia*, 48, 512-541; Gallop et al., (1994) *J. Med. Chem.*, 37, 1233-1251; Gordon et al., (1994) *J. Med. Chem.*, 37, 1385-1401; Carell et al., (1995) *Chem. Biol.*, 3, 171-183; Madden et al., *Perspectives in Drug Discovery and Design* 2, 269-282; Lebl et al., (1995) *Biopolymers*, 37 177-198); small molecules assembled around a shared molecular structure; collections of chemicals that have been assembled by various commercial and noncommercial groups, natural products; extracts of marine organisms, fungi, bacteria, and plants.

[0295] Preferred libraries can be prepared in a homogenous reaction mixture, and separation of unreacted reagents from members of the library is not required prior to screening. Although many combinatorial chemistry approaches are based on solid state chemistry, liquid phase combinatorial chemistry is capable of generating libraries (Sun CM., (1999) Recent advances in liquid-phase combinatorial chemistry, *Combinatorial Chemistry & High Throughput Screening*. 2:299-318).

[0296] Libraries of a variety of types of molecules are prepared in order to obtain members therefrom having one or more preselected attributes that can be prepared by a variety of techniques, including but not limited to parallel array synthesis (Houghton, (2000) *Annu Rev Pharmacol Toxicol* 40:273-82, Parallel array and mixture-based synthetic combinatorial chemistry; solution-phase combinatorial chemistry (Merritt, (1998) *Comb*

Chem High Throughput Screen 1(2):57-72, Solution phase combinatorial chemistry, Coe et al., (1998-99) *Mol Divers*; 4(1):31-8, Solution-phase combinatorial chemistry, Sun, (1999) *Comb Chem High Throughput Screen* 2(6):299-318, Recent advances in liquid-phase combinatorial chemistry); synthesis on soluble polymer (Gravert et al., (1997) *Curr Opin Chem Biol* 1(1):107-13, Synthesis on soluble polymers: new reactions and the construction of small molecules); and the like. See, e.g., Dolle et al., (1999) *J Comb Chem* 1(4):235-82, Comprehensive survey of combinatorial library synthesis: 1998. Freidinger RM., (1999) Nonpeptidic ligands for peptide and protein receptors, Current Opinion in Chemical Biology; and Kundu et al., *Prog Drug Res*;53:89-156, Combinatorial chemistry: polymer supported synthesis of peptide and non-peptide libraries). Compounds may be clinically tagged for ease of identification (Chabala, (1995) *Curr Opin Biotechnol* 6(6):633-9, Solid-phase combinatorial chemistry and novel tagging methods for identifying leads).

[0297] The combinatorial synthesis of carbohydrates and libraries containing oligosaccharides have been described (Schweizer et al., (1999) *Curr* Opin *Chem Biol* 3(3):291-8, Combinatorial synthesis of carbohydrates). The synthesis of natural-product based compound libraries has been described (Wessjohann, (2000) *Curr Opin Chem Biol* 4(3):303-9, Synthesis of natural-product based compound libraries).

[0298] Libraries of nucleic acids are prepared by various techniques, including by way of non-limiting example the ones described herein, for the isolation of aptamers. Libraries that include oligonucleotides and polyaminooligonucleotides (Markiewicz et al., (2000) Synthetic oligonucleotide combinatorial libraries and their applications, *Farmaco.* 55:174-7) displayed on streptavidin magnetic beads are known. Nucleic acid libraries are known that can be coupled to parallel sampling and be deconvoluted without complex procedures such as automated mass spectrometry (Enjalbal C. Martinez J. Aubagnac JL, (2000) Mass spectrometry in combinatorial chemistry, *Mass Spectrometry Reviews.* 19:139-61) and parallel tagging. (Perrin DM., Nucleic acids for recognition and catalysis: landmarks, limitations, and looking to the future, *Combinatorial Chemistry & High Throughput Screening* 3:243-69).

[0299] Peptidomimetics are identified using combinatorial chemistry and solid phase synthesis (Kim HO. Kahn M., (2000) A merger of rational drug design and combinatorial chemistry: development and application of peptide secondary structure mimetics, Combinatorial Chemistry & High Throughput Screening 3:167-83; al-Obeidi, (1998) *Mol*

Biotechnol 9(3):205-23, Peptide and peptidomimetic libraries. Molecular diversity and drug design). The synthesis may be entirely random or based in part on a known polypeptide.

[0300] Polypeptide libraries can be prepared according to various techniques. In brief, phage display techniques can be used to produce polypeptide ligands (Gram H., (1999) Phage display in proteolysis and signal transduction, Combinatorial Chemistry & High Throughput Screening. 2:19-28) that may be used as the basis for synthesis of peptidomimetics. Polypeptides, constrained peptides, proteins, protein domains, antibodies, single chain antibody fragments, antibody fragments, and antibody combining regions are displayed on filamentous phage for selection.

[0301] Large libraries of individual variants of human single chain Fv antibodies have been produced. See, e.g., Siegel RW. Allen B. Pavlik P. Marks JD. Bradbury A., (2000) Mass spectral analysis of a protein complex using single-chain antibodies selected on a peptide target: applications to functional genomics, *Journal of Molecular Biology* 302:285-93; Poul MA. Becerril B. Nielsen UB. Morisson P. Marks JD.,(2000) Selection of tumor-specific internalizing human antibodies from phage libraries. Source *Journal of Molecular Biology*. 301:1149-61; Amersdorfer P. Marks JD., (2001) Phage libraries for generation of anti-botulinum scFv antibodies, *Methods in Molecular Biology*. 145:219-40; Hughes-Jones NC. Bye JM. Gorick BD. Marks JD. Ouwehand WH., (1999) Synthesis of Rh Fv phage-antibodies using VH and VL germline genes, *British Journal of Haematology*. 105:811-6; McCall AM. Amoroso AR. Sautes C. Marks JD. Weiner LM., (1998) Characterization of anti-mouse Fc gamma RII single-chain Fv fragments derived from human phage display libraries, *Immunotechnology*. 4:71-87; Sheets MD. Amersdorfer P. Finnern R. Sargent P. Lindquist E. Schier R. Hemingsen G. Wong C. Gerhart JC. Marks JD. Lindquist E., (1998) Efficient construction of a large nonimmune phage antibody library: the production of high-affinity human single-chain antibodies to protein antigens (published erratum appears in *Proc Natl Acad Sci* USA 1999 96:795), *Proc Natl Acad Sci USA* 95:6157-62).

[0302] Focused or smart chemical and pharmacophore libraries can be designed with the help of sophisticated strategies involving computational chemistry (e.g., Kundu B. Khare SK. Rastogi SK., (1999) Combinatorial chemistry: polymer supported synthesis of peptide and non-peptide libraries, *Progress in Drug Research* 53:89-156) and the use of structure-based ligands using database searching and docking, de novo drug design and estimation of ligand binding affinities (Joseph-McCarthy D., (1999) Computational approaches to

structure-based ligand design, *Pharmacology & Therapeutics* 84:179-91; Kirkpatrick DL. Watson S. Ulhaq S., (1999) Structure-based drug design: combinatorial chemistry and molecular modeling, *Combinatorial Chemistry & High Throughput Screening*. 2:211-21; Eliseev AV. Lehn JM., (1999) Dynamic combinatorial chemistry: evolutionary formation and screening of molecular libraries, *Current Topics in Microbiology & Immunology* 243:159-72; Bolger et al., (1991) *Methods Enz.* 203:21-45; Martin, (1991) *Methods Enz.* 203:587-613; Neidle et al., (1991) *Methods Enz.* 203:433-458; U.S. Patent 6,178,384).

Crystallography

[0303] After binding compounds have been determined, the orientation of compound bound to target is determined. Preferably this determination involves crystallography on co-crystals of molecular scaffold compounds with target. Most protein crystallographic platforms can preferably be designed to analyze up to about 500 co-complexes of compounds, ligands, or molecular scaffolds bound to protein targets due to the physical parameters of the instruments and convenience of operation. If the number of scaffolds that have binding activity exceeds a number convenient for the application of crystallography methods, the scaffolds can be placed into groups based on having at least one common chemical structure or other desirable characteristics, and representative compounds can be selected from one or more of the classes. Classes can be made with increasingly exacting criteria until a desired number of classes (e.g., 500) is obtained. The classes can be based on chemical structure similarities between molecular scaffolds in the class, e.g., all possess a pyrrole ring, benzene ring, or other chemical feature. Likewise, classes can be based on shape characteristics, e.g., space-filling characteristics.

[0304] The co-crystallography analysis can be performed by co-complexing each scaffold with its target at concentrations of the scaffold that showed activity in the screening assay. This co-complexing can be accomplished with the use of low percentage organic solvents with the target molecule and then concentrating the target with each of the scaffolds. In preferred embodiments these solvents are less than 5% organic solvent such as dimethyl sulfoxide (DMSO), ethanol, methanol, or ethylene glycol in water or another aqueous solvent. Each scaffold complexed to the target molecule can then be screened with a suitable number of crystallization screening conditions at both 4 and 20 degrees. In preferred embodiments, about 96 crystallization screening conditions can be performed in order to obtain sufficient information about the co-complexation and crystallization conditions, and the orientation of the scaffold at the binding site of the target molecule.

Crystal structures can then be analyzed to determine how the bound scaffold is oriented physically within the binding site or within one or more binding pockets of the molecular family member.

[0305] It is desirable to determine the atomic coordinates of the compounds bound to the target proteins in order to determine which is a most suitable scaffold for the protein family. X-ray crystallographic analysis is therefore most preferable for determining the atomic coordinates. Those compounds selected can be further tested with the application of medicinal chemistry. Compounds can be selected for medicinal chemistry testing based on their binding position in the target molecule. For example, when the compound binds at a binding site, the compound's binding position in the binding site of the target molecule can be considered with respect to the chemistry that can be performed on chemically tractable structures or sub-structures of the compound, and how such modifications on the compound might interact with structures or sub-structures on the binding site of the target. Thus, one can explore the binding site of the target and the chemistry of the scaffold in order to make decisions on how to modify the scaffold to arrive at a ligand with higher potency and/or selectivity. This process allows for more direct design of ligands, by utilizing structural and chemical information obtained directly from the co-complex, thereby enabling one to more efficiently and quickly design lead compounds that are likely to lead to beneficial drug products. In various embodiments it may be desirable to perform co-crystallography on all scaffolds that bind, or only those that bind with a particular affinity, for example, only those that bind with high affinity, moderate affinity, low affinity, very low affinity, or extremely low affinity. It may also be advantageous to perform co-crystallography on a selection of scaffolds that bind with any combination of affinities.

[0306] Standard X-ray protein diffraction studies such as by using a Rigaku RU-200® (Rigaku, Tokyo, Japan) with an X-ray imaging plate detector or a synchrotron beam-line can be performed on co-crystals and the diffraction data measured on a standard X-ray detector, such as a CCD detector or an X-ray imaging plate detector.

[0307] Performing X-ray crystallography on about 200 co-crystals should generally lead to about 50 co-crystals structures, which should provide about 10 scaffolds for validation in chemistry, which should finally result in about 5 selective leads for target molecules.

Virtual Assays

[0308] Commercially available software that generates three-dimensional graphical representations of the complexed target and compound from a set of coordinates provided can be used to illustrate and study how a compound is oriented when bound to a target. (e.g., QUANTA®, Accelerys, San Diego, CA). Thus, the existence of binding pockets at the binding site of the targets can be particularly useful in the present invention. These binding pockets are revealed by the crystallographic structure determination and show the precise chemical interactions involved in binding the compound to the binding site of the target. The person of ordinary skill will realize that the illustrations can also be used to decide where chemical groups might be added, substituted, modified, or deleted from the scaffold to enhance binding or another desirable effect, by considering where unoccupied space is located in the complex and which chemical substructures might have suitable size and/or charge characteristics to fill it. The person of ordinary skill will also realize that regions within the binding site can be flexible and its properties can change as a result of scaffold binding, and that chemical groups can be specifically targeted to those regions to achieve a desired effect. Specific locations on the molecular scaffold can be considered with reference to where a suitable chemical substructure can be attached and in which conformation, and which site has the most advantageous chemistry available.

[0309] An understanding of the forces that bind the compounds to the target proteins reveals which compounds can most advantageously be used as scaffolds, and which properties can most effectively be manipulated in the design of ligands. The person of ordinary skill will realize that steric, ionic, hydrogen bond, and other forces can be considered for their contribution to the maintenance or enhancement of the target-compound complex. Additional data can be obtained with automated computational methods, such as docking and/or Free Energy Perturbations (FEP), to account for other energetic effects such as desolvation penalties. The compounds selected can be used to generate information about the chemical interactions with the target or for elucidating chemical modifications that can enhance selectivity of binding of the compound.

[0310] Computer models, such as homology models (*i.e.*, based on a known, experimentally derived structure) can be constructed using data from the co-crystal structures. When the target molecule is a protein or enzyme, preferred co-crystal structures for making homology models contain high sequence identity in the binding site of the

protein sequence being modeled, and the proteins will preferentially also be within the same class and/or fold family. Knowledge of conserved residues in active sites of a protein class can be used to select homology models that accurately represent the binding site. Homology models can also be used to map structural information from a surrogate protein where an apo or co-crystal structure exists to the target protein.

[0311] Virtual screening methods, such as docking, can also be used to predict the binding configuration and affinity of scaffolds, compounds, and/or combinatorial library members to homology models. Using this data, and carrying out "virtual experiments" using computer software can save substantial resources and allow the person of ordinary skill to make decisions about which compounds can be suitable scaffolds or ligands, without having to actually synthesize the ligand and perform co-crystallization. Decisions thus can be made about which compounds merit actual synthesis and co-crystallization. An understanding of such chemical interactions aids in the discovery and design of drugs that interact more advantageously with target proteins and/or are more selective for one protein family member over others. Thus, applying these principles, compounds with superior properties can be discovered.

[0312] Additives that promote co-crystallization can of course be included in the target molecule formulation in order to enhance the formation of co-crystals. In the case of proteins or enzymes, the scaffold to be tested can be added to the protein formulation, which is preferably present at a concentration of approximately 1 mg/ml. The formulation can also contain between 0%-10% (v/v) organic solvent, e.g. DMSO, methanol, ethanol, propane diol, or 1,3 dimethyl propane diol (MPD) or some combination of those organic solvents. Compounds are preferably solubilized in the organic solvent at a concentration of about 10 mM and added to the protein sample at a concentration of about 100 mM. The protein-compound complex is then concentrated to a final concentration of protein of from about 5 to about 20 mg/ml. The complexation and concentration steps can conveniently be performed using a 96-well formatted concentration apparatus (e.g., Amicon Inc., Piscataway, NJ). Buffers and other reagents present in the formulation being crystallized can contain other components that promote crystallization or are compatible with crystallization conditions, such as DTT, propane diol, glycerol.

[0313] The crystallization experiment can be set-up by placing small aliquots of the concentrated protein-compound complex (1 μl) in a 96 well format and sampling under 96

crystallization conditions. (Other screening formats can also be used, *e.g.*, plates with greater than 96 wells.) Crystals can typically be obtained using standard crystallization protocols that can involve the 96 well crystallization plate being placed at different temperatures. Co-crystallization varying factors other than temperature can also be considered for each protein-compound complex if desirable. For example, atmospheric pressure, the presence or absence of light or oxygen, a change in gravity, and many other variables can all be tested. The person of ordinary skill in the art will realize other variables that can advantageously be varied and considered.

Ligand Design and Preparation

[0314] The design and preparation of ligands can be performed with or without structural and/or co-crystallization data by considering the chemical structures in common between the active scaffolds of a set. In this process structure-activity hypotheses can be formed and those chemical structures found to be present in a substantial number of the scaffolds, including those that bind with low affinity, can be presumed to have some effect on the binding of the scaffold. This binding can be presumed to induce a desired biochemical effect when it occurs in a biological system (e.g., a treated mammal). New or modified scaffolds or combinatorial libraries derived from scaffolds can be tested to disprove the maximum number of binding and/or structure-activity hypotheses. The remaining hypotheses can then be used to design ligands that achieve a desired binding and biochemical effect.

[0315] But in many cases it will be preferred to have co-crystallography data for consideration of how to modify the scaffold to achieve the desired binding effect (e.g., binding at higher affinity or with higher selectivity). Using the case of proteins and enzymes, co-crystallography data shows the binding pocket of the protein with the molecular scaffold bound to the binding site, and it will be apparent that a modification can be made to a chemically tractable group on the scaffold. For example, a small volume of space at a protein binding site or pocket might be filled by modifying the scaffold to include a small chemical group that fills the volume. Filling the void volume can be expected to result in a greater binding affinity, or the loss of undesirable binding to another member of the protein family. Similarly, the co-crystallography data may show that deletion of a chemical group on the scaffold may decrease a hindrance to binding and result in greater binding affinity or specificity.

[0316] It can be desirable to take advantage of the presence of a charged chemical group located at the binding site or pocket of the protein. For example, a positively charged group can be complemented with a negatively charged group introduced on the molecular scaffold. This can be expected to increase binding affinity or binding specificity, thereby resulting in a more desirable ligand. In many cases, regions of protein binding sites or pockets are known to vary from one family member to another based on the amino acid differences in those regions. Chemical additions in such regions can result in the creation or elimination of certain interactions (e.g., hydrophobic, electrostatic, or entropic) that allow a compound to be more specific for one protein target over another or to bind with greater affinity, thereby enabling one to synthesize a compound with greater selectivity or affinity for a particular family member. Additionally, certain regions can contain amino acids that are known to be more flexible than others. This often occurs in amino acids contained in loops connecting elements of the secondary structure of the protein, such as alpha helices or beta strands. Additions of chemical moieties can also be directed to these flexible regions in order to increase the likelihood of a specific interaction occurring between the protein target of interest and the compound. Virtual screening methods can also be conducted *in silico* to assess the effect of chemical additions, subtractions, modifications, and/or substitutions on compounds with respect to members of a protein family or class.

[0317] The addition, subtraction, or modification of a chemical structure or sub-structure to a scaffold can be performed with any suitable chemical moiety. For example the following moieties, which are provided by way of example and are not intended to be limiting, can be utilized: hydrogen, alkyl, alkoxy, phenoxy, alkenyl, alkynyl, phenylalkyl, hydroxyalkyl, haloalkyl, aryl, arylalkyl, alkyloxy, alkylthio, alkenylthio, phenyl, phenylalkyl, phenylalkylthio, hydroxyalkyl-thio, alkylthiocarbbamylthio, cyclohexyl, pyridyl, piperidinyl, alkylamino, amino, nitro, mercapto, cyano, hydroxyl, a halogen atom, halomethyl, an oxygen atom (e.g., forming a ketone or N-oxide) or a sulphur atom (e.g., forming a thiol, thione, di-alkylsulfoxide or sulfone) are all examples of moieties that can be utilized.

[0318] Additional examples of structures or sub-structures that may be utilized are an aryl optionally substituted with one, two, or three substituents independently selected from the group consisting of alkyl, alkoxy, halogen, trihalomethyl, carboxylate, carboxamide, nitro, and ester moieties; an amine of formula $-NX_2X_3$, where X_2 and X_3 are independently selected from the group consisting of hydrogen, saturated or unsaturated alkyl, and

homocyclic or heterocyclic ring moieties; halogen or trihalomethyl; a ketone of formula -COX_4, where X_4 is selected from the group consisting of alkyl and homocyclic or heterocyclic ring moieties; a carboxylic acid of formula -$(X_5)_nCOOH$ or ester of formula $(X_6)_nCOOX_7$, where X_5, X_6, and X_7 and are independently selected from the group consisting of alkyl and homocyclic or heterocyclic ring moieties and where n is 0 or 1; an alcohol of formula $(X_8)_nOH$ or an alkoxy moiety of formula -$(X_8)_nOX_9$, where X_8 and X_9 are independently selected from the group consisting of saturated or unsaturated alkyl and homocyclic or heterocyclic ring moieties, wherein said ring is optionally substituted with one or more substituents independently selected from the group consisting of alkyl, alkoxy, halogen, trihalomethyl, carboxylate, nitro, and ester and where n is 0 or 1; an amide of formula $NHCOX_{10}$, where X_{10} is selected from the group consisting of alkyl, hydroxyl, and homocyclic or heterocyclic ring moieties, wherein said ring is optionally substituted with one or more substituents independently selected from the group consisting of alkyl, alkoxy, halogen, trihalomethyl, carboxylate, nitro, and ester; SO_2, NX_{11} X_{12}, where X_{11} and X_{12} are selected from the group consisting of hydrogen, alkyl, and homocyclic or heterocyclic ring moieties; a homocyclic or heterocyclic ring moiety optionally substituted with one, two, or three substituents independently selected from the group consisting of alkyl, alkoxy, halogen, trihalomethyl, carboxylate, carboxamide, nitro, and ester moieties; an aldehyde of formula -CHO; a sulfone of formula -SO_2X_{13}, where X_{13} is selected from the group consisting of saturated or unsaturated alkyl and homocyclic or heterocyclic ring moieties; and a nitro of formula -NO_2.

Identification of Attachment Sites on Molecular Scaffolds and Ligands

[0319] In addition to the identification and development of ligands for kinases and other enzymes, determination of the orientation of a molecular scaffold or other binding compound in a binding site allows identification of energetically allowed sites for attachment of the binding molecule to another component. For such sites, any free energy change associated with the presence of the attached component should not destablize the binding of the compound to the kinase to an extent that will disrupt the binding. Preferably, the binding energy with the attachment should be at least 4 kcal/mol., more preferably at least 6, 8, 10, 12, 15, or 20 kcal/mol. Preferably, the presence of the attachment at the particular site reduces binding energy by no more than 3, 4, 5, 8, 10, 12, or 15 kcal/mol.

[0320] In many cases, suitable attachment sites will be those that are exposed to solvent when the binding compound is bound in the binding site. In some cases, attachment sites

can be used that will result in small displacements of a portion of the enzyme without an excessive energetic cost. Exposed sites can be identified in various ways. For example, exposed sites can be identified using a graphic display or 3-dimensional model. In a graphic display, such as a computer display, an image of a compound bound in a binding site can be visually inspected to reveal atoms or groups on the compound that are exposed to solvent and oriented such that attachment at such atom or group would not preclude binding of the enzyme and binding compound. Energetic costs of attachment can be calculated based on changes or distortions that would be caused by the attachment as well as entropic changes.

[0321] Many different types of components can be attached. Persons with skill are familiar with the chemistries used for various attachments. Examples of components that can be attached include, without limitation: solid phase components such as beads, plates, chips, and wells; a direct or indirect label; a linker, which may be a traceless linker; among others. Such linkers can themselves be attached to other components, *e.g.*, to solid phase media, labels, and/or binding moieties.

[0322] The binding energy of a compound and the effects on binding energy for attaching the molecule to another component can be calculated approximately using any of a variety of available software or by manual calculation. An example is the following:

[0323] Calculations were performed to estimate binding energies of different organic molecules to two Kinases: Pim-1 and CDK2. The organic molecules considered included Staurosporine, identified compounds that bind to PIM-1, and several linkers.

[0324] Calculated binding energies between protein-ligand complexes were obtained using the FlexX score (an implementation of the Bohm scoring function) within the Tripos software suite. The form for that equation is shown in Eqn. 1 below:

$$\Delta G_{bind} = \Delta G_{tr} + \Delta G_{hb} + \Delta G_{ion} + \Delta G_{lipo} + \Delta G_{arom} + \Delta G_{rot}$$

[0325] where: ΔG_{tr} is a constant term that accounts for the overall loss of rotational and translational entropy of the ligand, ΔG_{hb} accounts for hydrogen bonds formed between the ligand and protein, ΔG_{ion} accounts for the ionic interactions between the ligand and protein, ΔG_{lipo} accounts for the lipophilic interaction that corresponds to the protein-ligand contact

surface, ΔG_{arom} accounts for interactions between aromatic rings in the protein and ligand, and ΔG_{rot} accounts for the entropic penalty of restricting rotatable bonds in the ligand upon binding.

[0326] This method estimates the free energy that a lead compound should have to a target protein for which there is a crystal structure, and it accounts for the entropic penalty of flexible linkers. It can therefore be used to estimate the free energy penalty incurred by attaching linkers to molecules being screened and the binding energy that a lead compound should have in order to overcome the free energy penalty of the linker. The method does not account for solvation and the entropic penalty is likely overestimated for cases where the linker is bound to a solid phase through another binding complex, such as a biotin:streptavidin complex.

[0327] Co-crystals were aligned by superimposing residues of PIM-1 with corresponding residues in CDK2. The PIM-1 structure used for these calculations was a co-crystal of PIM-1 with a binding compound. The CDK2:Staurosporine co-crystal used was from the Brookhaven database file 1aq1. Hydrogen atoms were added to the proteins and atomic charges were assigned using the AMBER95 parameters within Sybyl. Modifications to the compounds described were made within the Sybyl modeling suite from Tripos.

[0328] These calculations indicate that the calculated binding energy for compounds that bind strongly to a given target (such as Staurosporine:CDK2) can be lower than –25 kcal/mol, while the calculated binding affinity for a good scaffold or an unoptimized binding compound can be in the range of -15 to -20. The free energy penalty for attachment to a linker such as the ethylene glycol or hexatriene is estimated as typically being in the range of +5 to +15 kcal/mol.

Linkers

[0329] Linkers suitable for use in the invention can be of many different types. Linkers can be selected for particular applications based on factors such as linker chemistry compatible for attachment to a binding compound and to another component utilized in the particular application. Additional factors can include, without limitation, linker length, linker stability, and ability to remove the linker at an appropriate time. Exemplary linkers include, but are not limited to, hexyl, hexatrienyl, ethylene glycol, and peptide linkers. Traceless linkers can also be used, *e.g.*, as described in Plunkett, M. J., and Ellman, J. A., (1995), *J. Org. Chem.* 60:6006

[0330] Typical functional groups, that are utilized to link binding compound(s), include, but not limited to, carboxylic acid, amine, hydroxyl, and thiol. (Examples can be found in Solid-supported combinatorial and parallel synthesis of small molecular weight compound libraries; (1998) Tetrahedron organic chemistry series Vol.17; Pergamon; p85).

Labels

[0331] As indicated above, labels can also be attached to a binding compound or to a linker attached to a binding compound. Such attachment may be direct (attached directly to the binding compound) or indirect (attached to a component that is directly or indirectly attached to the binding compound). Such labels allow detection of the compound either directly or indirectly. Attachment of labels can be performed using conventional chemistries. Labels can include, for example, fluorescent labels, radiolabels, light scattering particles, light absorbent particles, magnetic particles, enzymes, and specific binding agents (*e.g.*, biotin or an antibody target moiety).

Solid Phase Media

[0332] Additional examples of components that can be attached directly or indirectly to a binding compound include various solid phase media. Similar to attachment of linkers and labels, attachment to solid phase media can be performed using conventional chemistries. Such solid phase media can include, for example, small components such as beads, nanoparticles, and fibers (*e.g.*, in suspension or in a gel or chromatographic matrix). Likewise, solid phase media can include larger objects such as plates, chips, slides, and tubes. In many cases, the binding compound will be attached in only a portion of such an objects, *e.g.*, in a spot or other local element on a generally flat surface or in a well or portion of a well.

Identification of Biological Agents

[0333] The possession of structural information about a protein also provides for the identification of useful biological agents, such as epitopes for development of antibodies, identification of mutation sites expected to affect activity, and identification of attachment sites allowing attachment of the protein to materials such as labels, linkers, peptides, and solid phase media.

[0334] Antibodies (Abs) finds multiple applications in a variety of areas including biotechnology, medicine and diagnosis, and indeed they are one of the most powerful tools

for life science research. Abs directed against protein antigens can recognize either linear or native three-dimensional (3D) epitopes. The obtention of Abs that recognize 3D epitopes require the use of whole native protein (or of a portion that assumes a native conformation) as immunogens. Unfortunately, this not always a choice due to various technical reasons: for example the native protein is just not available, the protein is toxic, or its is desirable to utilize a high density antigen presentation. In such cases, immunization with peptides is the alternative. Of course, Abs generated in this manner will recognize linear epitopes, and they might or might not recognize the source native protein, but yet they will be useful for standard laboratory applications such as western blots. The selection of peptides to use as immunogens can be accomplished by following particular selection rules and/or use of epitope prediction software.

[0335] Though methods to predict antigenic peptides are not infallible, there are several rules that can be followed to determine what peptide fragments from a protein are likely to be antigenic. These rules are also dictated to increase the likelihood that an Ab to a particular peptide will recognize the native protein.

- 1. Antigenic peptides should be located in solvent accessible regions and contain both hydrophobic and hydrophilic residues.
    - For proteins of known 3D structure, solvent accessibility can be determined using a variety of programs such as DSSP, NACESS, or WHATIF, among others.
    - If the 3D structure is not known, use any of the following web servers to predict accessibilities: PHD, JPRED, PredAcc (c) ACCpro
- 2. Preferably select peptides lying in long loops connecting Secondary Structure (SS) motifs, avoiding peptides located in helical regions. This will increase the odds that the Ab recognizes the native protein. Such peptides can, for example, be identified from a crystal structure or crystal structure-based homology model.
    - For protein with known 3D coordinates, SS can be obtained from the sequence link of the relevant entry at the Brookhaven data bank. The PDBsum server also offer SS analysis of pdb records.

- When no structure is available secondary structure predictions can be obtained from any of the following servers: PHD, JPRED, PSI-PRED, NNSP, etc

- 3. When possible, choose peptides that are in the N- and C-terminal region of the protein. Because the N- and C- terminal regions of proteins are usually solvent accessible and unstructured, Abs against those regions are also likely to recognize the native protein.

- 4. For cell surface glycoproteins, eliminate from initial peptides those containing consensus sites for N-glycosilation.

  - N-glycosilation sites can be detected using Scanprosite, or NetNGlyc

[0336] In addition, several methods based on various physio-chemical properties of experimental determined epitopes (flexibility, hydrophibility, accessibility) have been published for the prediction of antigenic determinants and can be used. The antigenic index and Preditop are example.

[0337] Perhaps the simplest method for the prediction of antigenic determinants is that of Kolaskar and Tongaonkar, which is based on the occurrence of amino acid residues in experimentally determined epitopes. (Kolaskar and Tongaonkar (1990) A semi-empirical method for prediction of antigenic determinants on protein antigens. *FEBBS Lett.* 276(1-2):172-174.) The prediction algorithm works as follows:

- 1. Calculate the average propensity for each overlapping 7-mer and assign the result to the central residue (i+3) of the 7-mer.

- 2. Calculate the average for the whole protein.

- 3. (a) If the average for the whole protein is above 1.0 then all residues having average propensity above 1.0 are potentially antigenic.

- 3. (b) If the average for the whole protein is below 1.0 then all residues having above the average for the whole protein are potentially antigenic.

- 4. Find 8-mers where all residues are selected by step 3 above (6-mers in the original paper)

[0338] The Kolaskar and Tongaonkar method is also available from the GCG package, and it runs using the command *egcg*.

[0339] Crystal structures also allow identification of residues at which mutation is likely to alter the activity of the protein. Such residues include, for example, residues that interact with substrate, conserved active site residues, and residues that are in a region of ordered secondary structure of involved in tertiary interactions. The mutations that are likely to affect activity will vary for different molecular contexts. Mutations in an active site that will affect activity are typically substitutions or deletions that eliminate a charge-charge or hydrogen bonding interaction, or introduce a steric interference. Mutations in secondary structure regions or molecular interaction regions that are likely to affect activity include, for example, substitutions that alter the hydrophobicity/hydrophilicity of a region, or that introduce a sufficient strain in a region near or including the active site so that critical residue(s) in the active site are displaced. Such substitutions and/or deletions and/or insertions are recognized, and the predicted structural and/or energetic effects of mutations can be calculated using conventional software.

IX. Kinase Activity Assays

[0340] A number of different assays for kinase activity can be utilized for assaying for active modulators and/or determining specificity of a modulator for a particular kinase or group or kinases. In addition to the assays mentioned below, one of ordinary skill in the art will know of other assays that can be utilized and can modify an assay for a particular application.

[0341] An assay for kinase activity that can be used for kinases, *e.g.*, PIM-1, can be performed according to the following procedure using purified kinase using myelin basic protein (MBP) as substrate. An exemplary assay can use the following materials: MBP (M-1891, Sigma); Kinase buffer (KB = HEPES 50 mM, pH7.2, $MgCl_2$:$MnCl_2$ (200 μM:200 μM); ATP (γ-^{33}P):NEG602H (10 mCi/mL)(Perkin-Elmer); ATP as 100 mM stock in kinase buffer; EDTA as 100 mM stock solution.

[0342] Coat scintillation plate suitable for radioactivity counting (*e.g.*, FlashPlate from Perkin-Elmer, such as the SMP200(basic)) with kinase+MBP mix (final 100 ng+300 ng/well) at 90 -μL/well in kinase buffer. Add compounds at 1 μL/well from 10 mM stock in DMSO. Positive control wells are added with 1 μL of DMSO. Negative control wells

are added with 2 μL of EDTA stock solution. ATP solution (10 μL) is added to each well to provide a final concentration of cold ATP is 2 μM, and 50 nCi ATPγ[^{33}P]. The plate is shaken briefly, and a count is taken to initiate count (IC) using an apparatus adapted for counting with the plate selected, *e.g.*, Perkin-Elmer Trilux. Store the plate at 37°C for 4 hrs, then count again to provide final count (FC).

[0343] Net 33P incorporation (NI) is calculated as: NI = FC – IC.

[0344] The effect of the present of a test compound can then be calculated as the percent of the positive control as: %PC = [(NI – NC) / (PC – NC)] x 100, where NC is the net incorporation for the negative control, and PC is the net incorporation for the positive control.

[0345] As indicated above, other assays can also be readily used. For example, kinase activity can be measured on standard polystyrene plates, using biotinylated MBP and ATPγ[^{33}P] and with Streptavidin-coated SPA (scintillation proximity) beads providing the signal.

[0346] Additional alternative assays can employ phospho-specific antibodies as detection reagents with biotinylated peptides as substrates for the kinase. This sort of assay can be formatted either in a fluorescence resonance energy transfer (FRET) format, or using an AlphaScreen (*a*mplified *l*uminescent *p*roximity *h*omogeneous *a*ssay) format by varying the donor and acceptor reagents that are attached to streptavidin or the phosphor-specific antibody.

X. Organic Synthetic Techniques

[0347] The versatility of computer-based modulator design and identification lies in the diversity of structures screened by the computer programs. The computer programs can search databases that contain very large numbers of molecules and can modify modulators already complexed with the enzyme with a wide variety of chemical functional groups. A consequence of this chemical diversity is that a potential modulator of kinase function may take a chemical form that is not predictable. A wide array of organic synthetic techniques exist in the art to meet the challenge of constructing these potential modulators. Many of these organic synthetic methods are described in detail in standard reference sources utilized by those skilled in the art. One example of such a reference is March, 1994, Advanced Organic Chemistry; Reactions, Mechanisms and Structure, New York, McGraw Hill. Thus,

the techniques useful to synthesize a potential modulator of kinase function identified by computer-based methods are readily available to those skilled in the art of organic chemical synthesis.

XI. Isomers, Prodrugs, and Active Metabolites

[0348] The present compounds are described herein with generic formulas and specific compounds. In addition, the present compounds may exist in a number of different forms or derivatives, all within the scope of the present invention. These include, for example, tautomers, enantiomers, stereoisomers, racemic mixtures, regioisomers, salts, prodrugs (e.g., carboxylic acid esters), solvated forms, different crystal forms or polymorphs, and active metabolites

A. Tautomers, Stereoisomers, Regioisomers, and Solvated Forms

[0349] It is understood that certain compounds may exhibit tautomerism. In such cases, the formula drawings within this specification expressly depict only one of the possible tautomeric forms. It is therefore to be understood that within the invention the formulas are intended to represent any tautomeric form of the depicted compounds and are not to be limited merely to the specific tautomeric form depicted by the formula drawings.

[0350] Likewise, some of the present compounds may contain one or more chiral centers, and therefore, may exist in two or more stereoisomeric forms. Thus, such compounds may be present as single stereoisomers (i.e., essentially free of other stereoisomers), racemates, and/or mixtures of enantiomers and/or diastereomers. All such single stereoisomers, racemates and mixtures thereof are intended to be within the scope of the present invention. Unless specified to the contrary, all such steroisomeric forms are included within the formulas provided herein.

[0351] In certain embodiments, a chiral compound of the present invention is in a form that contains at least 80% of a single isomer (60% enantiomeric excess ("e.e.") or diastereomeric excess ("d.e.")), or at least 85% (70% e.e. or d.e.), 90% (80% e.e. or d.e.), 95% (90% e.e. or d.e.), 97.5% (95% e.e. or d.e.), or 99% (98% e.e. or d.e.). As generally understood by those skilled in the art, an optically pure compound having one chiral center is one that consists essentially of one of the two possible enantiomers (i.e., is enantiomerically pure), and an optically pure compound having more than one chiral center

is one that is both diastereomerically pure and enantiomerically pure. In certain embodiments, the compound is present in optically pure form.

[0352] For compounds is which synthesis involves addition of a single group at a double bond, particularly a carbon-carbon double bond, the addition may occur at either of the double bond-linked atoms. For such compounds, the present invention includes both such regioisomers.

[0353] Additionally, the formulas are intended to cover solvated as well as unsolvated forms of the identified structures. For example, the indicated structures include both both hydrated and non-hydrated forms. Other examples of solvates include the structures in combination with isopropanol, ethanol, methanol, DMSO, ethyl acetate, acetic acid, or ethanolamine.

B. Prodrugs and Metabolites

[0354] In addition to the present formulas and compounds described herein, the invention also includes prodrugs (generally pharmaceutically acceptable prodrugs), active metabolic derivatives (active metabolites), and their pharmaceutically acceptable salts.

[0355] In this context, prodrugs are compounds that may be converted under physiological conditions or by solvolysis to the specified compound or to a pharmaceutically acceptable salt of such a compound. A common example is an alkyl ester of a carboxylic acid.

[0356] As described in The Practice of Medicinal Chemistry, Ch. 31-32 (Ed. Wermuth, Academic Press, San Diego, CA, 2001), prodrugs can be conceptually divided into two non-exclusive categories, bioprecursor prodrugs and carrier prodrugs. Generally, bioprecursor prodrugs are compounds are inactive or have low activity compared to the corresponding active drug compound, that contain one or more protective groups and are converted to an active form by metabolism or solvolysis. Both the active drug form and any released metabolic products should have acceptably low toxicity. Typically, the formation of active drug compound involves a metabolic process or reaction that is one of the follow types:

[0357] Oxidative reactions, such as oxidation of alcohol, carbonyl, and acid functions, hydroxylation of aliphatic carbons, hydroxylation of alicyclic carbon atoms, oxidation of aromatic carbon atoms, oxidation of carbon-carbon double bonds, oxidation of nitrogen-

containing functional groups, oxidation of silicon, phosphorus, arsenic, and sulfur, oxidative N-delakylation, oxidative O- and S-delakylation, oxidative deamination, as well as other oxidative reactions.

[0358] Reductive reactions, such as reduction of carbonyl groups, reduction of alcoholic groups and carbon-carbon double bonds, reduction of nitrogen-containing functions groups, and other reduction reactions.

[0359] Reactions without change in the state of oxidation, such as hydrolysis of esters and ethers, hydrolytic cleavage of carbon-nitrogen single bonds, hydrolytic cleavage of non-aromatic heterocycles, hydration and dehydration at multiple bonds, new atomic linkages resulting from dehydration reactions, hydrolytic dehalogenation, removal of hydrogen halide molecule, and other such reactions.

[0360] Carrier prodrugs are drug compounds that contain a transport moiety, e.g., that improves uptake and/or localized delivery to a site(s) of action. Desirably for such a carrier prodrug, the linkage between the drug moiety and the transport moiety is a covalent bond, the prodrug is inactive or less active than the drug compound, the prodrug and any release transport moiety are acceptably non-toxic. For prodrugs where the transport moiety in intended to enhance uptake, typically the release of the transport moiety should be rapid. In other cases, it is desirable to utilize a moiety that provides slow release, e.g., certain polymers or other moieties, such as cyclodextrins. (See, e.g., Cheng et al., U.S. Patent publ. 20040077595, appl. 10/656,838, incorporated herein by reference.) Such carrier prodrugs are often advantageous for orally administered drugs. Carrier prodrugs can, for example, be used to improve one or more of the following properties: increased lipophilicity, increased duration of pharmacological effects, increased site-specificity, decreased toxicity and adverse reactions, and/or improvement in drug formulation (e.g., stability, water solubility, suppression of an undesirable organoleptic or physiochemical property). For example, lipophilicity can be increased by esterification of hydroxyl groups with lipophilic carboxylic acids, or of carboxylic acid groups with alcohols, e.g., aliphatic alcohols. Wermuth, The Practice of Medicinal Chemistry, Ch. 31-32, Ed. Wermuth, Academic Press, San Diego, CA, 2001.

[0361] Prodrugs may proceed from prodrug form to active form in a single step or may have one or more intermediate forms which may themselves have activity or may be inactive.

[0362] Metabolites, e.g., active metabolites overlap with prodrugs as described above, e.g., bioprecursor prodrugs. Thus, such metabolites are pharmacologically active compounds or compounds that further metabolize to pharmacologically active compounds that are derivatives resulting from metabolic process in the body of a subject or patient. Of these, active metabolites are such pharmacologically active derivative compounds. For prodrugs, the prodrug compounds is generally inactive or of lower activity than the metabolic product. For active metabolites, the parent compound may be either an active compound or may be an inactive prodrug.

[0363] Prodrugs and active metabolites may be identified using routine techniques know in the art. See, e.g., Bertolini et al, 1997, *J Med Chem* 40:2011-2016; Shan et al., *J Pharm Sci* 86:756-757; Bagshawe, 1995, *Drug Dev Res* 34:220-230; Wermuth, The Practice of Medicinal Chemistry, Ch. 31-32, Academic Press, San Diego, CA, 2001.

C. Pharmaceutically acceptable salts

[0364] Compounds can be formulated as or be in the form of pharmaceutically acceptable salts. Pharmaceutically acceptable salts are non-toxic salts in the amounts and concentrations at which they are administered. The preparation of such salts can facilitate the pharmacological use by altering the physical characteristics of a compound without preventing it from exerting its physiological effect. Useful alterations in physical properties include lowering the melting point to facilitate transmucosal administration and increasing the solubility to facilitate administering higher concentrations of the drug.

[0365] Pharmaceutically acceptable salts include acid addition salts such as those containing sulfate, chloride, hydrochloride, fumarate, maleate, phosphate, sulfamate, acetate, citrate, lactate, tartrate, methanesulfonate, ethanesulfonate, benzenesulfonate, *p*-toluenesulfonate, cyclohexylsulfamate and quinate. Pharmaceutically acceptable salts can be obtained from acids such as hydrochloric acid, maleic acid, sulfuric acid, phosphoric acid, sulfamic acid, acetic acid, citric acid, lactic acid, tartaric acid, malonic acid, methanesulfonic acid, ethanesulfonic acid, benzenesulfonic acid, *p*-toluenesulfonic acid, cyclohexylsulfamic acid, fumaric acid, and quinic acid.

[0366] Pharmaceutically acceptable salts also include basic addition salts such as those containing benzathine, chloroprocaine, choline, diethanolamine, ethylenediamine, meglumine, procaine, aluminum, calcium, lithium, magnesium, potassium, sodium,

ammonium, alkylamine, and zinc, when acidic functional groups, such as carboxylic acid or phenol are present. For example, see Remington's Pharmaceutical Sciences, 19th ed., Mack Publishing Co., Easton, PA, Vol. 2, p. 1457, 1995. Such salts can be prepared using the appropriate corresponding bases.

[0367] Pharmaceutically acceptable salts can be prepared by standard techniques. For example, the free-base form of a compound is dissolved in a suitable solvent, such as an aqueous or aqueous-alcohol in solution containing the appropriate acid and then isolated by evaporating the solution. In another example, a salt is prepared by reacting the free base and acid in an organic solvent.

[0368] Thus, for example, if the particular compound is a base, the desired pharmaceutically acceptable salt may be prepared by any suitable method available in the art, for example, treatment of the free base with an inorganic acid, such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, or with an organic acid, such as acetic acid, maleic acid, succinic acid, mandelic acid, fumaric acid, malonic acid, pyruvic acid, oxalic acid, glycolic acid, salicylic acid, a pyranosidyl acid, such as glucuronic acid or galacturonic acid, an alpha-hydroxy acid, such as citric acid or tartaric acid, an amino acid, such as aspartic acid or glutamic acid, an aromatic acid, such as benzoic acid or cinnamic acid, a sulfonic acid, such as p-toluenesulfonic acid or ethanesulfonic acid, or the like.

[0369] Similarly, if the particular compound is an acid, the desired pharmaceutically acceptable salt may be prepared by any suitable method, for example, treatment of the free acid with an inorganic or organic base, such as an amine (primary, secondary or tertiary), an alkali metal hydroxide or alkaline earth metal hydroxide, or the like. Illustrative examples of suitable salts include organic salts derived from amino acids, such as glycine and arginine, ammonia, primary, secondary, and tertiary amines, and cyclic amines, such as piperidine, morpholine and piperazine, and inorganic salts derived from sodium, calcium, potassium, magnesium, manganese, iron, copper, zinc, aluminum and lithium.

[0370] The pharmaceutically acceptable salt of the different compounds may be present as a complex. Examples of complexes include 8-chlorotheophylline complex (analogous to, *e.g.*, dimenhydrinate: diphenhydramine 8-chlorotheophylline (1:1) complex; Dramamine) and various cyclodextrin inclusion complexes.

[0371] Unless specified to the contrary, specification of a compound herein includes pharmaceutically acceptable salts of such compound.

D. Polymorphic forms

[0372] In the case of agents that are solids, it is understood by those skilled in the art that the compounds and salts may exist in different crystal or polymorphic forms, all of which are intended to be within the scope of the present invention and specified formulas.

XII. Administration

[0373] The methods and compounds will typically be used in therapy for human patients. However, they may also be used to treat similar or identical diseases in other vertebrates such as other primates, sports animals, and pets such as horses, dogs and cats.

[0374] Suitable dosage forms, in part, depend upon the use or the route of administration, for example, oral, transdermal, transmucosal, or by injection (parenteral). Such dosage forms should allow the compound to reach target cells. Other factors are well known in the art, and include considerations such as toxicity and dosage forms that retard the compound or composition from exerting its effects. Techniques and formulations generally may be found in Remington's Pharmaceutical Sciences, 18th ed., Mack Publishing Co., Easton, PA, 1990 (hereby incorporated by reference herein).

[0375] Carriers or excipients can be used to produce pharmaceutical compositions. The carriers or excipients can be chosen to facilitate administration of the compound. Examples of carriers include calcium carbonate, calcium phosphate, various sugars such as lactose, glucose, or sucrose, or types of starch, cellulose derivatives, gelatin, vegetable oils, polyethylene glycols and physiologically compatible solvents. Examples of physiologically compatible solvents include sterile solutions of water for injection (WFI), saline solution, and dextrose.

[0376] The compounds can be administered by different routes including intravenous, intraperitoneal, subcutaneous, intramuscular, oral, transmucosal, rectal, or transdermal. Oral administration is preferred. For oral administration, for example, the compounds can be formulated into conventional oral dosage forms such as capsules, tablets, and liquid preparations such as syrups, elixirs, and concentrated drops.

[0377] Pharmaceutical preparations for oral use can be obtained, for example, by combining the active compounds with solid excipients, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose (CMC), and/or polyvinylpyrrolidone (PVP: povidone). If desired, disintegrating agents may be added, such as the cross—linked polyvinylpyrrolidone, agar, or alginic acid, or a salt thereof such as sodium alginate.

[0378] Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain, for example, gum arabic, talc, poly-vinylpyrrolidone, carbopol gel, polyethylene glycol (PEG), and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dye-stuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

[0379] Pharmaceutical preparations that can be used orally include push-fit capsules made of gelatin ("gelcaps"), as well as soft, sealed capsules made of gelatin, and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols (PEGs). In addition, stabilizers may be added.

[0380] Alternatively, injection (parenteral administration) may be used, *e.g.*, intramuscular, intravenous, intraperitoneal, and/or subcutaneous. For injection, the compounds of the invention are formulated in sterile liquid solutions, preferably in physiologically compatible buffers or solutions, such as saline solution, Hank's solution, or Ringer's solution. In addition, the compounds may be formulated in solid form and redissolved or suspended immediately prior to use. Lyophilized forms can also be produced.

[0381] Administration can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be

permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, bile salts and fusidic acid derivatives. In addition, detergents may be used to facilitate permeation. Transmucosal administration, for example, may be through nasal sprays or suppositories (rectal or vaginal).

[0382] The amounts of various compound to be administered can be determined by standard procedures taking into account factors such as the compound IC_{50}, the biological half-life of the compound, the age, size, and weight of the patient, and the disorder associated with the patient. The importance of these and other factors are well known to those of ordinary skill in the art. Generally, a dose will be between about 0.01 and 50 mg/kg, preferably 0.1 and 20 mg/kg of the patient being treated. Multiple doses may be used.

XIII. Manipulation of Kinase Coding Sequences

[0383] Through the availability of the coding sequences for many different kinases, any of a variety of different molecular techniques can be performed as desired, .e.g., cloning, construction of recombinant sequences, production and purification of recombinant protein, introduction of particular kinase sequences into other organisms, and the like.

[0384] Techniques for the manipulation of nucleic acids, such as, e.g., subcloning, labeling probes (e.g., random-primer labeling using Klenow polymerase, nick translation, amplification), sequencing, hybridization and the like are well disclosed in the scientific and patent literature, see, e.g., Sambrook, ed., Molecular Cloning: a Laboratory Manual (2nd ed.), Vols. 1-3, Cold Spring Harbor Laboratory, (1989); Current Protocols in Molecular Biology, Ausubel, ed. John Wiley & Sons, Inc., New York (1997); Laboratory Techniques in Biochemistry and Molecular Biology: Hybridization With Nucleic Acid Probes, Part I. Theory and Nucleic Acid Preparation, Tijssen, ed. Elsevier, N.Y. (1993).

[0100] Nucleic acid sequences can be amplified as necessary for further use using amplification methods, such as PCR, isothermal methods, rolling circle methods, etc., are well known to the skilled artisan. See, e.g., Saiki, "Amplification of Genomic DNA" in PCR Protocols, Innis et al., Eds., Academic Press, San Diego, CA 1990, pp 13-20; Wharam et al., *Nucleic Acids Res.* 2001 Jun 1;29(11):E54-E54; Hafner et al., *Biotechniques* 2001 Apr;30(4):852-6, 858, 860 passim; Zhong et al., *Biotechniques* 2001 Apr;30(4):852-6, 858, 860 passim.

[0385] Nucleic acids, vectors, capsids, polypeptides, and the like can be analyzed and quantified by any of a number of general means well known to those of skill in the art. These include, e.g., analytical biochemical methods such as NMR, spectrophotometry, radiography, electrophoresis, capillary electrophoresis, high performance liquid chromatography (HPLC), thin layer chromatography (TLC), and hyperdiffusion chromatography, various immunological methods, e.g. fluid or gel precipitin reactions, immunodiffusion, immuno-electrophoresis, radioimmunoassays (RIAs), enzyme-linked immunosorbent assays (ELISAs), immuno-fluorescent assays, Southern analysis, Northern analysis, dot-blot analysis, gel electrophoresis (e.g., SDS-PAGE), nucleic acid or target or signal amplification methods, radiolabeling, scintillation counting, and affinity chromatography.

[0386] Obtaining and manipulating nucleic acids used to practice the methods of the invention can be performed by cloning from genomic samples, and, if desired, screening and re-cloning inserts isolated or amplified from, e.g., genomic clones or cDNA clones. Sources of nucleic acid used in the methods of the invention include genomic or cDNA libraries contained in, e.g., mammalian artificial chromosomes (MACs), see, e.g., U.S. Patent Nos. 5,721,118; 6,025,155; human artificial chromosomes, see, e.g., Rosenfeld (1997) *Nat. Genet.* 15:333-335; yeast artificial chromosomes (YAC); bacterial artificial chromosomes (BAC); P1 artificial chromosomes, see, e.g., Woon (1998) *Genomics* 50:306-316; P1-derived vectors (PACs), see, e.g., Kern (1997) *Biotechniques* 23:120-124; cosmids, recombinant viruses, phages or plasmids.

[0387] The nucleic acids of the invention can be operatively linked to a promoter. A promoter can be one motif or an array of nucleic acid control sequences which direct transcription of a nucleic acid. A promoter can include necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter which is active under most environmental and developmental conditions. An "inducible" promoter is a promoter which is under environmental or developmental regulation. A "tissue specific" promoter is active in certain tissue types of an organism, but not in other tissue types from the same organism. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a

second nucleic acid sequence, wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

[0388] The nucleic acids of the invention can also be provided in expression vectors and cloning vehicles, e.g., sequences encoding the polypeptides of the invention. Expression vectors and cloning vehicles of the invention can comprise viral particles, baculovirus, phage, plasmids, phagemids, cosmids, fosmids, bacterial artificial chromosomes, viral DNA (e.g., vaccinia, adenovirus, foul pox virus, pseudorabies and derivatives of SV40), P1-based artificial chromosomes, yeast plasmids, yeast artificial chromosomes, and any other vectors specific for specific hosts of interest (such as bacillus, *Aspergillus* and yeast). Vectors of the invention can include chromosomal, non-chromosomal and synthetic DNA sequences. Large numbers of suitable vectors are known to those of skill in the art, and are commercially available.

[0389] The nucleic acids of the invention can be cloned, if desired, into any of a variety of vectors using routine molecular biological methods; methods for cloning *in vitro* amplified nucleic acids are disclosed, *e.g.*, U.S. Pat. No. 5,426,039. To facilitate cloning of amplified sequences, restriction enzyme sites can be "built into" a PCR primer pair. Vectors may be introduced into a genome or into the cytoplasm or a nucleus of a cell and expressed by a variety of conventional techniques, well described in the scientific and patent literature. See, e.g., Roberts (1987) *Nature* 328:731; Schneider (1995) *Protein Expr. Purif.* 6435:10; Sambrook, Tijssen or Ausubel. The vectors can be isolated from natural sources, obtained from such sources as ATCC or GenBank libraries, or prepared by synthetic or recombinant methods. For example, the nucleic acids of the invention can be expressed in expression cassettes, vectors or viruses which are stably or transiently expressed in cells (e.g., episomal expression systems). Selection markers can be incorporated into expression cassettes and vectors to confer a selectable phenotype on transformed cells and sequences. For example, selection markers can code for episomal maintenance and replication such that integration into the host genome is not required.

[0390] In one aspect, the nucleic acids of the invention are administered *in vivo* for *in situ* expression of the peptides or polypeptides of the invention. The nucleic acids can be administered as "naked DNA" (see, e.g., U.S. Patent No. 5,580,859) or in the form of an expression vector, e.g., a recombinant virus. The nucleic acids can be administered by any route, including peri- or intra-tumorally, as described below. Vectors administered *in vivo*

can be derived from viral genomes, including recombinantly modified enveloped or non-enveloped DNA and RNA viruses, preferably selected from baculoviridiae, parvoviridiae, picornoviridiae, herpesveridiae, poxviridae, adenoviridiae, or picornaviridiae. Chimeric vectors may also be employed which exploit advantageous merits of each of the parent vector properties (See e.g., Feng (1997) *Nature Biotechnology* 15:866-870). Such viral genomes may be modified by recombinant DNA techniques to include the nucleic acids of the invention; and may be further engineered to be replication deficient, conditionally replicating or replication competent. In alternative aspects, vectors are derived from the adenoviral (e.g., replication incompetent vectors derived from the human adenovirus genome, see, e.g., U.S. Patent Nos. 6,096,718; 6,110,458; 6,113,913; 5,631,236); adeno-associated viral and retroviral genomes. Retroviral vectors can include those based upon murine leukemia virus (MuLV), gibbon ape leukemia virus (GaLV), Simian Immuno deficiency virus (SIV), human immuno deficiency virus (HIV), and combinations thereof; see, e.g., U.S. Patent Nos. 6,117,681; 6,107,478; 5,658,775; 5,449,614; Buchscher (1992) J. Virol. 66:2731-2739; Johann (1992) *J. Virol.* 66:1635-1640). Adeno-associated virus (AAV)-based vectors can be used to transduce cells with target nucleic acids, e.g., in the *in vitro* production of nucleic acids and peptides, and in *in vivo* and *ex vivo* gene therapy procedures; see, e.g., U.S. Patent Nos. 6,110,456; 5,474,935; Okada (1996) *Gene Ther.* 3:957-964.

[0391] The present invention also relates to fusion proteins, and nucleic acids encoding them. A polypeptide of the invention can be fused to a heterologous peptide or polypeptide, such as N-terminal identification peptides which impart desired characteristics, such as increased stability or simplified purification. Peptides and polypeptides of the invention can also be synthesized and expressed as fusion proteins with one or more additional domains linked thereto for, e.g., producing a more immunogenic peptide, to more readily isolate a recombinantly synthesized peptide, to identify and isolate antibodies and antibody-expressing B cells, and the like. Detection and purification facilitating domains include, e.g., metal chelating peptides such as polyhistidine tracts and histidine-tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp, Seattle WA). The inclusion of a cleavable linker sequences such as Factor Xa or enterokinase (Invitrogen, San Diego CA) between a purification domain and the motif-comprising peptide or polypeptide to facilitate purification. For example, an expression vector can include an epitope-encoding nucleic

acid sequence linked to six histidine residues followed by a thioredoxin and an enterokinase cleavage site (see e.g., [illegible] (1995) *Biochemistry* 34:1787-1797; Dobeli (1998) *Protein Expr. Purif.* 12:404-414). The histidine residues facilitate detection and purification while the enterokinase cleavage site provides a means for purifying the epitope from the remainder of the fusion protein. In one aspect, a nucleic acid encoding a polypeptide of the invention is assembled in appropriate phase with a leader sequence capable of directing secretion of the translated polypeptide or fragment thereof. Technology pertaining to vectors encoding fusion proteins and application of fusion proteins are well disclosed in the scientific and patent literature, see e.g., Kroll (1993) *DNA Cell. Biol.* 12:441-53.

[0392] The nucleic acids and polypeptides of the invention can be bound to a solid support, e.g., for use in screening and diagnostic methods. Solid supports can include, e.g., membranes (e.g., nitrocellulose or nylon), a microtiter dish (e.g., PVC, polypropylene, or polystyrene), a test tube (glass or plastic), a dip stick (e.g., glass, PVC, polypropylene, polystyrene, latex and the like), a microfuge tube, or a glass, silica, plastic, metallic or polymer bead or other substrate such as paper. One solid support uses a meta (e.g., cobalt or nickel)-comprising column which binds with specificity to a histidine tag e gineered onto a peptide.

[0393] Adhesion of molecules to a solid support can be direct (i.e., the molecule conta ts the solid support) or indirect (a "linker" is bound to the support and the molecule of interest binds to this linker). Molecules can be immobilized either covalently (e.g., utilizing single reactive thiol groups of cysteine residues (see, e.g., Colliuod (1993) *Bioconjugate Chem.* 4:528-536) or non-covalently but specifically (e.g., via immobilized antibodies (see, e.g., Schuhmann (1991) *Adv. Mater.* 3:388-391; Lu (1995) *Anal. Chem.* 67:83-87; the biotin/strepavidin system (see, e.g., Iwane (1997) *Biophys. Biochem. Res.* Comm. 230:76-80); metal chelating, e.g., Langmuir-Blodgett films (see, e.g., Ng (1995) *Langmuir* 11:4048-55); metal-chelating self-assembled monolayers (see, e.g., Sigal (1996) *Anal. Chem.* 68:490-497) for binding of polyhistidine fusions.

[0394] Indirect binding can be achieved using a variety of linkers which are commercially available. The reactive ends can be any of a variety of functionalities including, but not limited to: amino reacting ends such as N-hydroxysuccinimide (NHS) active esters, imidoesters, aldehydes, epoxides, sulfonyl halides, isocyanate, isothiocyanate, and nitroaryl halides; and thiol reacting ends such as pyridyl disulfides, maleimides, thiophthalimides,

and active halogens. The heterobifunctional crosslinking reagents have two different reactive ends, e.g., an amino-reactive end and a thiol-reactive end, while homobifunctional reagents have two similar reactive ends, e.g., bismaleimidohexane (BMH) which permits the cross-linking of sulfhydryl-containing compounds. The spacer can be of varying length and be aliphatic or aromatic. Examples of commercially available homobifunctional cross-linking reagents include, but are not limited to, the imidoesters such as dimethyl adipimidate dihydrochloride (DMA); dimethyl pimelimidate dihydrochloride (DMP); and dimethyl suberimidate dihydrochloride (DMS). Heterobifunctional reagents include commercially available active halogen-NHS active esters coupling agents such as N-succinimidyl bromoacetate and N-succinimidyl (4-iodoacetyl)aminobenzoate (SIAB) and the sulfosuccinimidyl derivatives such as sulfosuccinimidyl(4-iodoacetyl)aminobenzoate (sulfo-SIAB) (Pierce). Another group of coupling agents is the heterobifunctional and thiol cleavable agents such as N-succinimidyl 3-(2-pyridyidithio)propionate (SPDP) (Pierce Chemicals, Rockford, IL).

[0395] Antibodies can also be used for binding polypeptides and peptides of the invention to a solid support. This can be done directly by binding peptide-specific antibodies to the column or it can be done by creating fusion protein chimeras comprising motif-containing peptides linked to, e.g., a known epitope (e.g., a tag (e.g., FLAG, myc) or an appropriate immunoglobulin constant domain sequence (an "immunoadhesin," see, e.g., Capon (1989) *Nature* 377:525-531 (1989).

[0396] Nucleic acids or polypeptides of the invention can be immobilized to or applied to an array. Arrays can be used to screen for or monitor libraries of compositions (e.g., small molecules, antibodies, nucleic acids, etc.) for their ability to bind to or modulate the activity of a nucleic acid or a polypeptide of the invention. For example, in one aspect of the invention, a monitored parameter is transcript expression of a gene comprising a nucleic acid of the invention. One or more, or, all the transcripts of a cell can be measured by hybridization of a sample comprising transcripts of the cell, or, nucleic acids representative of or complementary to transcripts of a cell, by hybridization to immobilized nucleic acids on an array, or "biochip." By using an "array" of nucleic acids on a microchip, some or all of the transcripts of a cell can be simultaneously quantified. Alternatively, arrays comprising genomic nucleic acid can also be used to determine the genotype of a newly engineered strain made by the methods of the invention. Polypeptide arrays" can also be used to simultaneously quantify a plurality of proteins.

[0397] The terms "array" or "microarray" or "biochip" or "chip" as used herein is a plurality of target elements, each target element comprising a defined amount of one or more polypeptides (including antibodies) or nucleic acids immobilized onto a defined area of a substrate surface. In practicing the methods of the invention, any known array and/or method of making and using arrays can be incorporated in whole or in part, or variations thereof, as disclosed, for example, in U.S. Patent Nos. 6,277,628; 6,277,489; 6,261,776; 6,258,606; 6,054,270; 6,048,695; 6,045,996; 6,022,963; 6,013,440; 5,965,452; 5,959,098; 5,856,174; 5,830,645; 5,770,456; 5,632,957; 5,556,752; 5,143,854; 5,807,522; 5,800,992; 5,744,305; 5,700,637; 5,556,752; 5,434,049; see also, e.g., WO 99/51773; WO 99/09217; WO 97/46313; WO 96/17958; see also, e.g., Johnston (1998) *Curr. Biol.* 8:R171-R174; Schummer (1997) *Biotechniques* 23:1087-1092; Kern (1997) *Biotechniques* 23:120-124; Solinas-Toldo (1997) *Genes, Chromosomes & Cancer* 20:399-407; Bowtell (1999) *Nature Genetics Supp.* 21:25-32. See also published U.S. patent applications Nos. 20010018642; 20010019827; 20010016322; 20010014449; 20010014448; 20010012537; 20010008765.

Host Cells and Transformed Cells Comprising Kinase Sequences

[0398] As indicated above, availability of kinase coding sequences also allows provision of a transformed cell comprising a kinase nucleic acid sequence, *e.g.*, a sequence encoding a kinase polypeptide, or a vector. The host cell may be any of the host cells familiar to those skilled in the art, including prokaryotic cells, eukaryotic cells, such as bacterial cells, fungal cells, yeast cells, mammalian cells, insect cells, or plant cells. Exemplary bacterial cells include *E. coli*, *Streptomyces*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*. Exemplary insect cells include *Drosophila* S2 and *Spodoptera* Sf9. Exemplary animal cells include CHO, COS or Bowes melanoma or any mouse or human cell line. The selection of an appropriate host is within the abilities of those skilled in the art.

[0399] Vectors may be introduced into the host cells using any of a variety of techniques, including transformation, transfection, transduction, viral infection, gene guns, or Ti-mediated gene transfer. Particular methods include calcium phosphate transfection, DEAE-Dextran mediated transfection, lipofection, or electroporation.

[0400] Engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants or amplifying the genes of the invention. Following transformation of a suitable host strain and growth of the host strain

to an appropriate cell density, the selected promoter may be induced by appropriate means (e.g., temperature shift or chemical induction) and the cells may be cultured for an additional period to allow them to produce the desired polypeptide or fragment thereof.

[0401] Cells can be harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract is retained for further purification. Microbial cells employed for expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents. Such methods are well known to those skilled in the art. The expressed polypeptide or fragment can be recovered and purified from recombinant cell cultures by methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Protein refolding steps can be used, as necessary, in completing configuration of the polypeptide. If desired, high performance liquid chromatography (HPLC) can be employed for final purification steps.

[0402] Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts and other cell lines capable of expressing proteins from a compatible vector, such as the C127, 3T3, CHO, HeLa and BHK cell lines.

[0403] The constructs in host cells can be used in a conventional manner to produce the gene product encoded by the recombinant sequence. Depending upon the host employed in a recombinant production procedure, the polypeptides produced by host cells containing the vector may be glycosylated or may be non-glycosylated. Polypeptides of the invention may or may not also include an initial methionine amino acid residue.

[0404] Cell-free translation systems can also be employed to produce a polypeptide of the invention. Cell-free translation systems can use mRNAs transcribed from a DNA construct comprising a promoter operably linked to a nucleic acid encoding the polypeptide or fragment thereof. In some aspects, the DNA construct may be linearized prior to conducting an *in vitro* transcription reaction. The transcribed mRNA is then incubated with an appropriate cell-free translation extract, such as a rabbit reticulocyte extract, to produce the desired polypeptide or fragment thereof.

[0405] The expression vectors can contain one or more selectable marker genes to provide a phenotypic trait for selection of transformed host cells such as dihydrofolate reductase or neomycin resistance for eukaryotic cell culture, or such as tetracycline or ampicillin resistance in *E. coli*.

[0406] For transient expression in mammalian cells, cDNA encoding a polypeptide of interest may be incorporated into a mammalian expression vector, e.g. pcDNA1, which is available commercially from Invitrogen Corporation (San Diego, Calif., U.S.A.; catalogue number V490-20). This is a multifunctional 4.2 kb plasmid vector designed for cDNA expression in eukaryotic systems, and cDNA analysis in prokaryotes, incorporated on the vector are the CMV promoter and enhancer, splice segment and polyadenylation signal, an SV40 and Polyoma virus origin of replication, and M13 origin to rescue single strand DNA for sequencing and mutagenesis, Sp6 and T7 RNA promoters for the production of sense and anti-sense RNA transcripts and a Col E1-like high copy plasmid origin. A polylinker is located appropriately downstream of the CMV promoter (and 3' of the T7 promoter).

[0407] The cDNA insert may be first released from the above phagemid incorporated at appropriate restriction sites in the pcDNAI polylinker. Sequencing across the junctions may be performed to confirm proper insert orientation in pcDNAI. The resulting plasmid may then be introduced for transient expression into a selected mammalian cell host, for example, the monkey-derived, fibroblast like cells of the COS-1 lineage (available from the American Type Culture Collection, Rockville, Md. as ATCC CRL 1650).

[0408] For transient expression of the protein-encoding DNA, for example, COS-1 cells may be transfected with approximately 8 μg DNA per 10^6 COS cells, by DEAE-mediated DNA transfection and treated with chloroquine according to the procedures described by Sambrook et al, Molecular Cloning: A Laboratory Manual, 1989, Cold Spring Harbor Laboratory Press, Cold Spring Harbor N.Y, pp. 16.30-16.37. An exemplary method is as follows. Briefly, COS-1 cells are plated at a density of 5 x 10^6 cells/dish and then grown for 24 hours in FBS-supplemented DMEM/F12 medium. Medium is then removed and cells are washed in PBS and then in medium. A transfection solution containing DEAE dextran (0.4 mg/ml), 100 μM chloroquine, 10% NuSerum, DNA (0.4 mg/ml) in DMEM/F12 medium is then applied on the cells 10 ml volume. After incubation for 3 hours at 37 °C, cells are washed in PBS and medium as just described and then shocked for 1 minute with 10% DMSO in DMEM/F12 medium. Cells are allowed to grow for 2-3 days in 10% FBS-

supplemented medium, and at the end of incubation dishes are placed on ice, washed with ice cold PBS and then removed by scraping. Cells are then harvested by centrifugation at 1000 rpm for 10 minutes and the cellular pellet is frozen in liquid nitrogen, for subsequent use in protein expression. Northern blot analysis of a thawed aliquot of frozen cells may be used to confirm expression of receptor-encoding cDNA in cells under storage.

[0409] In a like manner, stably transfected cell lines can also prepared, for example, using two different cell types as host: CHO K1 and CHO Pro5. To construct these cell lines, cDNA coding for the relevant protein may be incorporated into the mammalian expression vector pRC/CMV (Invitrogen), which enables stable expression. Insertion at this site places the cDNA under the expression control of the cytomegalovirus promoter and upstream of the polyadenylation site and terminator of the bovine growth hormone gene, and into a vector background comprising the neomycin resistance gene (driven by the SV40 early promoter) as selectable marker.

[0410] An exemplary protocol to introduce plasmids constructed as described above is as follows. The host CHO cells are first seeded at a density of $5x10^5$ in 10% FBS-supplemented MEM medium. After growth for 24 hours, fresh medium is added to the plates and three hours later, the cells are transfected using the calcium phosphate-DNA co-precipitation procedure (Sambrook et al, supra). Briefly, 3 μg of DNA is mixed and incubated with buffered calcium solution for 10 minutes at room temperature. An equal volume of buffered phosphate solution is added and the suspension is incubated for 15 minutes at room temperature. Next, the incubated suspension is applied to the cells for 4 hours, removed and cells were shocked with medium containing 15% glycerol. Three minutes later, cells are washed with medium and incubated for 24 hours at normal growth conditions. Cells resistant to neomycin are selected in 10% FBS-supplemented alpha-MEM medium containing G418 (1 mg/ml). Individual colonies of G418-resistant cells are isolated about 2-3 weeks later, clonally selected and then propagated for assay purposes.

EXAMPLES

EXAMPLE 1: Cloning of PIM-1

[0411] The PIM-1 DNA encoding amino acids 1-313 and 29- 313 were amplified from human brain cDNA (Clonetech) by PCR protocols and cloned into a modified pET 29 vector (Novagen) between NdeI and SalI restriction enzyme sites. The amino acid

sequences of the cloned DNA were confirmed by DNA sequencing and the expressed proteins contain a hexa-histidine sequence at the C terminus. The protein was expressed in *E. coli* BL21(DE3)pLysS (Novagen). The bacteria were grown at 22°C in Terrific broth to 1-1.2 OD600 and protein was induced by 1 mM IPTG for 16-18 h. The bacterial pellet was collected by centrifugation and stored at -70°C until used for protein purification. PIM-2 and PIM-3 are cloned similarly.

EXAMPLE 2: Purification of PIM-1

[0412] The bacterial pellet of approximately 250-300g (usually from 16 L) expressing PIM-1 kinase domain (29-313) was suspended in 0.6 L of Lysis buffer (0.1 M potassium phosphate buffer, pH 8.0, 10 % glycerol, 1 mM PMSF) and the cells were lysed in a French Pressure cell at 20,000 psi. The cell extract was clarified at 17,000 rpm in a Sorval SA 600 rotor for 1 h. The supernatant was re-centrifuged at 17000 rpm for another extra hour. The clear supernatant was added with imidazole (pH 8.0) to 5 mM and 2 ml of cobalt beads (50% slurry) to each 40 ml cell extract. The beads were mixed at 4°C for 3-4 h on a nutator. The cobalt beads were recovered by centrifugation at 4000 rpm for 5 min. The pelleted beads were washed several times with lysis buffer and the beads were packed on a Byroad disposable column. The bound protein was eluted with 3-4 column volumes of 0.1 M imidazole followed by 0.25 M imidazole prepared in lysis buffer. The eluted protein was analyzed by SDS gel electrophoresis for purity and yield.

[0413] The eluted protein from cobalt beads was concentrated by Centriprep-10 (Amicon) and separated on Pharmacia Superdex 200 column (16/60) in low salt buffer (25 mM Tris-HCl, pH 8.0, 150 mM NaCl, 14 mM beta mercaptoethanol). The peak fractions containing PIM-1 kinase was further purified on a Pharmacia Source Q column (10/10) in 20 mM Tris-HCl pH 7.5 and 14 mM beta mercaptoethanol using a NaCl gradient in an AKTA-FPLC (Pharmacia). The PIM-1 kinase eluted approximately at 0.2 M NaCl gradient. The peak fractions were analyzed by SDS gel electrophoresis and were pooled and concentrated by Centriprep 10. The concentrated PIM-1 protein (usually 50-60 A280/ml) was aliquoted into many tubes (60ul), flash frozen in liquid nitrogen and stored at -70°C until used for crystallization. The frozen PIM-1 kinase still retained kinase activity as concluded from activity assays. PIM-2 and PIM-3 can be purified in the same way with small adjustments to conditions, *e.g.*, elution conditions.

Example 3: Variants and Derivatives of PIM-1

[0414] In mouse, PIM-1 is expressed as two forms of 44 kDa and 33 kDa. The p44 kDa PIM-1 is encoded by the same gene as p33 kDa PIM-1 but the translation is initiated at an upstream CUG codon (Saris CJ, Domen J, and Berns A. (1991) The PIM-1 oncogene encodes two related protein-serine/threonine kinases by alternative initiation at AUG and CUG. EMBO J. 10: 655-664.) This results in expression of p44 PIM-1 having a unique 11 kDa N terminal extension that is followed by the p33 PIM-1 sequence. The p33 kDa PIM-1 contains almost the entire kinase domain and both p33 and p44 kDa have comparable kinase activity and both can prevent apoptosis (Lilly M, Sandholm J, Cooper JJ, Koskinen PJ, and Kraft A. (1999) The PIM-1 serine kinase prolongs survival and inhibits apoptosis-related mitochondrial dysfunction in part through a bcl-2-dependent pathway. Oncogene., 18: 4022-4031). CD40 engagement caused significant increase in the levels of both 33 and 44 kDa forms of PIM1 in cytoplasmic extracts of WEHI-231 cells (Zhu N, Ramirez LM, Lee RL, Magnuson NS, Bishop GA, and Gold MR.(2002) CD40 signaling in B cells regulates the expression of the PIM-1 kinase via the NF-kappa B pathway. J Immunol. 168: 744-754). Recently it has been shown that the p33kDa form was more strongly associated with Socs-1 than the p44 kDa form (Chen XP, Losman JA, Cowan S, Donahue E, Fay S, Vuong BQ, Nawijn MC, Capece D, Cohan VL, Rothman P. (2002) PIM serine/threonine kinases regulate the stability of Socs-1 protein. Proc Natl Acad Sci U S A., 99:2175-2180).

[0415] There are no reports of PIM-1 existing in more than one form in human. Analysis of PIM-1 gene sequence reveals that the presence of in-frame stop codons block synthesis of proteins with N terminal extensions. However, the human PIM-2 gene contains no in-frame stop codon, based on the reported DNA sequence. Therefore, alternate initiation at an upstream start codon is possible. We have expressed the PIM-2 kinase domain in *E.coli* and purified the protein by the same methods as described for PIM-1 kinase.

Example 4: Crystallization of PIM-1.

PIM-1 protein crystal growth:

[0416] All materials were purchased through Hampton Research, Inc. (Laguna Niguel, CA) unless otherwise noted.PIM-1 protein @ 7 and 14 mg/ml was screened against Hampton Crystal Screen 1 and 2 kits (HS1 and HS2) and yielded successful crystals growing in at least 10 conditions from HS1 alone. Crystals were grown initially using

sitting drops against the Hampton screening conditions set in Greiner 96 well CrystalQuick crystallization plates with 100 ul reservoir and 1 ul protein + 1 ul reservoir added per platform (1 of 3 available). Conditions from Hampton Screen 1 yielded obvious protein crystals in conditions: #2,7,14,17,23,25,29,36,44,and 49. These crystals were grown at 4°C, and grew in size to varying dimensions, all hexagonal rod shaped and hardy.

[0417] Crystals of larger dimensions, 100 uM wide x 400 uM long, were then grown in larger drop volumes and in larger dimension plates. Refined grids were performed with both hanging and sitting drop methods in VDX plates (cat. # HR3- 140) or CrysChem plates (cat. # HR3-160). There appeared to be no obvious difference of crystal size or quality between the two methods, but there was a preference to use hanging drops to facilitate mounting procedures.

[0418] We proceeded with refining conditions by gridding 4 independent reservoir conditions initially obtained from the screening kits.

1) HS1 # 17 was optimized to 0.2 M LiCl, 0.1 M Tris pH 8.5 and 5%- 15% Polyethylene glycol 4000;
2) HS1 # 25 was optimized to 0.4 M – 0.9 M Sodium Acetate trihydrate pH 6.5 and 0.1 M Imidazole;
3) HS1 # 29 was optimized to 0.2M – 0.7 M Sodium Potassium tartrate and 0.1 M MES buffer pH 6.5;
4) HS1 # 44 was optimized to 0.25 M Magnesium formate.

[0419] These optimized conditions produced crystals with the most consistent size and quality of appearance. Conditions were further evaluated by x-ray diffraction analysis of the resulting protein crystals, and keeping in mind the utility for forming compound co-crystals in these conditions as well (ie. salt composition and concentration effects are important to develop suitable compound solubility in the crystallization experiments). Native crystals grew as rods in many drops to large dimensions of approximately 100 um wide and 500 um long.

Seleno Methionine labeled PIM-1 protein crystal growth.

[0420] Se-Met labeled PIM protein was expressed and purified as described by Hendrickson, W. A., and Ogata, C. M. (1997) "Phase determination from multiwavelength anomalous diffraction measurements, *Methods Enzymol.*, **276**, 494-523, and Hendrickson,

W. A., Horton, J. R., and LeMaster, D. M. (1990) "Selenomethionyl proteins produced for analysis by multiwavelength anomalous diffraction (MAD): a vehicle for direct determination of three-dimentional structure, *EMBO J.*, **9**, 1665-1672. This preparation appeared to be less soluble as evidenced by more pronounced nucleation within the screen drops and due to the hydrophobic nature of Se labeled proteins. Crystals grew small and in showers compared to the previously evaluated similar drop conditions that the native protein grew well in. Upon finer gridding, 20 μm wide x 100 μm long crystals were obtained in condition HS1 # 17 optimized at 0.2 M LiCl, 0.1 M Tris pH 8.5 and 5% -15% PEG 4000. These crystals and all others were carefully mounted in 50 – 100 uM nylon loops on copper stem magnetic bases that were flash frozen in liquid nitrogen in appropriate cryogenic buffer and taken to the Lawerence Berkeley Lab synchrotron, the Advanced Light Source (ALS) beamline 8.3.1.

PIM-1 protein/Molecular Scaffolds Co-crystal growth:

[0421] In order to add compounds to PIM-1 protein, compounds were added directly from their DMSO stocks (20-200 mM) into the protein solution at high concentration. The procedure involved adding the DMSO stocks containing compound as a thin layer to the wall of the 1.5 ml eppendorf tube that contains the protein. The solution was then gently rolled over the wall of the tube until the compound was in the protein solution. The final concentration of compounds in the PIM-1 solution usually achieved was between 0.5 and 1 mM with DMSO concentrations less than 2% being added. The solutions were then set-up in trays immediately as previously described.

PIM-1/Compound Co-crystal Screening in HS1:

[0422] Two conditions for crystal growth have resulted in the best results with PIM-1 protein and added compounds. The optimized Na-K tartrate and Na-acetate tetrahydrate solutions listed above. Crystals varied greatly in size but data has been collected on various crystals that are between 20 uM and 100 uM in width. These crystals were typically several hundred microns long and some required manipulation as well as being broken to facilitate mounting procedures into loops. Interestingly, some crystals that were grown in the presence of colored compounds were also colored the same way.

Example 5: Diffraction Analysis of PIM-1.

[0423] Crystals were first determined to diffract on a Rigaku RU-200 rotating copper anode x-ray source equipped with Yale focusing optics and an R-AXIS 2C imaging plate system. A crystal grown in the optimized condition HS1 # 17 (DY plate 12/14/01) was used to conduct initial diffraction experiments.

[0424] After x-ray diffraction was initially determined as described above, large native protein crystals grown in Mg-Formate (DY plate) and were frozen in cryoprotectant by submersion in liquid nitrogen and then tested for diffraction at ALS beamline 8.3.1. Data was originally collected, indexed and reduced using Mosflm. The spacegroup was determined to be P65.

[0425] We have collected 3 native data sets, the highest resolution obtained with good statistics after merging is to 2.0 angstroms.

[0426] We have collected a MAD data set on the Se-Met labeled PIM-1 crystal using the experimentally determined 12668 eV peak and 11000 eV remote for selenium to 3.2 angstroms. Subsequently a 2.6 angstrom Se peak data set was collected at the experimentally determined peak of 12668 eV radiation.

[0427] We have collected more than 50 PIM-1/binding compound co-crystal data sets. All data was indexed and reduced as indicated in the computational crystallographic work that follows.

PIM-1 Structure Determination and Refinement

Data set: Native, Resolution: 2.13 Å

[0428] The primary structure determination was carried out using Molecular Replacement method with programs

EPMR (Public domain)

AmoRe (from CCP4))

And a homology model of PIM-1 based on the protein Phosphorylase Kinase (PDB ID: 1PHK – Owen et al., 1995, *Structure* 3:467)

[0429] The molecular replacement was carried out in all of the P6 space groups (P61, P62, ... P65). The best solution was obtained in P65.

[0430] The molecular replacement solution was improved by several rounds of the cycles of

Model Building in O (from DatOno AB)
Annealing in CNX (from Accelerys)
SigmaA weighting and Solvent Flattening the resultant map with DM (from CCP4)

[0431] The statistics at the end of these cycles were R ~ 36 %.

Data set: SeMet (2 wavelengths), Resolution: 3.3 Å

[0432] The MAD phased data (with SOLVE (from Los Alamos National Laboratory)) helped improve the model in the refinement with REFMAC (from CCP4).

Data set: SeMet (1 wavelength), Resolution: 2.6 Å

[0433] Further improvement of the model was obtained using SAD Phasing with SOLVE and subsequent improvement with RESOLVE produced an excellent map into which the PIM1 model could be rebuilt completely.

[0434] The newly built model refined with CNX/Anneal and then with CCP4/Refmac to give R = 27.7% and Rfree = 31.9 %

Data set: Native, Resolution: 2.1 Å

[0435] The above model has been further refined against the native data with CCP4/Refmac, giving R = 22.1 %, Rfree = 24.2 %.

Example 6: Co-Crystal Structures

[0436] Exemplary co-crystal structures have been determined for 7 compounds with PIM-1, using methods as generally described above. Those co-crystals are the following (the number indicates the compound id and the compound source is provided in parentheses):

PIM1_5321980 (Chembridge)
PIM1_RB00137 (Maybridge)
PIM1_5264241(Chembridge)
PIM1_RJF00907 (Maybridge)
PIM1_5140994 (Chembridge)
PIM1_5108305 (Chembridge)
PIM1_BTB02713 (Maybridge)

Example 7: PIM Binding Assays

[0437] Such binding assays can be performed in a variety of ways, including a variety of ways known in the art. For example, competitive binding to PIM-1 can be measured on Nickel-FlashPlates, using His-tagged PIM-1 (~ 100 ng) and ATPγ[^{35}S] (~ 10 nCi). As compound is added, the signal decreases, since less ATPγ[^{35}S] is bound to PIM1 which is proximal to the scintillant in the FlashPlate. The binding assay can be performed by the addition of compound (10 µl; 20 mM) to PIM-1 protein (90 10 µl) followed by the addition of ATPγ[^{35}S] and incubating for 1 hr at 37°C. The radioactivity is measured through scintillation counting in Trilus (Perkin-Elmer).

[0438] Alternatively, any method which can measure binding of a ligand to the ATP-binding site can be used. For example, a fluorescent ligand can be used. When bound to PIM1, the emitted fluorescence is polarized. Once displaced by inhibitor binding, the polarization decreases.

[0439] Determination of IC50 for compounds by competitive binding assays. (Note that K_I is the dissociation constant for inhibitor binding; K_D is the dissociation constant for substrate binding.) For this system, the IC50, inhibitor binding constant and substrate binding constant can be interrelated according to the following formula:

[0440] When using radiolabeled substrate $K_I = \frac{IC50}{1 + [L^*]/K_D}$,

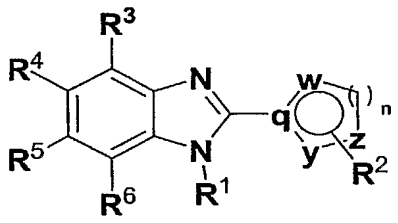
the IC50 ~ K_I when there is a small amount of labeled substrate.

Example 8: PIM Activity Assays

[0441] Inhibitory or exhitory activity of compounds binding to PIM-1 was determined using the kinase activity assay described in the detailed description.

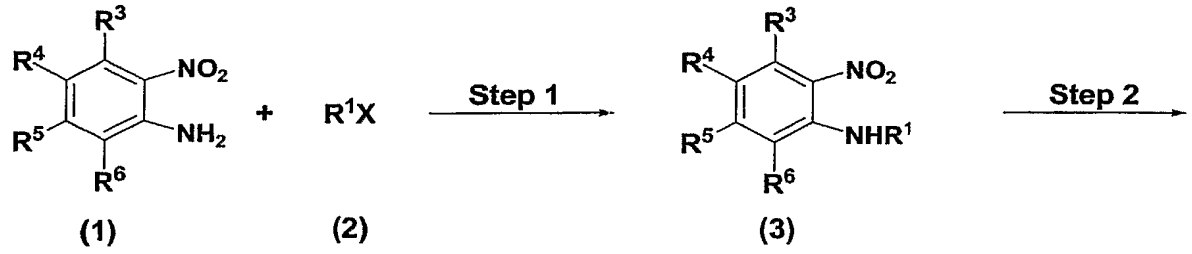
[0442] Exemplary compounds within Formula I, Formula II, and Formula III were assayed for inhibitory activity with PIM-1. The ability to develop ligands is illustrated by 2 compounds from the quinolinone molecular scaffold group (Formula III). A compound with R1, R2, R3, R4, R5, and R6 = H, had 100% inhibition of PIM-1 at 200 μM concentration, while a compound with R1 = phenyl group, R2, R3, R5, and R7 = H, and R4 = OCF_3, had only 3% inhibition of PIM-1 at 200 μM.

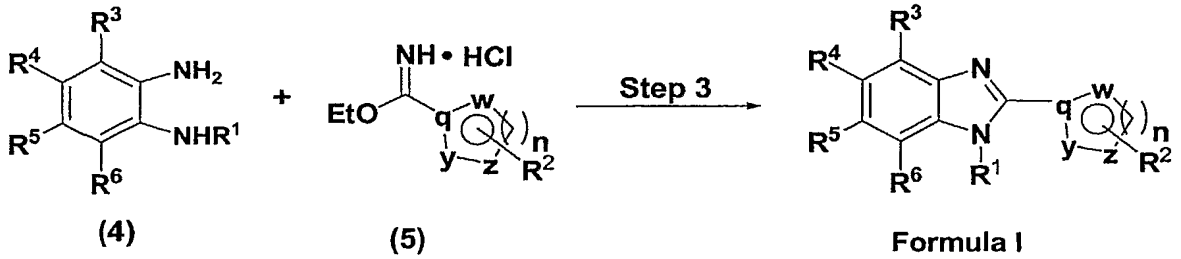
Example 9: Synthesis of the Compounds of Formula I:



Formula I

1. Synthesis of the Compounds of Formula I - Scheme 1





[0443] The 2-arylbenzimidazoles derivatives, represented by Formula I, can be prepared as shown in Scheme 1.

Step 1 Preparation of formula (3)

[0444] Compound of formula (3) was prepared by a reaction of a compound of formula (1) with an alkyl halide of formula (2)(e.g. X = Br) in an inert solvent (e.g. DMF), in the presence of a base (e.g. NaH) and heated near 100 ^{0}C for 24-36 h. Compound of formula (3) was purified by column chromatography.

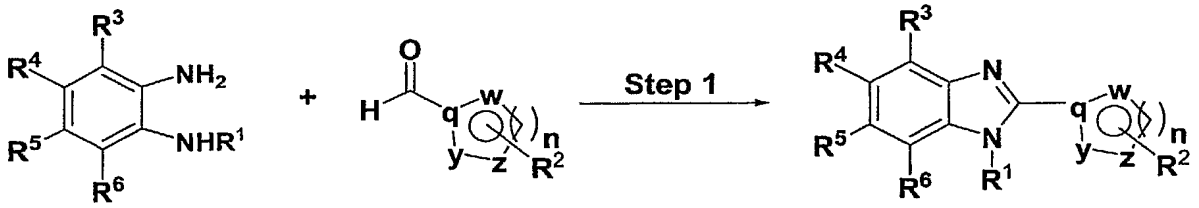
Step 2 Preparation of formula (4)

[0445] Compound of formula (4) was prepared by a reaction of a compound of formula (3) with a reducing agent (e.g. $SnCl_2$) in a polar solvent (e.g. EtOH)and heated near 100 ^{0}C for 5-12 h. When the reaction is completed, the product of formula (4) is isolated by conventional means (e.g. aqueous base workup).

Step 3 Preparation of formula I

[0446] Compound of formula I was prepared by the reaction of the compound of formula (4) with an imidate of formula (5) in a polar solvent (e.g. EtOH) and heated near 80°C for 12-18 h. Compound of formula I was purified by column chromatography.

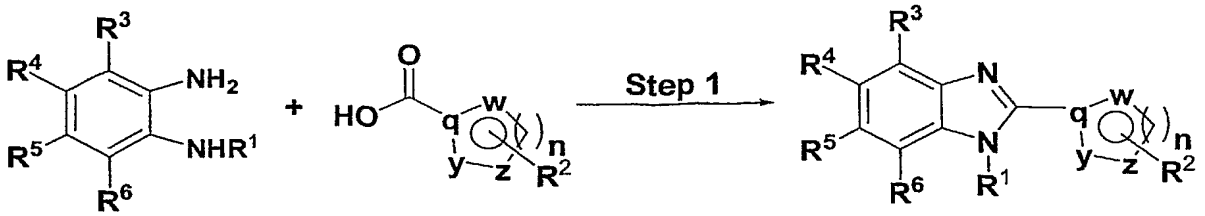
2. Alternate synthesis of the Compounds of Formula I - Scheme 2



Step 1 Preparation of formula I

[0447] Compound of formula I was prepared by the reaction of the compound of formula (4) with an aldehyde of formula (6) in a polar solvent (e.g. EtOH) and heated near 80°C for 12-22 h. Compound of formula I was purified by column chromatography.

3. Alternate synthesis of the Compounds of Formula I - Scheme 3

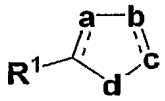


(4) (7) Formula I

Step 1 Preparation of formula I

[0448] Compound of formula I was prepared by the reaction of the compound of formula (4) with an aldehyde of formula (7) in an inorganic acid (e.g. polyphosphoric acid) and heating near 190-220 ^{0}C for 5-12 h. Compound of formula I was purified by column chromatography.

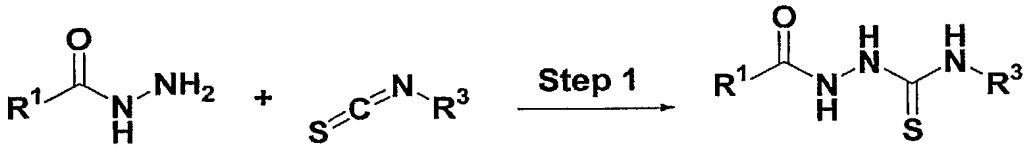
Example 10: Synthesis of the Compounds of Formula II:



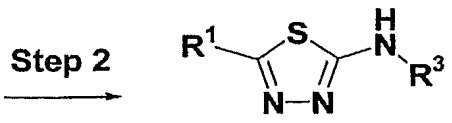
Formula II

[0449] Synthesis schemes for exemplary groups of compounds within Formula II are provided below. Persons skilled in chemical synthesis will readily understand how to synthesize additional compounds within Formula II.

1. Synthesis of the Compounds of Formula IIa (where a and b are nitrogen, d is sulfur, and c is CR^{11}) - Scheme 4



(8) (9) (10)



Formula IIa

[0450] The thiadiazole derivative, represented by formula IIa, can be prepared as shown in Scheme 4.

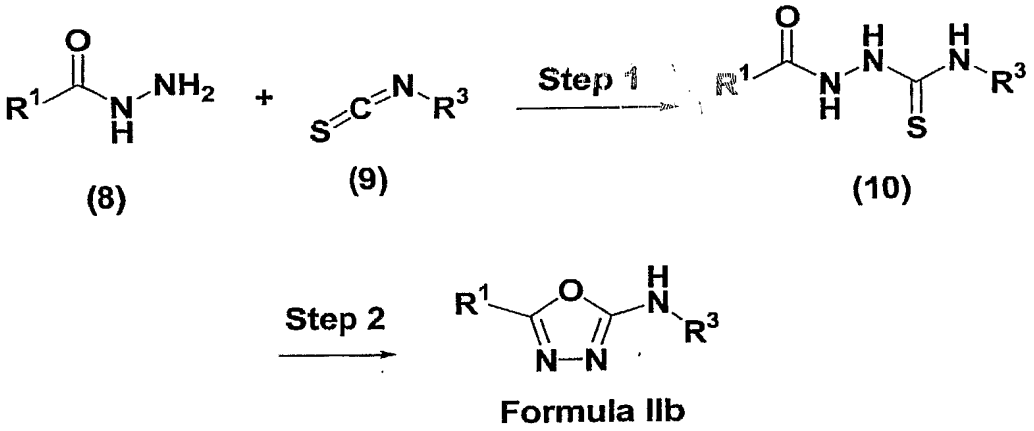
Step-1 Preparation of formula (10)

[0451] Compound of formula (10) was prepared by reaction of a compound of formula (8) (e.g. *m*-toluic hydrazide) with an isothiocyanate of formula (9), in a basic solvent (e.g. pyridine), typically heated near 65 °C for 2-6 hours.

Step-2 Preparation of formula IIa

[0452] Compound of formula IIa was prepared by dissolving a compound of formula (10) in $POCl_3$ and heated near 80 °C for 2 -4 hours. When the reaction is substantially complete, the product of formula IIa is isolated by conventional means (e.g. reverse phase HPLC).

2. Synthesis of the Compounds of Formula IIb (where a and b are nitrogen, d is oxygen, and c is CR^{11}) - Scheme 5



[0453] The oxadiazole derivatives, represented by formula IIb, can be prepared as shown in Scheme 5.

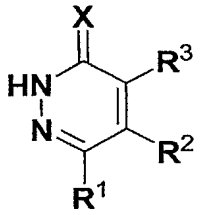
Step-1 Preparation of formula (10)

[0454] Compound of formula (10) was prepared by reaction of a compound of formula (8), e.g. *m*-toluic hydrazide, with an isothiocyanate of formula (9), in a basic solvent (e.g. pyridine), typically heated near 65 °C for 2-6 hours.

Step-2 Preparation of formula IIb

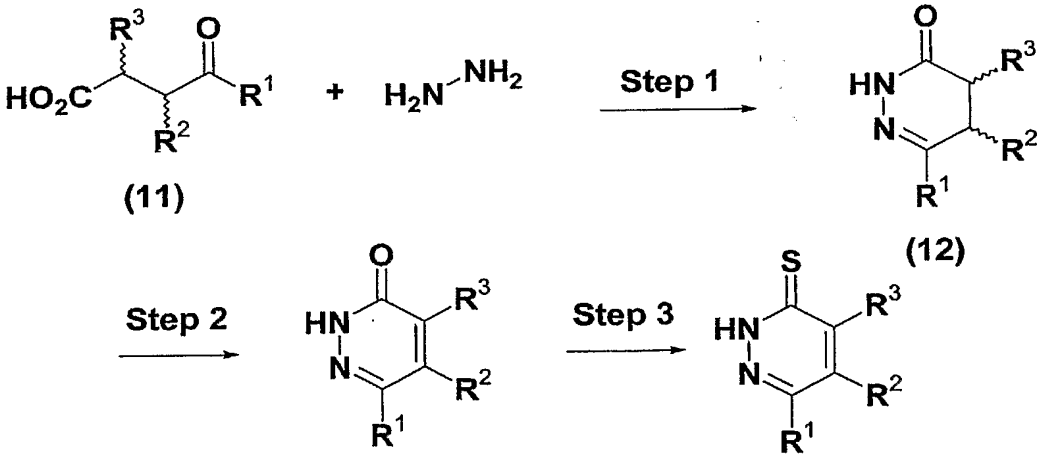
[0455] Compound of formula IIb was prepared by dissolving a compound of formula (10) in $SOCl_2$ and heated near 80 °C for 2 -4 hours. When the reaction is substantially complete, the product of formula II was isolated by conventional means (e.g. reverse phase HPLC).

Example 11: Synthesis of the Compounds of Formula IIIa, where n = 0:



Formula IIIa

1. Synthesis of the Compounds of Formula IIIa - Scheme 6



Formula IIIaa **Formula IIIab**

where the squiggly lines indicate a mixture of stereoisomers.

[0456] The Pyridazinone derivatives, represented by formula IIIa, can be prepared as shown in Scheme 6.

Step-1 Preparation of formula (12)

[0457] The compound of formula (12) was prepared by reaction of a 4-oxo-butyric acid derivative of formula (11) with hydrazine, in a basic solvent (e.g. pyridine), typically heated near 65 °C for 2-6 hours.

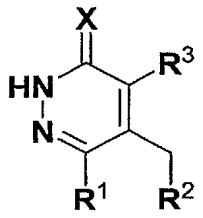
Step-2 Preparation of formula IIIaa

[0458] The compound of formula IIIaa was prepared by dissolving a compound of formula (12) in an inert solvent and adding an oxidizing agent (e.g. Br_2, chloranil, or Pd(C) under an air atmosphere. When the reaction is substantially complete, the product of formula IIIaa is isolated by conventional means (e.g. reverse phase HPLC).

Step-3 Preparation of Formula IIIab

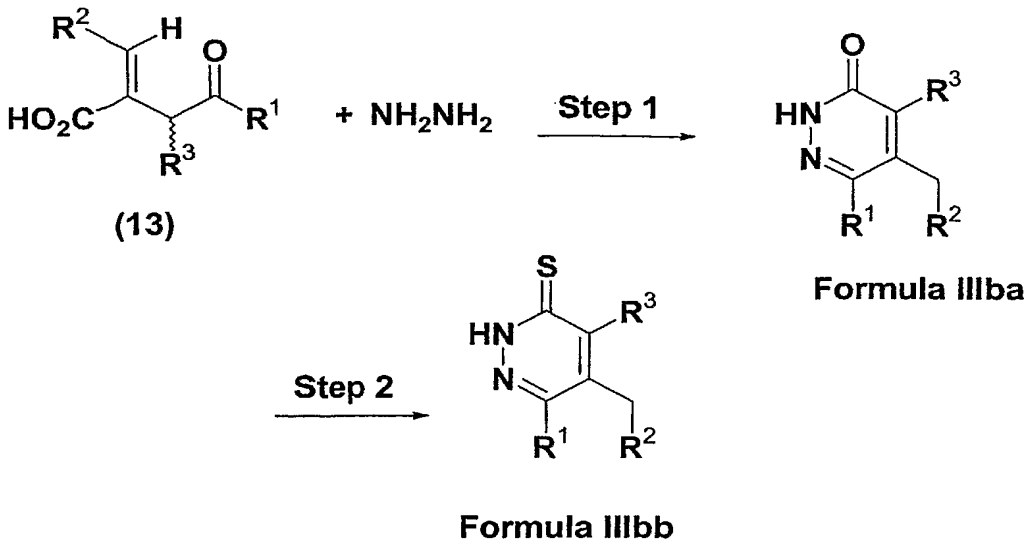
[0459] Compounds of Formula IIIaa (X = 0) can be converted into compounds where X = S, by treatment with Lawesson's reagent or P_2S_5 stirred in an inert solvent at ambient temperature for 2-6 hours. When the reaction is substantially complete, the product of formula IIIb is isolated by conventional means (e.g. reverse phase HPLC).

[0460] Synthesis of the compounds of Formula IIIb, where n = 1:



Formula IIIb

2. Synthesis of Compounds of Formula IIIb (IIIba and IIIbb) - Scheme 7



[0461] The Pyridazinone derivatives, represented by formula IIIba, can be prepared as shown in Scheme 7.

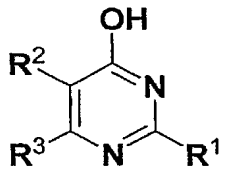
Step-1 Preparation of formula IIIba

[0462] The compound of formula IIIba was prepared by reaction of an acyl-acrylic acid of formula (13) with hydrazine, in a basic solvent (e.g. aqueous NaOH), typically stirred at ambient temperature for 2-6 hours. When the reaction is substantially complete, the product of formula IIIa (X = 0) is isolated by conventional means (e.g. reverse phase HPLC).

Step-2 Preparation of Formula IIIbb

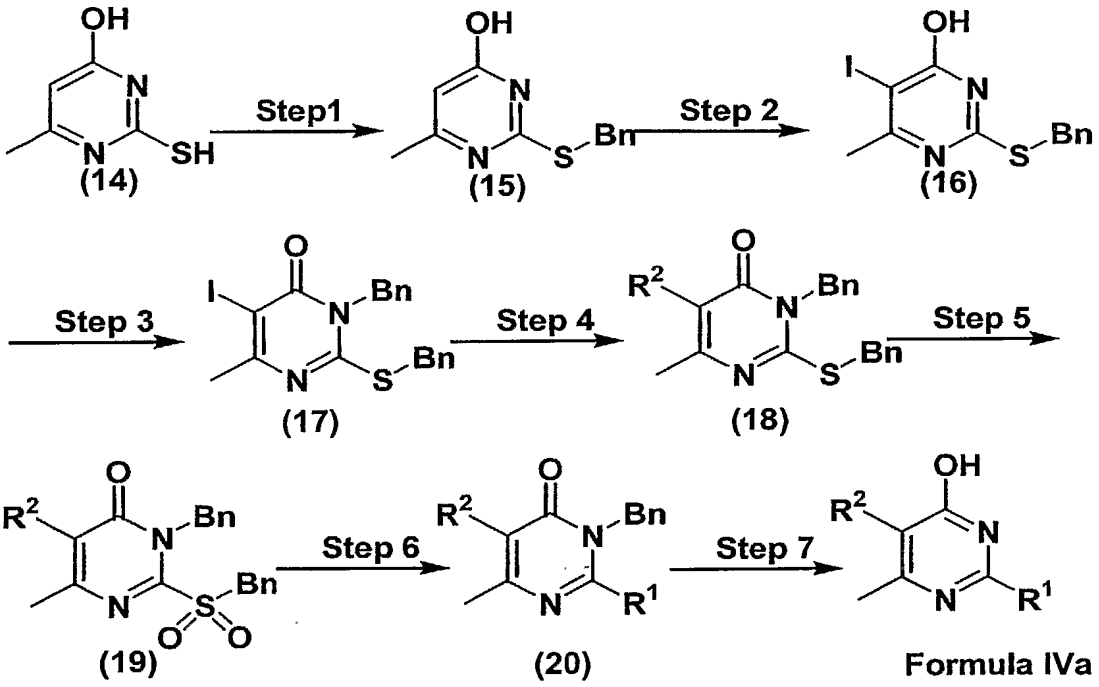
[0463] Compounds of Formula IIIba (X = 0) can be converted into compounds where X = S, by treatment with Lawesson's reagent or P_2S_5 stirred in an inert solvent at ambient temperature for 2-6 hours. When the reaction is substantially complete, the product of formula IIIbb is isolated by conventional means (e.g. reverse phase HPLC).

Example 12: Synthesis of the Compounds of Formula IV:



Formula IV

1. Synthesis of the Compounds of Formula IVa, where R^3 is Methyl - Scheme 8



[0464] The 4-hydroxypyrimidine derivatives, represented by formula IVa, can be prepared as shown in Scheme 8.

Step-1 Preparation of formula (15)

[0465] Compound (15) was prepared by reaction of compound (14) with benzyl bromide in an inert solvent (e.g. DMF), in the presence of a base (e.g. Et_3N), at room temperature for 4 hours. Product (15) is purified by a conventional way (e.g. recrystallization).

Step-2 Preparation of formula (16)

[0466] Compound (16) was prepared by reaction of compound (15) with N-iodosuccinimide in chloroform under reflux for several hours. Product (16) was purified by a conventional way (e.g. recrystallization).

Step-3 Preparation of formula (17)

[0467] Compound (17) was prepared by reaction of compound (16) with benzyl bromide in an inert solvent (e.g. DMF), in the presence of a base (e.g. NaH) at room temperature for several hours.

Step4 Preparation of formula (18)

[0468] The compound of formula (18) was prepared by reaction of compound (17), with a suitable reagent for coupling reaction (e.g. phenylboronic acid) in a suitable mixture of solvent (e.g. dimethoxyethane and water), in the presence of a base (e.g. K_2CO_3), typically heated to 100 ^{0}C for several hours. The product was isolated by a conventional way (e.g. flash chromatography).

Step5 Preparation of formula (19

[0469] The compound of formula (19) was prepared by reaction of a compound of formula (18), with an oxidizing reagent (e.g. MCPBA) in a suitable solvent (e.g. CH_2Cl_2), typically at room temperature for a few hours.

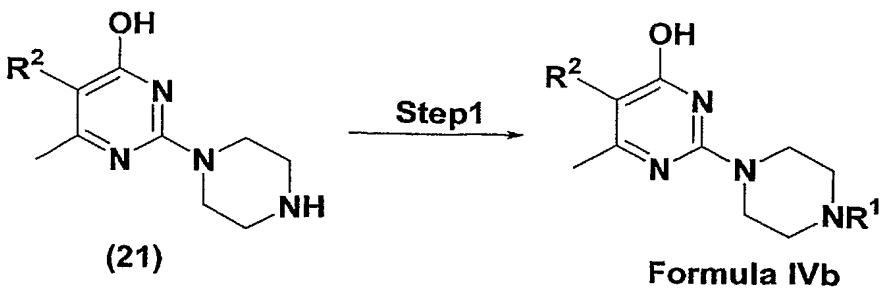
Step6 Preparation of formula (20)

[0470] The compound of formula (20) was prepared by reaction of a compound of formula (19) with a nucleophilic reagent (e.g. piperazine), in the presence of a base (e.g. Cs_2CO_3) in a suitable solvent (e.g. dioxane) reflux for several hours. The product is purified in a conventional way (e.g. flash chromatography).

Step7 Preparation of formula IV

[0471] The compound of formula IVa was prepared conventionally by hydrogenation of a compound of formula (20) in the presence of a catalyst (e.g. $Pd(OH)_2/C$), under hydrogen in a suitable solvent (e.g. methanol) at room temperature for several hours.

2. **Synthesis of the Compounds of Formula IVb - Scheme 9**

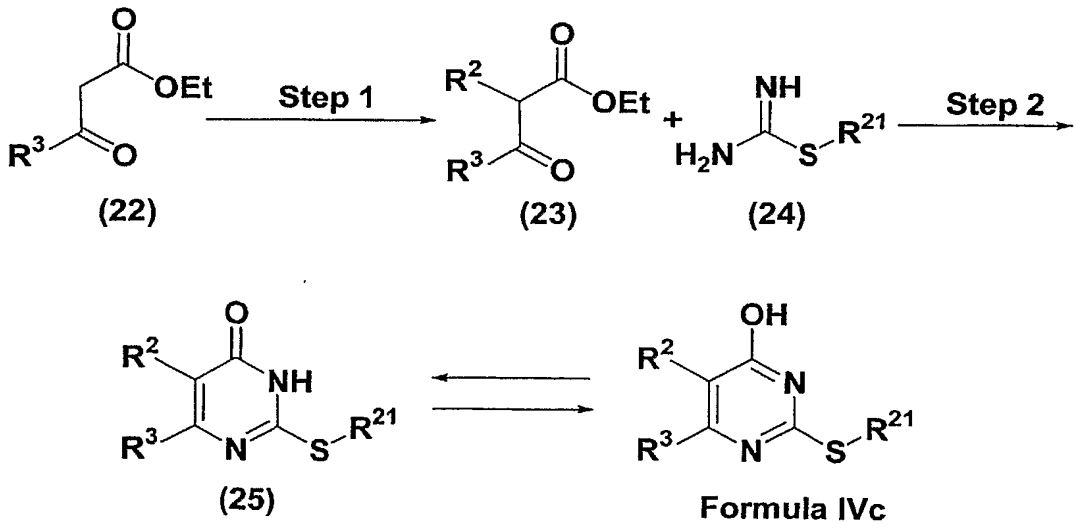


[0472] The 4-hydroxypyrimidine derivatives, represented by formula IV, can be prepared as shown in Scheme 9.

Step1 Preparation of formula IVb

[0473] The compound of formula IVb was prepared by reaction of a compound of formula (21) with an electrophilic reagent (phenyl isocyanate), in the presence of a base (e.g. Et_3N) in a suitable solvent (e.g. CH_2Cl_2) at room temperature for several hours. When the reaction is substantially complete, the product of formula IVb was isolated by conventional means (e.g. flash chromatography).

3. **Synthesis of the Compounds of Formula IVc - Scheme 10**



[0474] The 4-hydroxypyrimidine derivatives, represented by formula IVc, were prepared as shown in Scheme 10.

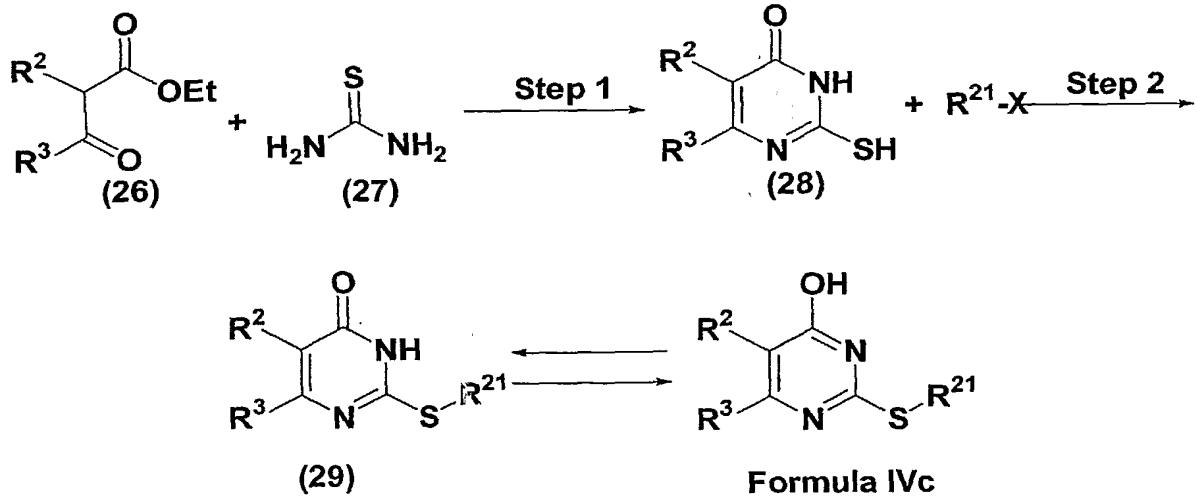
Step-1 Preparation of formula (23)

[0475] The compound of formula (23) was prepared by reaction of a compound of formula (22), with an alkyl halide reagent (e.g. methyl iodide) in an inert solvent (e.g. DMF), in the presence of a base (e.g. K_2CO_3), typically heated near 80 °C for 12-36 hours.

Step-2 Preparation of formula IVc

[0476] The compound of formula (25) was prepared y by reaction of a compound of formula (23) with an alkylisothiourea (e.g. S-methylisothiourea, $H_2NCNHSCH_3$), while heating in a suitable solvent (e.g. ethanol) at 75 ^{0}C for several hours. When the reaction is substantially complete, the product of formula IVc was isolated by conventional means; for example, recrystallization.

4. Alternate synthesis of the Compounds of Formula IV - Scheme 11



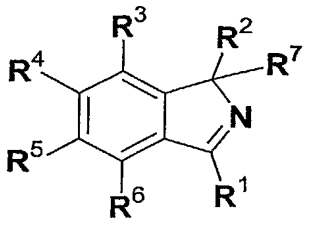
Step-1 Preparation of formula (28)

[0477] Compound of formula (28) was prepared conventionally by reaction of a compound of formula (26), with thiourea of formula (27), in a polar solvent (e.g. ethanol), and typically heated near 80 °C for 12-36 hours and isolating the product by column chromatography.

Step-2 Preparation of formula (29)

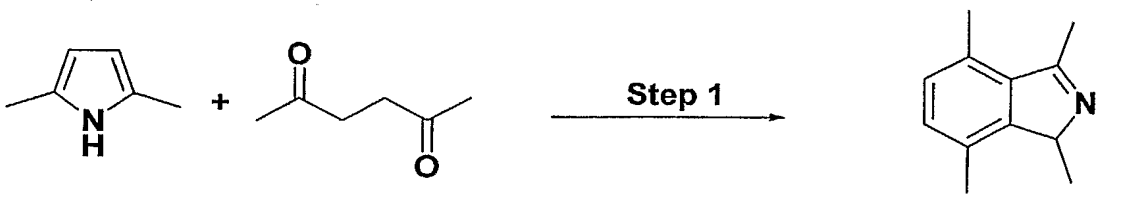
[0478] Compound of formula (29) was prepared by reaction of a compound of formula (28) with an alkylating agent (e.g. ethylbromoacetate), in the presence of a base (e.g. K_2CO_3) in a suitable solvent (e.g. acetonitrile) at room temperature or reflux for several hours. When the reaction is substantially complete, the product of formula IVc was isolated by conventional means.

Example 13: Synthesis of the Compounds of Formula V:



Formula V

1. Synthesis of the Compounds of Formula Va, where R^1, R^2, R^3, and R^6 are Methyl; R^4 and $R^5$are Hydrogen - Scheme 12



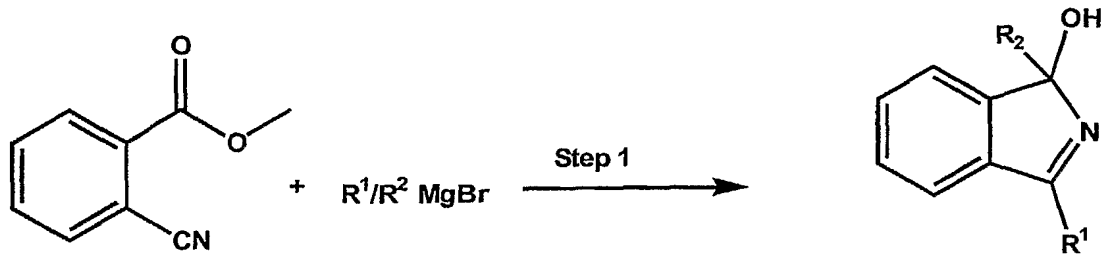
(30) (31) Formula Va

[0479] The isoindole derivatives, represented by formula Va, can be prepared as shown in Scheme 12.

Step-1 Preparation of Formula Va

[0480] The compound of formula (30) can be reacted with diketone compounds of formula (31), in aqueous acetic acid and typically heated near 100 °C for 12-36 hours. The compound can be isolated by conventional methods (e.g. recrystallization).

2. Synthesis of the Compounds of Formula Vb, where R^3, R^6, R^4 and $R^5$are Hydrogen; R^7 is hydroxy - Scheme 13

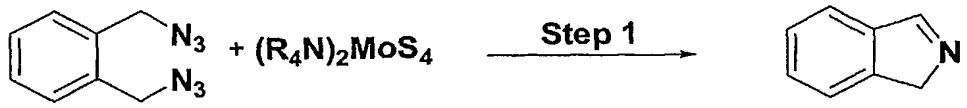


(32) (33) Formula Vb

Step-1 Preparation of Formula Vb

[0481] The compound of Formula Vb is prepared conventionally by reaction of a compound of formula (32) with a Grignard reagent (e.g. Phenyl magnesium bromide), in a suitable solvent (e.g. benzene) and refluxed for 1 hour. When the reaction is substantially complete, the product of is isolated by conventional means (e.g., column chromatography).

3. Synthesis of the Compounds of Formula Vc, where where R^1, R^2, R^3, R^4, R^5, R^6, and R^7 are Hydrogen - Scheme 14



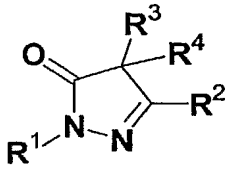
(34) (35) Formula Vc

Step-1 Preparation of Vc

[0482] The compound (34) and the ammonium tetrathiomolybdate of formula (35) are reacted at room temperature with aqueous CH_3CN as the solvent. When the reaction is substantially complete (typically 1 hour), the solvent is removes by evaporation at reduced

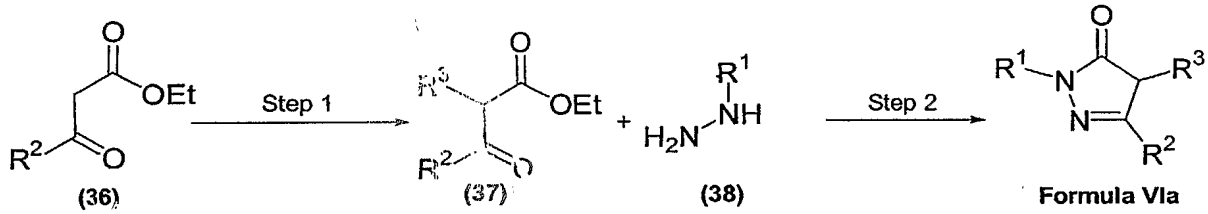
pressure. The product Vc is isolated by conventional means (e.g. ether extraction). (Ramesha, et. al., *J. Org. Chem.*, 1995,60, 7682-7683; and references therein).

Example 14: Synthesis of the Compounds of Formula VI:



Formula VI

1. Synthesis of the Compounds of Formula VIa, where R^4 = H - Scheme 15



[0483] Pyrazolidinone derivatives, represented by formula VI, can be prepared as shown in Scheme-15.

Step-1 Preparation of formula (37)

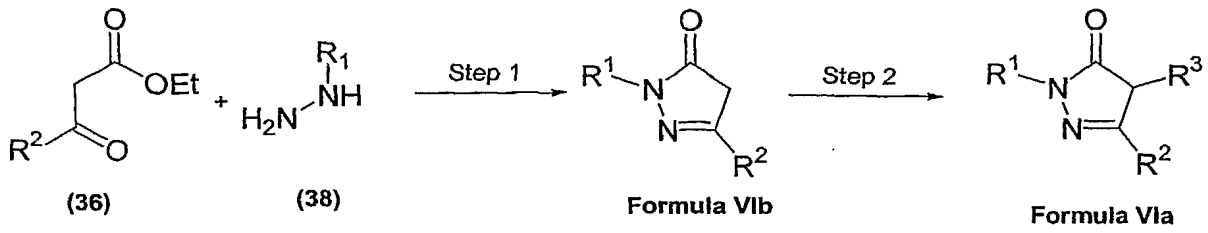
[0484] The compound of formula (37) is prepared conventionally by reaction of a compound of formula (36), with an alkyl halide reagent (e.g. methyl iodide) in an inert solvent (e.g. DMF), in the presence of a base (e.g. K_2CO_3), typically heated near 80 °C for 12-36 hours.

Step-2 Preparation of formula VIa

[0485] Compound of formula (37) is reacted with hydrazine of formula (38) along with a catalytic amount of concentrated acid (e.g. hydrochloric acid) at 120 °C. The liberation of alcohol and water results in the formation of the product of formula VIa, can be isolated through conventional means, for example column chromatography.

2. Alternate synthesis of the Compounds of Formula VI, where R^4=H: -

Scheme 16



(36) (38) Formula VIb Formula VIa

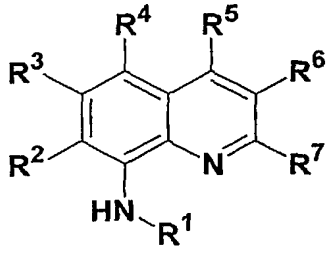
Step-1 Preparation of formula VIb

[0486] Compound of formula (36) is reacted with hydrazine of formula (38) along with a catalytic amount of concentrated acid (e.g. hydrochloric acid) at 120 °C. The liberation of alcohol and water results in the formation of the product of formula VIb, can be isolated through conventional means, for example column chromatography.

Step-2 Preparation of formula VIa:

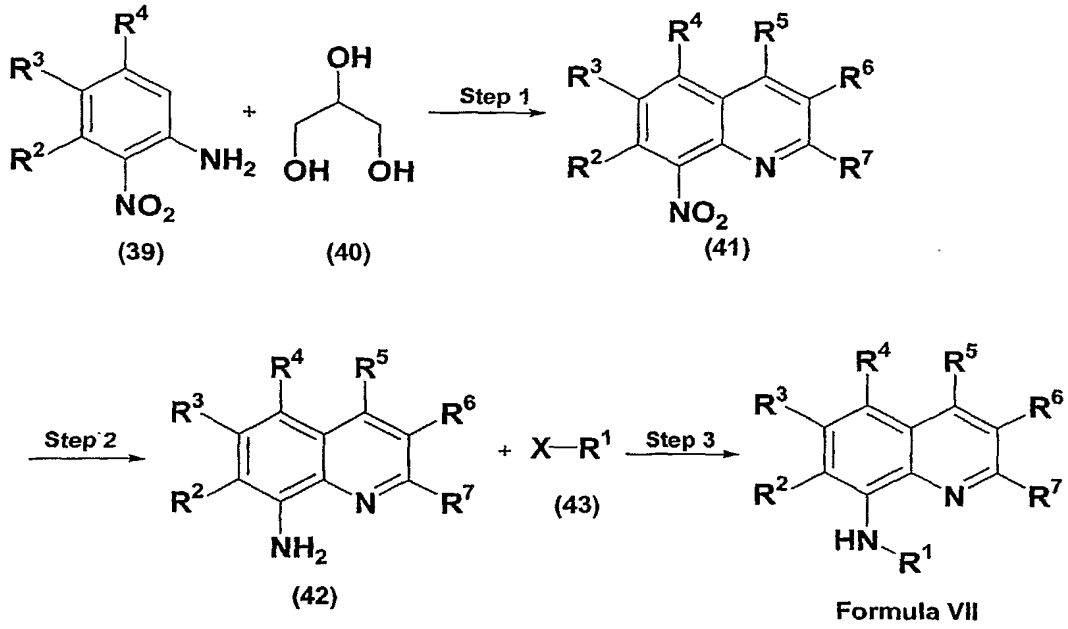
[0487] The compound of formula VI is prepared conventionally by reaction of a compound of formula (42) with an alkylating agent of formula (43) (e.g. ethylbromoacetate), in the presence of a base (e.g. K_2CO_3) in a suitable solvent (e.g. acetonitrile) at room temperature or reflux for several hours. When the reaction is substantially complete, the product of Formula VI is isolated by conventional means; for example, recrystallization.

Example 15: Synthesis of the Compounds of Formula VII:



Formula VII

1. Synthesis of the Compounds of Formula VII - Scheme 17



[0488] The 8-aminoquinoline derivatives, represented by formula VII, can be prepared as shown in Scheme-17. In this particular scheme, R^5, R^6, and R^7 are hydrogen.

Step-1 Preparation of formula (41)

[0489] The compound of formula (41) can be prepared via a Skraup reaction by reaction of a compound of formula (39) (e.g. 2-nitroaniline), with glycerol (40), in the presence of sulfuric acid in an inert solvent (e.g. dioxane) and typically heated to > 100 °C for 2-24 hours. The addition of nitrobenzene or arsenic oxide can aid the reaction (Claus and Schoeller, *J. Prakt. Chem.* 1893, *48*, 140. Mosher, H.S. *et. al.*, *Org. Syn.* CV 3, 568).

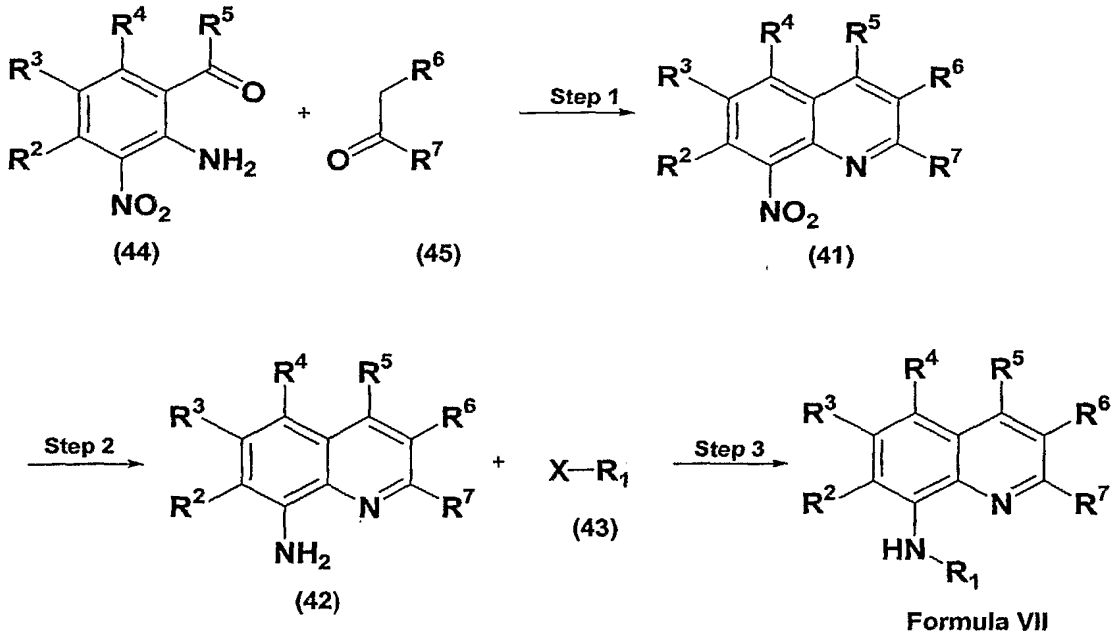
Step-2 Preparation of formula (42)

[0490] The compound of formula (42) can be prepared conventionally by reaction of a compound of formula (41) with a reducing agent (e.g. hydrogen gas, ammonium formate, HCO_2NH_4), in the presence of a catalyst (e.g. Pd/C), in a suitable solvent (e.g. methanol) at room temperature for several hours. When the reaction is substantially complete, the product of formula (41) can be isolated by conventional means, (e.g. filtration through Celite).

Step-3 Preparation of formula VII

[0491] The compound of formula (42) can be reacted with a compound of formula (43) where X is a leaving group (e.g. bromide, chloride) or an electrophilic substituent (e.g. isocyanate, isothiocyanate), in the presence of base (e.g. K_2CO_3), in an inert solvent (e.g. DMF). Representaive examples of compounds of formula (43) include benzoyl chloride, benzenesulfonyl chloride, 3-bromo-2-methylpropane, benzyl bromide, phenyl isocyanate, and phenyl isothiocyanate. When the reaction is substantially complete, the product of formula VII can be isolated by conventional means (e.g. silica gel chromatography).

2. Alternative Exemplary Synthesis of Compounds of Formula VII - Scheme 18



[0492] The 8-aminoquinoline derivatives, represented by formula VII, can be prepared as shown in Scheme-18.

Step-1 Preparation of formula (41)

[0493] The compound of formula (41) can be prepared via a Friedländer synthesis by reaction of a compound of formula (44) (e.g. 2-amino-3-nitro-acetophenone), with a compound of formula (45) (e.g. acetone), in the presence of base (e.g. potassium hydroxide,

piperidine) in an inert solvent (e.g. ethanol) and possible with heating for 2-24 hours (Eckert, K. *Angew. Chem. Int. Ed.* 1981, *20*, 208).

Step-2 Preparation of formula (42)

[0494] The compound of formula (42) can be prepared conventionally by reaction of a compound of formula (41) with a reducing agent (e.g. hydrogen gas, ammonium formate, HCO_2NH_4), in the presence of a catalyst (e.g. Pd/C), in a suitable solvent (e.g. methanol) at room temperature for several hours. When the reaction is substantially complete, the product of formula (42) can be isolated by conventional means, (e.g. filtration through Celite).

Step-3 Preparation of formula VII

[0495] The compound of formula (42) can be reacted with a compound of formula (48) where X is a leaving group (e.g. bromide, chloride) or an electrophilic substituent (e.g. isocyanate, isothiocyanate), in the presence of base (e.g. K_2CO_3), in an inert solvent (e.g. DMF). Representaive examples of compounds of formula (43) include benzoyl chloride, benzenesulfonyl chloride, 3-bromo-2-methylpropane, benzyl bromide, phenyl isocyanate, and phenyl isothiocyanate. When the reaction is substantially complete, the product of formula VII can be isolated by conventional means (e.g. silica gel chromatography).

Example 16: Site-directed Mutagenesis of Kinases

[0496] Mutagenesis of kinases, e.g. PIM kinases, such as the P123M mutation of PIM-1 can be carried out according to the following procedure (or other procedures available persons performing molecular biological techniques) as described in *Molecular Biology: Current Innovations and Future Trends.* Eds. A.M. Griffin and H.G.Griffin. (1995) ISBN 1-898486-01-8, Horizon Scientific Press, PO Box 1, Wymondham, Norfolk, U.K., among others.

[0497] *In vitro* site-directed mutagenesis is an invaluable technique for studying protein structure-function relationships, gene expression and vector modification. Several methods have appeared in the literature, but many of these methods require single-stranded DNA as the template. The reason for this, historically, has been the need for separating the complementary strands to prevent reannealing. Use of PCR in site-directed mutagenesis

accomplishes strand separation by using a denaturing step to separate the complementing strands and allowing efficient polymerization of the PCR primers. PCR site-directed methods thus allow site-specific mutations to be incorporated in virtually any double-stranded plasmid; eliminating the need for M13-based vectors or single-stranded rescue.

[0498] It is often desirable to reduce the number of cycles during PCR when performing PCR-based site-directed mutagenesis to prevent clonal expansion of any (undesired) second-site mutations. Limited cycling which would result in reduced product yield, is offset by increasing the starting template concentration. A selection is used to reduce the number of parental molecules coming through the reaction. Also, in order to use a single PCR primer set, it is desirable to optimize the long PCR method. Further, because of the extendase activity of some thermostable polymerases it is often necessary to incorporate an end-polishing step into the procedure prior to end-to-end ligation of the PCR-generated product containing the incorporated mutations in one or both PCR primers.

[0499] The following protocol provids as a facile method for site-directed mutagenesis and accomplishes the above desired features by the incorporation of the following steps: (i) increasing template concentration approximately 1000-fold over conventional PCR conditions; (ii) reducing the number of cycles from 25-30 to 5-10; (iii) adding the restriction endonuclease *Dpn*I (recognition target sequence: 5-Gm6ATC-3, where the A residue is methylated) to select against parental DNA (note: DNA isolated from almost all common strains of *E. coli* is *Dam*-methylated at the sequence 5-GATC-3); (iv) using Taq Extender in the PCR mix for increased reliability for PCR to 10 kb; (v) using *Pfu* DNA polymerase to polish the ends of the PCR product, and (vi) efficient intramolecular ligation in the presence of T4 DNA ligase.

[0500] Plasmid template DNA (approximately 0.5 pmole) is added to a PCR cocktail containing, in 25 ul of 1x mutagenesis buffer: (20 mM Tris HCl, pH 7.5; 8 mM MgCl2; 40 ug/ml BSA); 12-20 pmole of each primer (one of which must contain a 5-prime phosphate), 250 uM each dNTP, 2.5 U *Taq* DNA polymerase, 2.5 U of *Taq* Extender (Stratagene).

[0501] The PCR cycling parameters are 1 cycle of: 4 min at 94 C, 2 min at 50 C and 2 min at 72 C; followed by 5-10 cycles of 1 min at 94 C, 2 min at 54 C and 1 min at 72 C (step 1).

[0502] The parental template DNA and the linear, mutagenesis primer incorporating newly synthesized DNA are treated with *Dpn*I (10 U) and *Pfu* DNA polymerase (2.5U).

This results in the *Dpn*I digestion of the *in vivo* methylated parental template and hybrid DNA and the removal, by *Pfu* DNA polymerase, of the *Taq* DNA polymerase-extended base(s) on the linear PCR product.

[0503] The reaction is incubated at 37 C for 30 min and then transferred to 72 C for an additional 30 min (step 2).

[0504] Mutagenesis buffer (1x, 115 ul, containing 0.5 mM ATP) is added to the *Dpn*I-digested, *Pfu* DNA polymerase-polished PCR products.

[0505] The solution is mixed and 10 ul is removed to a new microfuge tube and T4 DNA ligase (2-4 U) added.

[0506] The ligation is incubated for greater than 60 min at 37 C (step 3).

[0507] The treated solution is transformed into competent *E. coli* (step 4).

[0508] In addition to the PCT-based site-directed mutagenesis described above, other methods are available. Examples include those described in Kunkel (1985) *Proc. Natl. Acad. Sci.* 82:488-492; Eckstein et al. (1985) *Nucl. Acids Res.* 13:8764-8785; and using the GeneEditor™ Site-Directed Mutageneis Sytem from Promega.

[0509] All patents and other references cited in the specification are indicative of the level of skill of those skilled in the art to which the invention pertains, and are incorporated by reference in their entireties, including any tables and figures, to the same extent as if each reference had been incorporated by reference in its entirety individually.

[0510] One skilled in the art would readily appreciate that the present invention is well adapted to obtain the ends and advantages mentioned, as well as those inherent therein. The methods, variances, and compositions described herein as presently representative of preferred embodiments are exemplary and are not intended as limitations on the scope of the invention. Changes therein and other uses will occur to those skilled in the art, which are encompassed within the spirit of the invention, are defined by the scope of the claims.

[0511] It will be readily apparent to one skilled in the art that varying substitutions and modifications may be made to the invention disclosed herein without departing from the

scope and spirit of the invention. For example, variations can be made to crystallization or co-crystallization conditions for PIM proteins. Thus, such additional embodiments are within the scope of the present invention and the following claims.

[0512] The invention illustratively described herein suitably may be practiced in the absence of any element or elements, limitation or limitations which is not specifically disclosed herein. Thus, for example, in each instance herein any of the terms "comprising", "consisting essentially of" and "consisting of" may be replaced with either of the other two terms. The terms and expressions which have been employed are used as terms of description and not of limitation, and there is no intention that in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, but it is recognized that various modifications are possible within the scope of the invention claimed. Thus, it should be understood that although the present invention has been specifically disclosed by preferred embodiments and optional features, modification and variation of the concepts herein disclosed may be resorted to by those skilled in the art, and that such modifications and variations are considered to be within the scope of this invention as defined by the appended claims.

[0513] In addition, where features or aspects of the invention are described in terms of Markush groups or other grouping of alternatives, those skilled in the art will recognize that the invention is also thereby described in terms of any individual member or subgroup of members of the Markush group or other group.

[0514] Also, unless indicated to the contrary, where various numerical values are provided for embodiments, additional embodiments are described by taking any 2 different values as the endpoints of a range. Such ranges are also within the scope of the described invention.

[0515] Thus, additional embodiments are within the scope of the invention and within the following claims.

Table 1

```
HEADER    ----                                        XX-XXX-XX    xxxx
COMPND    ---
REMARK    3
REMARK    3 REFINEMENT.
REMARK    3   PROGRAM     : REFMAC 5.1.19
REMARK    3   AUTHORS     : MURSHUDOV,VAGIN,DODSON
REMARK    3
REMARK    3    REFINEMENT TARGET : MAXIMUM LIKELIHOOD
REMARK    3
REMARK    3  DATA USED IN REFINEMENT.
REMARK    3   RESOLUTION RANGE HIGH (ANGSTROMS) :   2.00
REMARK    3   RESOLUTION RANGE LOW  (ANGSTROMS) :  84.52
REMARK    3   DATA CUTOFF            (SIGMA(F)) : NONE
REMARK    3   COMPLETENESS FOR RANGE        (%) :  99.27
REMARK    3   NUMBER OF REFLECTIONS             :   28693
REMARK    3
REMARK    3  FIT TO DATA USED IN REFINEMENT.
REMARK    3   CROSS-VALIDATION METHOD          : THROUGHOUT
REMARK    3   FREE R VALUE TEST SET SELECTION  : RANDOM
REMARK    3   R VALUE      (WORKING + TEST SET) : 0.22119
REMARK    3   R VALUE           (WORKING SET) :  0.22012
REMARK    3   FREE R VALUE                     :  0.24194
REMARK    3   FREE R VALUE TEST SET SIZE   (%) :  5.0
REMARK    3   FREE R VALUE TEST SET COUNT      :  1498
REMARK    3
REMARK    3  FIT IN THE HIGHEST RESOLUTION BIN.
REMARK    3   TOTAL NUMBER OF BINS USED           :      20
REMARK    3   BIN RESOLUTION RANGE HIGH          :    2.000
REMARK    3   BIN RESOLUTION RANGE LOW           :    2.052
REMARK    3   REFLECTION IN BIN     (WORKING SET) :     2096
REMARK    3   BIN R VALUE           (WORKING SET) :    0.344
REMARK    3   BIN FREE R VALUE SET COUNT          :      102
REMARK    3   BIN FREE R VALUE                    :    0.359
REMARK    3
REMARK    3  NUMBER OF NON-HYDROGEN ATOMS USED IN REFINEMENT.
REMARK    3   ALL ATOMS                 :     2382
REMARK    3
REMARK    3  B VALUES.
REMARK    3   FROM WILSON PLOT           (A**2) : NULL
REMARK    3   MEAN B VALUE      (OVERALL, A**2) :  49.236
REMARK    3   OVERALL ANISOTROPIC B VALUE.
REMARK    3    B11 (A**2) :     1.32
REMARK    3    B22 (A**2) :     1.32
REMARK    3    B33 (A**2) :    -1.99
REMARK    3    B12 (A**2) :     0.66
REMARK    3    B13 (A**2) :     0.00
REMARK    3    B23 (A**2) :     0.00
REMARK    3
REMARK    3  ESTIMATED OVERALL COORDINATE ERROR.
REMARK    3   ESU BASED ON R VALUE                                (A):   0.158
REMARK    3   ESU BASED ON FREE R VALUE                          (A):   0.142
REMARK    3   ESU BASED ON MAXIMUM LIKELIHOOD                     (A):   0.127
REMARK    3   ESU FOR B VALUES BASED ON MAXIMUM LIKELIHOOD (A**2):   4.758
REMARK    3
REMARK    3 CORRELATION COEFFICIENTS.
REMARK    3   CORRELATION COEFFICIENT FO-FC      :   0.954
REMARK    3   CORRELATION COEFFICIENT FO-FC FREE :   0.947
REMARK    3
REMARK    3  RMS DEVIATIONS FROM IDEAL VALUES        COUNT    RMS    WEIGHT
REMARK    3   BOND LENGTHS REFINED ATOMS        (A):  2296 ; 0.011 ; 0.021
REMARK    3   BOND ANGLES REFINED ATOMS    (DEGREES):  3114 ; 1.088 ; 1.945
REMARK    3   TORSION ANGLES, PERIOD 1     (DEGREES):   273 ; 3.838 ; 5.000
REMARK    3   CHIRAL-CENTER RESTRAINTS       (A**3):   332 ; 0.081 ; 0.200
REMARK    3   GENERAL PLANES REFINED ATOMS      (A):  1784 ; 0.004 ; 0.020
REMARK    3   NON-BONDED CONTACTS REFINED ATOMS (A):  1094 ; 0.215 ; 0.200
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REMARK   3   H-BOND (X...Y) REFINED ATOMS       (A):    138 ; 0.121 ; 0.200
REMARK   3   SYMMETRY VDW REFINED ATOMS         (A):     60 ; 0.282 ; 0.200
REMARK   3   SYMMETRY H-BOND REFINED ATOMS      (A):     19 ; 0.247 ; 0.200
REMARK   3
REMARK   3  ISOTROPIC THERMAL FACTOR RESTRAINTS.      COUNT   RMS    WEIGHT
REMARK   3   MAIN-CHAIN BOND REFINED ATOMS  (A**2):  1365 ; 1.058 ; 1.500
REMARK   3   MAIN-CHAIN ANGLE REFINED ATOMS (A**2):  2212 ; 2.010 ; 2.000
REMARK   3   SIDE-CHAIN BOND REFINED ATOMS  (A**2):   931 ; 2.240 ; 3.000
REMARK   3   SIDE-CHAIN ANGLE REFINED ATOMS (A**2):   902 ; 3.766 ; 4.500
REMARK   3
REMARK   3  NCS RESTRAINTS STATISTICS
REMARK   3   NUMBER OF NCS GROUPS : NULL
REMARK   3
REMARK   3
REMARK   3  TLS DETAILS
REMARK   3   NUMBER OF TLS GROUPS  : NULL
REMARK   3
REMARK   3
REMARK   3  BULK SOLVENT MODELLING.
REMARK   3   METHOD USED : BABINET MODEL WITH MASK
REMARK   3   PARAMETERS FOR MASK CALCULATION
REMARK   3   VDW PROBE RADIUS   :   1.40
REMARK   3   ION PROBE RADIUS   :   0.80
REMARK   3   SHRINKAGE RADIUS   :   0.80
REMARK   3
REMARK   3  OTHER REFINEMENT REMARKS: NULL
REMARK   3
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CRYST1   99.210   99.210   80.285  90.00  90.00 120.00 P 65
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SCALE2      0.000000  0.011639  0.000000        0.00000
SCALE3      0.000000  0.000000  0.012456        0.00000
ATOM      1  N   PRO A  33       9.285 100.137  -4.493  1.00 93.84           N
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ATOM      3  CB  PRO A  33       9.624  97.864  -3.896  1.00 93.79           C
ATOM      4  CG  PRO A  33      10.732  98.328  -4.833  1.00 93.76           C
ATOM      5  CD  PRO A  33      10.201  99.562  -5.499  1.00 93.83           C
ATOM      6  C   PRO A  33       9.413  99.588  -2.038  1.00 93.22           C
ATOM      7  O   PRO A  33       8.647 100.212  -1.288  1.00 93.33           O
ATOM      8  N   LEU A  34      10.667  99.251  -1.716  1.00 92.55           N
ATOM      9  CA  LEU A  34      11.325  99.616  -0.457  1.00 91.82           C
ATOM     10  CB  LEU A  34      11.402 101.150  -0.303  1.00 92.11           C
ATOM     11  CG  LEU A  34      12.362 101.709   0.756  1.00 92.47           C
ATOM     12  CD1 LEU A  34      13.829 101.513   0.349  1.00 92.34           C
ATOM     13  CD2 LEU A  34      12.044 103.183   1.024  1.00 93.01           C
ATOM     14  C   LEU A  34      10.758  98.941   0.808  1.00 90.98           C
ATOM     15  O   LEU A  34      11.164  97.828   1.157  1.00 91.10           O
ATOM     16  N   GLU A  35       9.837  99.614   1.498  1.00 89.80           N
ATOM     17  CA  GLU A  35       9.346  99.114   2.780  1.00 88.50           C
ATOM     18  CB  GLU A  35      10.297  99.526   3.901  1.00 88.76           C
ATOM     19  CG  GLU A  35      10.444 101.039   4.047  1.00 89.07           C
ATOM     20  CD  GLU A  35      11.208 101.436   5.292  1.00 89.82           C
ATOM     21  OE1 GLU A  35      10.603 101.403   6.400  1.00 90.45           O
ATOM     22  OE2 GLU A  35      12.411 101.780   5.162  1.00 89.60           O
ATOM     23  C   GLU A  35       7.963  99.672   3.060  1.00 87.48           C
ATOM     24  O   GLU A  35       7.220  99.114   3.875  1.00 87.62           O
ATOM     25  N   SER A  36       7.640 100.781   2.382  1.00 85.74           N
ATOM     26  CA  SER A  36       6.316 101.427   2.424  1.00 83.76           C
ATOM     27  CB  SER A  36       6.258 102.576   1.402  1.00 84.10           C
ATOM     28  OG  SER A  36       7.465 103.332   1.399  1.00 84.47           O
ATOM     29  C   SER A  36       5.170 100.444   2.150  1.00 81.91           C
ATOM     30  O   SER A  36       3.997 100.755   2.389  1.00 81.51           O
ATOM     31  N   GLN A  37       5.535  99.262   1.651  1.00 79.60           N
ATOM     32  CA  GLN A  37       4.600  98.179   1.363  1.00 77.25           C
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ATOM     34  CG  GLN A  37       6.195  97.509  -0.554  1.00 77.20           C
ATOM     35  CD  GLN A  37       6.645  96.330  -1.414  1.00 77.20           C
ATOM     36  OE1 GLN A  37       5.827  95.483  -1.799  1.00 77.03           O
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```

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ATOM	39	O	GLN	A	37	2.879	97.043	2.567	1.00	75.51	O
ATOM	40	N	TYR	A	38	4.655	97.747	3.756	1.00	73.43	N
ATOM	41	CA	TYR	A	38	4.208	97.129	5.004	1.00	71.44	C
ATOM	42	CB	TYR	A	38	5.100	95.931	5.373	1.00	70.49	C
ATOM	43	CG	TYR	A	38	5.227	94.919	4.255	1.00	67.67	C
ATOM	44	CD1	TYR	A	38	4.258	93.929	4.067	1.00	65.14	C
ATOM	45	CE1	TYR	A	38	4.361	93.019	3.032	1.00	63.31	C
ATOM	46	CZ	TYR	A	38	5.446	93.087	2.177	1.00	62.94	C
ATOM	47	OH	TYR	A	38	5.568	92.191	1.151	1.00	64.24	O
ATOM	48	CE2	TYR	A	38	6.417	94.054	2.339	1.00	63.82	C
ATOM	49	CD2	TYR	A	38	6.304	94.967	3.371	1.00	65.13	C
ATOM	50	C	TYR	A	38	4.125	98.099	6.169	1.00	71.00	C
ATOM	51	O	TYR	A	38	5.021	98.914	6.385	1.00	70.68	O
ATOM	52	N	GLN	A	39	3.026	97.986	6.913	1.00	70.43	N
ATOM	53	CA	GLN	A	39	2.797	98.756	8.124	1.00	69.86	C
ATOM	54	CB	GLN	A	39	1.298	99.021	8.279	1.00	70.46	C
ATOM	55	CG	GLN	A	39	0.934	100.007	9.385	1.00	73.80	C
ATOM	56	CD	GLN	A	39	0.378	99.319	10.635	1.00	77.97	C
ATOM	57	OE1	GLN	A	39	-0.750	98.794	10.625	1.00	79.52	O
ATOM	58	NE2	GLN	A	39	1.161	99.330	11.717	1.00	78.94	N
ATOM	59	C	GLN	A	39	3.333	97.967	9.322	1.00	68.49	C
ATOM	60	O	GLN	A	39	2.704	97.003	9.777	1.00	68.58	O
ATOM	61	N	VAL	A	40	4.491	98.390	9.834	1.00	66.87	N
ATOM	62	CA	VAL	A	40	5.141	97.688	10.940	1.00	65.53	C
ATOM	63	CB	VAL	A	40	6.600	98.137	11.138	1.00	65.20	C
ATOM	64	CG1	VAL	A	40	7.310	97.201	12.100	1.00	64.63	C
ATOM	65	CG2	VAL	A	40	7.336	98.174	9.804	1.00	65.16	C
ATOM	66	C	VAL	A	40	4.376	97.837	12.255	1.00	64.96	C
ATOM	67	O	VAL	A	40	3.833	98.893	12.547	1.00	65.27	O
ATOM	68	N	GLY	A	41	4.339	96.766	13.042	1.00	64.02	N
ATOM	69	CA	GLY	A	41	3.640	96.764	14.310	1.00	62.22	C
ATOM	70	C	GLY	A	41	4.545	96.341	15.451	1.00	61.31	C
ATOM	71	O	GLY	A	41	5.747	96.572	15.406	1.00	60.92	O
ATOM	72	N	PRO	A	42	3.966	95.725	16.478	1.00	60.62	N
ATOM	73	CA	PRO	A	42	4.723	95.313	17.666	1.00	60.91	C
ATOM	74	CB	PRO	A	42	3.636	94.755	18.602	1.00	60.81	C
ATOM	75	CG	PRO	A	42	2.347	95.332	18.089	1.00	60.97	C
ATOM	76	CD	PRO	A	42	2.529	95.401	16.599	1.00	60.64	C
ATOM	77	C	PRO	A	42	5.759	94.235	17.385	1.00	60.96	C
ATOM	78	O	PRO	A	42	5.626	93.478	16.424	1.00	60.93	O
ATOM	79	N	LEU	A	43	6.783	94.180	18.226	1.00	61.11	N
ATOM	80	CA	LEU	A	43	7.737	93.084	18.200	1.00	61.79	C
ATOM	81	CB	LEU	A	43	8.924	93.411	19.110	1.00	61.59	C
ATOM	82	CG	LEU	A	43	10.162	92.511	19.107	1.00	62.19	C
ATOM	83	CD1	LEU	A	43	11.000	92.704	17.848	1.00	61.21	C
ATOM	84	CD2	LEU	A	43	11.003	92.782	20.344	1.00	62.67	C
ATOM	85	C	LEU	A	43	7.027	91.795	18.643	1.00	62.48	C
ATOM	86	O	LEU	A	43	6.143	91.824	19.511	1.00	62.19	O
ATOM	87	N	LEU	A	44	7.396	90.671	18.030	1.00	63.26	N
ATOM	88	CA	LEU	A	44	6.811	89.378	18.387	1.00	63.89	C
ATOM	89	CB	LEU	A	44	6.257	88.663	17.154	1.00	63.70	C
ATOM	90	CG	LEU	A	44	5.135	89.362	16.379	1.00	63.05	C
ATOM	91	CD1	LEU	A	44	4.801	88.562	15.131	1.00	62.30	C
ATOM	92	CD2	LEU	A	44	3.894	89.539	17.241	1.00	62.27	C
ATOM	93	C	LEU	A	44	7.791	88.474	19.110	1.00	64.82	C
ATOM	94	O	LEU	A	44	7.386	87.669	19.951	1.00	65.08	O
ATOM	95	N	GLY	A	45	9.071	88.602	18.784	1.00	66.08	N
ATOM	96	CA	GLY	A	45	10.088	87.734	19.357	1.00	68.09	C
ATOM	97	C	GLY	A	45	11.517	88.122	19.027	1.00	69.52	C
ATOM	98	O	GLY	A	45	11.763	88.937	18.124	1.00	69.05	O
ATOM	99	N	SER	A	46	12.448	87.517	19.774	1.00	71.08	N
ATOM	100	CA	SER	A	46	13.891	87.764	19.662	1.00	72.58	C
ATOM	101	CB	SER	A	46	14.311	88.922	20.588	1.00	72.92	C
ATOM	102	OG	SER	A	46	15.655	89.327	20.364	1.00	74.04	O
ATOM	103	C	SER	A	46	14.688	86.513	20.027	1.00	73.06	C
ATOM	104	O	SER	A	46	14.265	85.720	20.875	1.00	73.26	O
ATOM	105	N	GLY	A	47	15.849	86.349	19.394	1.00	73.67	N
ATOM	106	CA	GLY	A	47	16.733	85.234	19.707	1.00	74.04	C

ATOM	107	C	GLY	A	47	17.739	84.965	18.608	1.00	74.12	C
ATOM	108	O	GLY	A	47	18.133	85.889	17.883	1.00	74.48	O
ATOM	109	N	GLY	A	48	18.150	83.698	18.490	1.00	73.84	N
ATOM	110	CA	GLY	A	48	19.109	83.257	17.478	1.00	73.16	C
ATOM	111	C	GLY	A	48	18.602	83.392	16.048	1.00	72.45	C
ATOM	112	O	GLY	A	48	19.391	83.374	15.093	1.00	72.37	O
ATOM	113	N	PHE	A	49	17.282	83.531	15.911	1.00	71.52	N
ATOM	114	CA	PHE	A	49	16.647	83.755	14.612	1.00	70.43	C
ATOM	115	CB	PHE	A	49	15.215	83.187	14.590	1.00	70.83	C
ATOM	116	CG	PHE	A	49	14.301	83.752	15.661	1.00	73.19	C
ATOM	117	CD1	PHE	A	49	13.584	84.933	15.439	1.00	74.32	C
ATOM	118	CE1	PHE	A	49	12.738	85.453	16.419	1.00	75.71	C
ATOM	119	CZ	PHE	A	49	12.587	84.787	17.638	1.00	75.96	C
ATOM	120	CE2	PHE	A	49	13.290	83.605	17.874	1.00	75.42	C
ATOM	121	CD2	PHE	A	49	14.139	83.090	16.883	1.00	74.82	C
ATOM	122	C	PHE	A	49	16.696	85.231	14.157	1.00	68.55	C
ATOM	123	O	PHE	A	49	16.785	85.509	12.963	1.00	69.15	O
ATOM	124	N	GLY	A	50	16.663	86.164	15.106	1.00	66.20	N
ATOM	125	CA	GLY	A	50	16.625	87.588	14.795	1.00	62.55	C
ATOM	126	C	GLY	A	50	15.562	88.351	15.578	1.00	59.75	C
ATOM	127	O	GLY	A	50	15.316	88.056	16.754	1.00	59.86	O
ATOM	128	N	SER	A	51	14.945	89.332	14.916	1.00	56.20	N
ATOM	129	CA	SER	A	51	13.866	90.148	15.480	1.00	51.75	C
ATOM	130	CB	SER	A	51	14.300	91.614	15.587	1.00	51.18	C
ATOM	131	OG	SER	A	51	15.454	91.750	16.401	1.00	48.30	O
ATOM	132	C	SER	A	51	12.699	90.076	14.537	1.00	49.79	C
ATOM	133	O	SER	A	51	12.848	90.341	13.344	1.00	48.22	O
ATOM	134	N	VAL	A	52	11.538	89.724	15.064	1.00	47.77	N
ATOM	135	CA	VAL	A	52	10.345	89.551	14.243	1.00	46.96	C
ATOM	136	CB	VAL	A	52	9.795	88.091	14.312	1.00	46.48	C
ATOM	137	CG1	VAL	A	52	8.570	87.924	13.397	1.00	45.18	C
ATOM	138	CG2	VAL	A	52	10.873	87.082	13.955	1.00	45.83	C
ATOM	139	C	VAL	A	52	9.265	90.515	14.701	1.00	47.44	C
ATOM	140	O	VAL	A	52	8.874	90.493	15.869	1.00	48.09	O
ATOM	141	N	TYR	A	53	8.784	91.346	13.779	1.00	47.68	N
ATOM	142	CA	TYR	A	53	7.723	92.315	14.055	1.00	48.21	C
ATOM	143	CB	TYR	A	53	8.102	93.711	13.532	1.00	47.13	C
ATOM	144	CG	TYR	A	53	9.290	94.335	14.223	1.00	46.28	C
ATOM	145	CD1	TYR	A	53	10.593	93.949	13.897	1.00	43.98	C
ATOM	146	CE1	TYR	A	53	11.689	94.495	14.532	1.00	42.59	C
ATOM	147	CZ	TYR	A	53	11.498	95.475	15.521	1.00	43.72	C
ATOM	148	OH	TYR	A	53	12.598	96.012	16.159	1.00	43.55	O
ATOM	149	CE2	TYR	A	53	10.226	95.884	15.864	1.00	44.06	C
ATOM	150	CD2	TYR	A	53	9.117	95.305	15.221	1.00	45.68	C
ATOM	151	C	TYR	A	53	6.436	91.886	13.363	1.00	49.25	C
ATOM	152	O	TYR	A	53	6.466	91.335	12.258	1.00	48.07	O
ATOM	153	N	SER	A	54	5.306	92.162	14.008	1.00	50.84	N
ATOM	154	CA	SER	A	54	3.996	91.959	13.398	1.00	53.09	C
ATOM	155	CB	SER	A	54	2.889	92.092	14.445	1.00	53.24	C
ATOM	156	OG	SER	A	54	1.609	91.939	13.854	1.00	55.73	O
ATOM	157	C	SER	A	54	3.826	93.019	12.342	1.00	54.41	C
ATOM	158	O	SER	A	54	4.303	94.129	12.510	1.00	55.46	O
ATOM	159	N	GLY	A	55	3.151	92.691	11.248	1.00	56.17	N
ATOM	160	CA	GLY	A	55	3.043	93.625	10.143	1.00	58.09	C
ATOM	161	C	GLY	A	55	1.800	93.391	9.327	1.00	60.22	C
ATOM	162	O	GLY	A	55	1.164	92.343	9.433	1.00	60.35	O
ATOM	163	N	ILE	A	56	1.457	94.381	8.513	1.00	62.12	N
ATOM	164	CA	ILE	A	56	0.307	94.305	7.635	1.00	64.34	C
ATOM	165	CB	ILE	A	56	-0.847	95.188	8.169	1.00	64.42	C
ATOM	166	CG1	ILE	A	56	-1.391	94.639	9.500	1.00	65.47	C
ATOM	167	CD1	ILE	A	56	-2.240	95.670	10.281	1.00	66.61	C
ATOM	168	CG2	ILE	A	56	-1.969	95.273	7.149	1.00	65.46	C
ATOM	169	C	ILE	A	56	0.759	94.780	6.267	1.00	65.56	C
ATOM	170	O	ILE	A	56	1.422	95.805	6.155	1.00	65.96	O
ATOM	171	N	ARG	A	57	0.419	94.017	5.233	1.00	67.26	N
ATOM	172	CA	ARG	A	57	0.731	94.386	3.858	1.00	68.96	C
ATOM	173	CB	ARG	A	57	0.628	93.161	2.946	1.00	68.74	C
ATOM	174	CG	ARG	A	57	1.139	93.361	1.520	1.00	68.49	C
ATOM	175	CD	ARG	A	57	0.433	92.424	0.532	1.00	68.56	C

ATOM	176	NE	ARG	A	57	1.266	91.272	0.179	1.00	68.20	N
ATOM	177	CZ	ARG	A	57	0.777	90.086	-0.208	1.00	68.80	C
ATOM	178	NH1	ARG	A	57	-0.551	89.870	-0.291	1.00	69.12	N
ATOM	179	NH2	ARG	A	57	1.616	89.106	-0.517	1.00	69.04	N
ATOM	180	C	ARG	A	57	-0.259	95.448	3.422	1.00	70.41	C
ATOM	181	O	ARG	A	57	-1.430	95.146	3.171	1.00	70.64	O
ATOM	182	N	VAL	A	58	0.218	96.691	3.345	1.00	72.30	N
ATOM	183	CA	VAL	A	58	-0.626	97.844	2.998	1.00	73.91	C
ATOM	184	CB	VAL	A	58	0.193	99.177	2.969	1.00	73.84	C
ATOM	185	CG1	VAL	A	58	-0.704	100.373	2.670	1.00	73.85	C
ATOM	186	CG2	VAL	A	58	0.924	99.394	4.297	1.00	73.45	C
ATOM	187	C	VAL	A	58	-1.348	97.602	1.666	1.00	74.98	C
ATOM	188	O	VAL	A	58	-2.468	98.081	1.465	1.00	75.68	O
ATOM	189	N	SER	A	59	-0.710	96.822	0.788	1.00	75.93	N
ATOM	190	CA	SER	A	59	-1.268	96.456	-0.521	1.00	76.51	C
ATOM	191	CB	SER	A	59	-0.255	95.617	-1.320	1.00	76.86	C
ATOM	192	OG	SER	A	59	1.103	96.061	-1.049	1.00	78.49	O
ATOM	193	C	SER	A	59	-2.617	95.721	-0.460	1.00	76.40	C
ATOM	194	O	SER	A	59	-3.382	95.775	-1.422	1.00	76.81	O
ATOM	195	N	ASP	A	60	-2.902	95.026	0.645	1.00	75.89	N
ATOM	196	CA	ASP	A	60	-4.174	94.299	0.790	1.00	75.35	C
ATOM	197	CB	ASP	A	60	-4.230	93.077	-0.148	1.00	75.67	C
ATOM	198	CG	ASP	A	60	-3.124	92.064	0.126	1.00	76.95	C
ATOM	199	OD1	ASP	A	60	-2.835	91.788	1.307	1.00	78.19	O
ATOM	200	OD2	ASP	A	60	-2.488	91.483	-0.788	1.00	77.92	O
ATOM	201	C	ASP	A	60	-4.543	93.872	2.217	1.00	74.33	C
ATOM	202	O	ASP	A	60	-5.339	92.947	2.398	1.00	74.34	O
ATOM	203	N	ASN	A	61	-3.965	94.541	3.215	1.00	72.99	N
ATOM	204	CA	ASN	A	61	-4.194	94.219	4.633	1.00	71.45	C
ATOM	205	CB	ASN	A	61	-5.599	94.651	5.074	1.00	72.10	C
ATOM	206	CG	ASN	A	61	-5.790	96.158	5.026	1.00	73.42	C
ATOM	207	OD1	ASN	A	61	-5.333	96.885	5.926	1.00	74.58	O
ATOM	208	ND2	ASN	A	61	-6.471	96.636	3.975	1.00	74.28	N
ATOM	209	C	ASN	A	61	-3.928	92.759	5.035	1.00	69.65	C
ATOM	210	O	ASN	A	61	-4.535	92.242	5.975	1.00	69.76	O
ATOM	211	N	LEU	A	62	-3.020	92.098	4.323	1.00	67.18	N
ATOM	212	CA	LEU	A	62	-2.623	90.738	4.680	1.00	64.33	C
ATOM	213	CB	LEU	A	62	-1.901	90.057	3.518	1.00	64.74	C
ATOM	214	CG	LEU	A	62	-1.291	88.685	3.821	1.00	65.22	C
ATOM	215	CD1	LEU	A	62	-2.383	87.635	4.009	1.00	65.88	C
ATOM	216	CD2	LEU	A	62	-0.325	88.264	2.725	1.00	65.33	C
ATOM	217	C	LEU	A	62	-1.698	90.766	5.883	1.00	61.89	C
ATOM	218	O	LEU	A	62	-0.682	91.453	5.863	1.00	61.51	O
ATOM	219	N	PRO	A	63	-2.044	90.010	6.920	1.00	59.57	N
ATOM	220	CA	PRO	A	63	-1.164	89.840	8.083	1.00	57.75	C
ATOM	221	CB	PRO	A	63	-1.963	88.888	8.983	1.00	57.73	C
ATOM	222	CG	PRO	A	63	-3.376	89.106	8.573	1.00	58.58	C
ATOM	223	CD	PRO	A	63	-3.303	89.261	7.080	1.00	59.38	C
ATOM	224	C	PRO	A	63	0.180	89.221	7.694	1.00	55.60	C
ATOM	225	O	PRO	A	63	0.211	88.163	7.075	1.00	55.56	O
ATOM	226	N	VAL	A	64	1.274	89.902	8.025	1.00	53.21	N
ATOM	227	CA	VAL	A	64	2.609	89.375	7.773	1.00	50.67	C
ATOM	228	CB	VAL	A	64	3.306	90.097	6.590	1.00	50.93	C
ATOM	229	CG1	VAL	A	64	2.441	90.040	5.326	1.00	50.56	C
ATOM	230	CG2	VAL	A	64	3.641	91.537	6.943	1.00	49.88	C
ATOM	231	C	VAL	A	64	3.492	89.445	9.025	1.00	49.15	C
ATOM	232	O	VAL	A	64	3.175	90.150	9.981	1.00	49.44	O
ATOM	233	N	ALA	A	65	4.587	88.692	9.015	1.00	46.68	N
ATOM	234	CA	ALA	A	65	5.604	88.774	10.046	1.00	44.84	C
ATOM	235	CB	ALA	A	65	5.881	87.384	10.654	1.00	45.04	C
ATOM	236	C	ALA	A	65	6.834	89.315	9.356	1.00	43.92	C
ATOM	237	O	ALA	A	65	7.123	88.912	8.218	1.00	43.40	O
ATOM	238	N	ILE	A	66	7.547	90.233	10.012	1.00	42.88	N
ATOM	239	CA	ILE	A	66	8.716	90.883	9.405	1.00	42.53	C
ATOM	240	CB	ILE	A	66	8.494	92.410	9.252	1.00	43.51	C
ATOM	241	CG1	ILE	A	66	7.260	92.679	8.383	1.00	44.11	C
ATOM	242	CD1	ILE	A	66	6.685	94.112	8.501	1.00	47.03	C
ATOM	243	CG2	ILE	A	66	9.704	93.067	8.636	1.00	42.39	C
ATOM	244	C	ILE	A	66	9.958	90.572	10.214	1.00	42.61	C

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ATOM    245  O   ILE A  66      10.119  91.057  11.342  1.00 41.89           O
ATOM    246  N   LYS A  67      10.820  89.731   9.641  1.00 41.21           N
ATOM    247  CA  LYS A  67      11.971  89.193  10.353  1.00 41.66           C
ATOM    248  CB  LYS A  67      12.052  87.664  10.164  1.00 41.05           C
ATOM    249  CG  LYS A  67      13.288  87.013  10.761  1.00 42.61           C
ATOM    250  CD  LYS A  67      13.165  85.495  10.666  1.00 44.83           C
ATOM    251  CE  LYS A  67      14.213  84.780  11.488  1.00 46.29           C
ATOM    252  NZ  LYS A  67      14.165  83.309  11.228  1.00 46.83           N
ATOM    253  C   LYS A  67      13.243  89.833   9.867  1.00 41.57           C
ATOM    254  O   LYS A  67      13.548  89.773   8.671  1.00 40.97           O
ATOM    255  N   HIS A  68      13.988  90.415  10.807  1.00 41.97           N
ATOM    256  CA  HIS A  68      15.254  91.087  10.553  1.00 43.17           C
ATOM    257  CB  HIS A  68      15.343  92.419  11.318  1.00 42.46           C
ATOM    258  CG  HIS A  68      14.352  93.440  10.858  1.00 40.77           C
ATOM    259  ND1 HIS A  68      13.018  93.384  11.203  1.00 43.58           N
ATOM    260  CE1 HIS A  68      12.376  94.393  10.640  1.00 41.67           C
ATOM    261  NE2 HIS A  68      13.247  95.100   9.942  1.00 41.02           N
ATOM    262  CD2 HIS A  68      14.489  94.522  10.062  1.00 37.93           C
ATOM    263  C   HIS A  68      16.408  90.217  10.960  1.00 45.01           C
ATOM    264  O   HIS A  68      16.466  89.744  12.089  1.00 44.97           O
ATOM    265  N   VAL A  69      17.340  90.027  10.030  1.00 46.61           N
ATOM    266  CA  VAL A  69      18.516  89.225  10.272  1.00 49.40           C
ATOM    267  CB  VAL A  69      18.538  87.969   9.359  1.00 49.48           C
ATOM    268  CG1 VAL A  69      19.738  87.093   9.675  1.00 50.89           C
ATOM    269  CG2 VAL A  69      17.266  87.146   9.529  1.00 49.70           C
ATOM    270  C   VAL A  69      19.746  90.103  10.038  1.00 51.36           C
ATOM    271  O   VAL A  69      19.879  90.721   8.983  1.00 50.89           O
ATOM    272  N   GLU A  70      20.634  90.162  11.026  1.00 53.97           N
ATOM    273  CA  GLU A  70      21.870  90.924  10.896  1.00 57.27           C
ATOM    274  CB  GLU A  70      22.480  91.219  12.272  1.00 57.98           C
ATOM    275  CG  GLU A  70      21.674  92.205  13.105  1.00 61.81           C
ATOM    276  CD  GLU A  70      22.524  93.240  13.839  1.00 66.09           C
ATOM    277  OE1 GLU A  70      21.982  93.928  14.744  1.00 67.00           O
ATOM    278  OE2 GLU A  70      23.729  93.377  13.518  1.00 68.05           O
ATOM    279  C   GLU A  70      22.861  90.148  10.057  1.00 58.15           C
ATOM    280  O   GLU A  70      23.115  88.977  10.332  1.00 57.86           O
ATOM    281  N   LYS A  71      23.420  90.807   9.041  1.00 60.40           N
ATOM    282  CA  LYS A  71      24.433  90.193   8.174  1.00 62.67           C
ATOM    283  CB  LYS A  71      24.982  91.207   7.166  1.00 62.59           C
ATOM    284  CG  LYS A  71      23.999  91.544   6.056  1.00 63.22           C
ATOM    285  CD  LYS A  71      24.634  92.387   4.973  1.00 64.60           C
ATOM    286  CE  LYS A  71      23.644  92.635   3.848  1.00 65.13           C
ATOM    287  NZ  LYS A  71      24.159  93.586   2.831  1.00 66.01           N
ATOM    288  C   LYS A  71      25.567  89.589   8.987  1.00 64.37           C
ATOM    289  O   LYS A  71      25.990  88.462   8.737  1.00 64.24           O
ATOM    290  N   ASP A  72      26.029  90.336   9.986  1.00 67.27           N
ATOM    291  CA  ASP A  72      27.153  89.928  10.820  1.00 70.03           C
ATOM    292  CB  ASP A  72      27.483  91.037  11.814  1.00 70.83           C
ATOM    293  CG  ASP A  72      28.294  92.162  11.177  1.00 73.07           C
ATOM    294  OD1 ASP A  72      27.828  92.764  10.174  1.00 75.44           O
ATOM    295  OD2 ASP A  72      29.412  92.511  11.611  1.00 74.89           O
ATOM    296  C   ASP A  72      26.923  88.614  11.551  1.00 71.40           C
ATOM    297  O   ASP A  72      27.875  87.895  11.851  1.00 71.59           O
ATOM    298  N   ARG A  73      25.658  88.287  11.805  1.00 73.23           N
ATOM    299  CA  ARG A  73      25.304  87.068  12.540  1.00 74.86           C
ATOM    300  CB  ARG A  73      24.241  87.380  13.602  1.00 75.53           C
ATOM    301  CG  ARG A  73      24.741  88.293  14.718  1.00 79.03           C
ATOM    302  CD  ARG A  73      23.959  88.151  16.043  1.00 84.58           C
ATOM    303  NE  ARG A  73      23.692  86.752  16.394  1.00 88.34           N
ATOM    304  CZ  ARG A  73      24.598  85.901  16.878  1.00 89.85           C
ATOM    305  NH1 ARG A  73      25.857  86.293  17.083  1.00 90.48           N
ATOM    306  NH2 ARG A  73      24.239  84.650  17.161  1.00 90.61           N
ATOM    307  C   ARG A  73      24.839  85.929  11.630  1.00 75.02           C
ATOM    308  O   ARG A  73      24.067  85.067  12.054  1.00 75.13           O
ATOM    309  N   ILE A  74      25.321  85.926  10.386  1.00 75.26           N
ATOM    310  CA  ILE A  74      24.969  84.885   9.420  1.00 75.36           C
ATOM    311  CB  ILE A  74      24.359  85.503   8.127  1.00 75.17           C
ATOM    312  CG1 ILE A  74      23.188  86.425   8.465  1.00 74.84           C
ATOM    313  CD1 ILE A  74      22.660  87.204   7.280  1.00 75.37           C
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ATOM	314	CG2	ILE	A	74	23.893	84.408	7.166	1.00	74.86	C
ATOM	315	C	ILE	A	74	26.189	84.022	9.088	1.00	75.92	C
ATOM	316	O	ILE	A	74	27.201	84.519	8.578	1.00	76.08	O
ATOM	317	N	SER	A	75	26.090	82.730	9.386	1.00	76.26	N
ATOM	318	CA	SER	A	75	27.155	81.784	9.072	1.00	76.63	C
ATOM	319	CB	SER	A	75	27.184	80.641	10.094	1.00	77.05	C
ATOM	320	OG	SER	A	75	26.007	79.839	10.009	1.00	78.24	O
ATOM	321	C	SER	A	75	26.990	81.226	7.660	1.00	76.35	C
ATOM	322	O	SER	A	75	27.918	81.285	6.855	1.00	76.40	O
ATOM	323	N	ASP	A	76	25.798	80.703	7.372	1.00	75.95	N
ATOM	324	CA	ASP	A	76	25.512	80.025	6.109	1.00	75.64	C
ATOM	325	CB	ASP	A	76	24.528	78.875	6.332	1.00	76.36	C
ATOM	326	CG	ASP	A	76	25.112	77.756	7.157	1.00	78.38	C
ATOM	327	OD1	ASP	A	76	25.828	76.906	6.579	1.00	80.43	O
ATOM	328	OD2	ASP	A	76	24.900	77.642	8.391	1.00	81.66	O
ATOM	329	C	ASP	A	76	24.948	80.952	5.043	1.00	74.58	C
ATOM	330	O	ASP	A	76	23.946	81.635	5.262	1.00	74.37	O
ATOM	331	N	TRP	A	77	25.592	80.945	3.879	1.00	73.73	N
ATOM	332	CA	TRP	A	77	25.148	81.728	2.730	1.00	72.88	C
ATOM	333	CB	TRP	A	77	26.159	82.826	2.398	1.00	72.08	C
ATOM	334	CG	TRP	A	77	26.345	83.854	3.455	1.00	68.72	C
ATOM	335	CD1	TRP	A	77	27.105	83.748	4.582	1.00	67.14	C
ATOM	336	NE1	TRP	A	77	27.038	84.911	5.313	1.00	66.79	N
ATOM	337	CE2	TRP	A	77	26.228	85.800	4.657	1.00	66.47	C
ATOM	338	CD2	TRP	A	77	25.776	85.163	3.478	1.00	66.40	C
ATOM	339	CE3	TRP	A	77	24.926	85.870	2.620	1.00	65.70	C
ATOM	340	CZ3	TRP	A	77	24.557	87.169	2.958	1.00	65.66	C
ATOM	341	CH2	TRP	A	77	25.023	87.770	4.139	1.00	65.79	C
ATOM	342	CZ2	TRP	A	77	25.858	87.104	5.000	1.00	65.98	C
ATOM	343	C	TRP	A	77	25.020	80.808	1.529	1.00	73.58	C
ATOM	344	O	TRP	A	77	25.727	79.802	1.434	1.00	73.41	O
ATOM	345	N	GLY	A	78	24.127	81.159	0.610	1.00	74.27	N
ATOM	346	CA	GLY	A	78	23.959	80.407	-0.623	1.00	75.77	C
ATOM	347	C	GLY	A	78	23.491	81.313	-1.740	1.00	77.06	C
ATOM	348	O	GLY	A	78	23.426	82.534	-1.567	1.00	77.12	O
ATOM	349	N	GLU	A	79	23.157	80.725	-2.887	1.00	78.52	N
ATOM	350	CA	GLU	A	79	22.685	81.517	-4.022	1.00	80.32	C
ATOM	351	CB	GLU	A	79	23.710	81.532	-5.170	1.00	80.86	C
ATOM	352	CG	GLU	A	79	24.083	80.152	-5.723	1.00	83.43	C
ATOM	353	CD	GLU	A	79	24.713	80.234	-7.108	1.00	85.86	C
ATOM	354	OE1	GLU	A	79	25.813	80.822	-7.235	1.00	86.43	O
ATOM	355	OE2	GLU	A	79	24.107	79.708	-8.071	1.00	86.75	O
ATOM	356	C	GLU	A	79	21.311	81.091	-4.518	1.00	80.80	C
ATOM	357	O	GLU	A	79	20.948	79.917	-4.453	1.00	80.46	O
ATOM	358	N	LEU	A	80	20.558	82.069	-5.012	1.00	81.81	N
ATOM	359	CA	LEU	A	80	19.233	81.837	-5.582	1.00	82.81	C
ATOM	360	CB	LEU	A	80	18.441	83.152	-5.596	1.00	82.78	C
ATOM	361	CG	LEU	A	80	18.289	83.870	-4.254	1.00	83.30	C
ATOM	362	CD1	LEU	A	80	17.545	85.189	-4.432	1.00	83.40	C
ATOM	363	CD2	LEU	A	80	17.588	82.965	-3.238	1.00	83.57	C
ATOM	364	C	LEU	A	80	19.343	81.256	-6.998	1.00	83.29	C
ATOM	365	O	LEU	A	80	20.440	81.256	-7.570	1.00	83.54	O
ATOM	366	N	PRO	A	81	18.235	80.753	-7.567	1.00	83.78	N
ATOM	367	CA	PRO	A	81	18.221	80.340	-8.986	1.00	83.97	C
ATOM	368	CB	PRO	A	81	16.758	79.937	-9.218	1.00	83.94	C
ATOM	369	CG	PRO	A	81	16.267	79.535	-7.871	1.00	84.00	C
ATOM	370	CD	PRO	A	81	16.927	80.513	-6.923	1.00	83.86	C
ATOM	371	C	PRO	A	81	18.623	81.488	-9.926	1.00	84.09	C
ATOM	372	O	PRO	A	81	18.910	81.267	-11.102	1.00	84.07	O
ATOM	373	N	ASN	A	82	18.644	82.700	-9.376	1.00	84.20	N
ATOM	374	CA	ASN	A	82	19.070	83.916	-10.064	1.00	83.96	C
ATOM	375	CB	ASN	A	82	18.276	85.106	-9.492	1.00	84.25	C
ATOM	376	CG	ASN	A	82	18.738	86.449	-10.026	1.00	85.14	C
ATOM	377	OD1	ASN	A	82	18.869	86.643	-11.241	1.00	85.89	O
ATOM	378	ND2	ASN	A	82	18.979	87.393	-9.115	1.00	84.89	N
ATOM	379	C	ASN	A	82	20.586	84.137	-9.935	1.00	83.40	C
ATOM	380	O	ASN	A	82	21.190	84.889	-10.709	1.00	83.24	O
ATOM	381	N	GLY	A	83	21.191	83.461	-8.958	1.00	82.90	N
ATOM	382	CA	GLY	A	83	22.597	83.634	-8.626	1.00	82.10	C

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ATOM    383  C   GLY A  83      22.845  84.924  -7.863  1.00 81.49           C
ATOM    384  O   GLY A  83      23.382  85.883  -8.430  1.00 81.74           O
ATOM    385  N   THR A  84      22.437  84.944  -6.590  1.00 80.61           N
ATOM    386  CA  THR A  84      22.609  86.097  -5.687  1.00 79.41           C
ATOM    387  CB  THR A  84      21.290  86.893  -5.543  1.00 79.60           C
ATOM    388  OG1 THR A  84      20.718  87.127  -6.836  1.00 80.05           O
ATOM    389  CG2 THR A  84      21.561  88.322  -5.007  1.00 79.91           C
ATOM    390  C   THR A  84      23.081  85.643  -4.302  1.00 78.07           C
ATOM    391  O   THR A  84      22.728  84.557  -3.841  1.00 78.47           O
ATOM    392  N   ARG A  85      23.866  86.489  -3.643  1.00 75.99           N
ATOM    393  CA  ARG A  85      24.443  86.177  -2.338  1.00 73.77           C
ATOM    394  CB  ARG A  85      25.768  86.943  -2.184  1.00 74.21           C
ATOM    395  CG  ARG A  85      26.453  86.829  -0.833  1.00 75.15           C
ATOM    396  CD  ARG A  85      27.404  85.638  -0.725  1.00 75.91           C
ATOM    397  NE  ARG A  85      28.213  85.731   0.487  1.00 76.30           N
ATOM    398  CZ  ARG A  85      28.957  84.739   0.972  1.00 77.02           C
ATOM    399  NH1 ARG A  85      29.005  83.560   0.352  1.00 76.24           N
ATOM    400  NH2 ARG A  85      29.655  84.929   2.086  1.00 77.19           N
ATOM    401  C   ARG A  85      23.457  86.502  -1.199  1.00 71.72           C
ATOM    402  O   ARG A  85      23.415  87.632  -0.696  1.00 71.91           O
ATOM    403  N   VAL A  86      22.653  85.514  -0.809  1.00 68.61           N
ATOM    404  CA  VAL A  86      21.660  85.693   0.262  1.00 65.46           C
ATOM    405  CB  VAL A  86      20.191  85.642  -0.265  1.00 65.32           C
ATOM    406  CG1 VAL A  86      19.977  86.633  -1.394  1.00 64.79           C
ATOM    407  CG2 VAL A  86      19.822  84.250  -0.709  1.00 65.00           C
ATOM    408  C   VAL A  86      21.866  84.656   1.372  1.00 63.06           C
ATOM    409  O   VAL A  86      22.543  83.649   1.144  1.00 63.20           O
ATOM    410  N   PRO A  87      21.301  84.887   2.563  1.00 60.50           N
ATOM    411  CA  PRO A  87      21.399  83.907   3.649  1.00 58.23           C
ATOM    412  CB  PRO A  87      20.570  84.544   4.774  1.00 58.22           C
ATOM    413  CG  PRO A  87      20.590  85.999   4.478  1.00 59.47           C
ATOM    414  CD  PRO A  87      20.535  86.082   2.986  1.00 60.10           C
ATOM    415  C   PRO A  87      20.797  82.564   3.237  1.00 56.09           C
ATOM    416  O   PRO A  87      19.802  82.524   2.513  1.00 55.24           O
ATOM    417  N   MET A  88      21.416  81.479   3.681  1.00 54.23           N
ATOM    418  CA  MET A  88      20.866  80.142   3.458  1.00 53.19           C
ATOM    419  CB  MET A  88      21.638  79.111   4.295  1.00 54.18           C
ATOM    420  CG  MET A  88      21.273  77.645   4.025  1.00 57.50           C
ATOM    421  SD  MET A  88      21.341  77.213   2.247  1.00 65.32           S
ATOM    422  CE  MET A  88      23.113  77.148   2.002  1.00 62.88           C
ATOM    423  C   MET A  88      19.363  80.103   3.775  1.00 50.99           C
ATOM    424  O   MET A  88      18.565  79.594   2.979  1.00 49.59           O
ATOM    425  N   GLU A  89      18.982  80.688   4.918  1.00 48.97           N
ATOM    426  CA  GLU A  89      17.575  80.754   5.317  1.00 46.86           C
ATOM    427  CB  GLU A  89      17.392  81.686   6.522  1.00 45.85           C
ATOM    428  CG  GLU A  89      15.944  81.803   6.991  1.00 45.51           C
ATOM    429  CD  GLU A  89      15.803  82.541   8.303  1.00 44.03           C
ATOM    430  OE1 GLU A  89      16.819  83.008   8.856  1.00 47.34           O
ATOM    431  OE2 GLU A  89      14.671  82.638   8.790  1.00 44.02           O
ATOM    432  C   GLU A  89      16.653  81.168   4.171  1.00 46.50           C
ATOM    433  O   GLU A  89      15.612  80.548   3.962  1.00 46.41           O
ATOM    434  N   VAL A  90      17.031  82.215   3.429  1.00 46.05           N
ATOM    435  CA  VAL A  90      16.243  82.669   2.275  1.00 45.86           C
ATOM    436  CB  VAL A  90      16.759  84.018   1.725  1.00 46.25           C
ATOM    437  CG1 VAL A  90      15.966  84.431   0.491  1.00 45.50           C
ATOM    438  CG2 VAL A  90      16.663  85.102   2.800  1.00 46.57           C
ATOM    439  C   VAL A  90      16.234  81.639   1.137  1.00 45.66           C
ATOM    440  O   VAL A  90      15.210  81.399   0.525  1.00 45.75           O
ATOM    441  N   VAL A  91      17.389  81.053   0.851  1.00 45.99           N
ATOM    442  CA  VAL A  91      17.490  80.034  -0.197  1.00 46.17           C
ATOM    443  CB  VAL A  91      18.913  79.465  -0.279  1.00 46.54           C
ATOM    444  CG1 VAL A  91      18.975  78.292  -1.284  1.00 47.68           C
ATOM    445  CG2 VAL A  91      19.892  80.556  -0.674  1.00 48.34           C
ATOM    446  C   VAL A  91      16.496  78.909   0.094  1.00 44.94           C
ATOM    447  O   VAL A  91      15.631  78.603  -0.729  1.00 45.36           O
ATOM    448  N   LEU A  92      16.591  78.352   1.302  1.00 43.94           N
ATOM    449  CA  LEU A  92      15.704  77.260   1.749  1.00 42.33           C
ATOM    450  CB  LEU A  92      16.106  76.772   3.137  1.00 40.99           C
ATOM    451  CG  LEU A  92      17.577  76.417   3.316  1.00 40.75           C
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ATOM	452	CD1	LEU	A	92	17.798	75.867	4.711	1.00	37.63	C
ATOM	453	CD2	LEU	A	92	18.061	75.410	2.247	1.00	40.38	C
ATOM	454	C	LEU	A	92	14.245	77.641	1.742	1.00	42.09	C
ATOM	455	O	LEU	A	92	13.401	76.888	1.243	1.00	41.96	O
ATOM	456	N	LEU	A	93	13.936	78.812	2.289	1.00	42.17	N
ATOM	457	CA	LEU	A	93	12.556	79.280	2.328	1.00	43.42	C
ATOM	458	CB	LEU	A	93	12.461	80.632	3.051	1.00	42.52	C
ATOM	459	CG	LEU	A	93	12.416	80.645	4.589	1.00	42.30	C
ATOM	460	CD1	LEU	A	93	12.576	82.074	5.095	1.00	39.64	C
ATOM	461	CD2	LEU	A	93	11.117	80.069	5.107	1.00	39.20	C
ATOM	462	C	LEU	A	93	11.947	79.382	0.921	1.00	44.51	C
ATOM	463	O	LEU	A	93	10.823	78.940	0.691	1.00	44.42	O
ATOM	464	N	LYS	A	94	12.690	79.981	-0.012	1.00	46.08	N
ATOM	465	CA	LYS	A	94	12.222	80.098	-1.391	1.00	47.69	C
ATOM	466	CB	LYS	A	94	13.266	80.807	-2.254	1.00	48.80	C
ATOM	467	CG	LYS	A	94	13.146	82.329	-2.195	1.00	52.89	C
ATOM	468	CD	LYS	A	94	14.133	83.009	-3.126	1.00	57.20	C
ATOM	469	CE	LYS	A	94	13.761	82.810	-4.598	1.00	58.87	C
ATOM	470	NZ	LYS	A	94	12.411	83.360	-4.919	1.00	60.23	N
ATOM	471	C	LYS	A	94	11.903	78.730	-1.981	1.00	47.52	C
ATOM	472	O	LYS	A	94	10.870	78.564	-2.633	1.00	48.02	O
ATOM	473	N	LYS	A	95	12.792	77.766	-1.733	1.00	47.55	N
ATOM	474	CA	LYS	A	95	12.615	76.380	-2.185	1.00	48.35	C
ATOM	475	CB	LYS	A	95	13.836	75.536	-1.829	1.00	48.23	C
ATOM	476	CG	LYS	A	95	15.023	75.801	-2.747	1.00	48.74	C
ATOM	477	CD	LYS	A	95	16.293	75.188	-2.212	1.00	50.92	C
ATOM	478	CE	LYS	A	95	16.392	73.705	-2.529	1.00	53.76	C
ATOM	479	NZ	LYS	A	95	16.339	73.414	-3.999	1.00	55.34	N
ATOM	480	C	LYS	A	95	11.351	75.706	-1.659	1.00	48.52	C
ATOM	481	O	LYS	A	95	10.770	74.872	-2.358	1.00	48.90	O
ATOM	482	N	VAL	A	96	10.921	76.056	-0.444	1.00	48.20	N
ATOM	483	CA	VAL	A	96	9.759	75.395	0.149	1.00	48.68	C
ATOM	484	CB	VAL	A	96	10.001	74.989	1.620	1.00	48.64	C
ATOM	485	CG1	VAL	A	96	11.105	73.977	1.718	1.00	45.61	C
ATOM	486	CG2	VAL	A	96	10.301	76.238	2.498	1.00	47.01	C
ATOM	487	C	VAL	A	96	8.469	76.211	0.082	1.00	50.79	C
ATOM	488	O	VAL	A	96	7.412	75.751	0.544	1.00	50.14	O
ATOM	489	N	SER	A	97	8.547	77.419	-0.476	1.00	52.75	N
ATOM	490	CA	SER	A	97	7.384	78.301	-0.523	1.00	55.97	C
ATOM	491	CB	SER	A	97	7.820	79.751	-0.306	1.00	56.04	C
ATOM	492	OG	SER	A	97	8.364	79.912	0.999	1.00	53.48	O
ATOM	493	C	SER	A	97	6.572	78.124	-1.816	1.00	58.83	C
ATOM	494	O	SER	A	97	7.097	78.270	-2.921	1.00	60.33	O
ATOM	495	N	SER	A	98	5.294	77.767	-1.667	1.00	61.85	N
ATOM	496	CA	SER	A	98	4.397	77.478	-2.805	1.00	63.61	C
ATOM	497	CB	SER	A	98	5.081	76.573	-3.822	1.00	63.67	C
ATOM	498	OG	SER	A	98	5.317	75.300	-3.246	1.00	63.53	O
ATOM	499	C	SER	A	98	3.120	76.797	-2.304	1.00	65.08	C
ATOM	500	O	SER	A	98	2.764	76.902	-1.125	1.00	65.04	O
ATOM	501	N	GLY	A	99	2.442	76.091	-3.204	1.00	66.21	N
ATOM	502	CA	GLY	A	99	1.192	75.403	-2.892	1.00	67.46	C
ATOM	503	C	GLY	A	99	0.948	74.924	-1.464	1.00	67.88	C
ATOM	504	O	GLY	A	99	-0.086	75.258	-0.860	1.00	68.29	O
ATOM	505	N	PHE	A	100	1.877	74.127	-0.924	1.00	68.05	N
ATOM	506	CA	PHE	A	100	1.723	73.626	0.436	1.00	67.53	C
ATOM	507	CB	PHE	A	100	2.873	72.738	0.871	1.00	68.29	C
ATOM	508	CG	PHE	A	100	2.530	71.844	2.047	1.00	69.62	C
ATOM	509	CD1	PHE	A	100	1.249	71.278	2.168	1.00	70.09	C
ATOM	510	CE1	PHE	A	100	0.933	70.435	3.245	1.00	70.04	C
ATOM	511	CZ	PHE	A	100	1.906	70.147	4.214	1.00	69.68	C
ATOM	512	CE2	PHE	A	100	3.181	70.698	4.103	1.00	69.67	C
ATOM	513	CD2	PHE	A	100	3.488	71.552	3.025	1.00	70.39	C
ATOM	514	C	PHE	A	100	1.617	74.720	1.453	1.00	66.54	C
ATOM	515	O	PHE	A	100	1.946	75.873	1.193	1.00	68.10	O
ATOM	516	N	SER	A	101	1.174	74.341	2.637	1.00	64.56	N
ATOM	517	CA	SER	A	101	0.954	75.295	3.693	1.00	61.98	C
ATOM	518	CB	SER	A	101	-0.524	75.693	3.717	1.00	62.34	C
ATOM	519	OG	SER	A	101	-1.344	74.533	3.712	1.00	64.11	O
ATOM	520	C	SER	A	101	1.379	74.726	5.036	1.00	59.07	C

ATOM	521	O	SER A 101	0.982	75.260	6.087	1.00	60.11	O
ATOM	522	N	GLY A 102	2.170	73.649	5.013	1.00	55.16	N
ATOM	523	CA	GLY A 102	2.732	73.096	6.245	1.00	49.51	C
ATOM	524	C	GLY A 102	3.986	73.857	6.676	1.00	46.58	C
ATOM	525	O	GLY A 102	4.576	73.592	7.726	1.00	43.90	O
ATOM	526	N	VAL A 103	4.411	74.794	5.840	1.00	44.62	N
ATOM	527	CA	VAL A 103	5.521	75.673	6.162	1.00	44.58	C
ATOM	528	CB	VAL A 103	6.738	75.384	5.255	1.00	44.89	C
ATOM	529	CG1	VAL A 103	7.832	76.366	5.505	1.00	46.40	C
ATOM	530	CG2	VAL A 103	7.282	73.964	5.503	1.00	45.56	C
ATOM	531	C	VAL A 103	5.057	77.124	6.013	1.00	43.92	C
ATOM	532	O	VAL A 103	4.370	77.458	5.049	1.00	43.86	O
ATOM	533	N	ILE A 104	5.427	77.982	6.961	1.00	43.35	N
ATOM	534	CA	ILE A 104	5.168	79.411	6.824	1.00	42.66	C
ATOM	535	CB	ILE A 104	5.520	80.165	8.122	1.00	43.40	C
ATOM	536	CG1	ILE A 104	4.339	80.057	9.077	1.00	44.47	C
ATOM	537	CD1	ILE A 104	4.527	80.787	10.332	1.00	50.46	C
ATOM	538	CG2	ILE A 104	5.877	81.660	7.853	1.00	41.37	C
ATOM	539	C	ILE A 104	5.961	79.925	5.622	1.00	42.85	C
ATOM	540	O	ILE A 104	7.184	79.743	5.536	1.00	41.68	O
ATOM	541	N	ARG A 105	5.241	80.535	4.691	1.00	42.70	N
ATOM	542	CA	ARG A 105	5.807	80.875	3.395	1.00	44.62	C
ATOM	543	CB	ARG A 105	4.690	80.815	2.360	1.00	46.35	C
ATOM	544	CG	ARG A 105	5.065	81.242	0.972	1.00	53.53	C
ATOM	545	CD	ARG A 105	4.460	80.351	-0.099	1.00	61.61	C
ATOM	546	NE	ARG A 105	3.071	80.019	0.185	1.00	65.80	N
ATOM	547	CZ	ARG A 105	2.156	79.818	-0.763	1.00	68.07	C
ATOM	548	NH1	ARG A 105	2.489	79.894	-2.060	1.00	69.01	N
ATOM	549	NH2	ARG A 105	0.907	79.535	-0.414	1.00	68.72	N
ATOM	550	C	ARG A 105	6.464	82.255	3.412	1.00	43.35	C
ATOM	551	O	ARG A 105	5.955	83.180	4.045	1.00	40.91	O
ATOM	552	N	LEU A 106	7.597	82.359	2.722	1.00	42.75	N
ATOM	553	CA	LEU A 106	8.288	83.624	2.481	1.00	43.28	C
ATOM	554	CB	LEU A 106	9.746	83.349	2.126	1.00	42.30	C
ATOM	555	CG	LEU A 106	10.653	84.564	1.905	1.00	42.45	C
ATOM	556	CD1	LEU A 106	10.906	85.341	3.204	1.00	40.95	C
ATOM	557	CD2	LEU A 106	11.993	84.148	1.293	1.00	40.34	C
ATOM	558	C	LEU A 106	7.601	84.394	1.350	1.00	44.07	C
ATOM	559	O	LEU A 106	7.620	83.960	0.206	1.00	44.25	O
ATOM	560	N	LEU A 107	6.979	85.521	1.683	1.00	44.63	N
ATOM	561	CA	LEU A 107	6.241	86.316	0.712	1.00	45.98	C
ATOM	562	CB	LEU A 107	5.123	87.107	1.401	1.00	46.13	C
ATOM	563	CG	LEU A 107	4.143	86.246	2.202	1.00	46.97	C
ATOM	564	CD1	LEU A 107	3.237	87.069	3.085	1.00	47.43	C
ATOM	565	CD2	LEU A 107	3.330	85.376	1.239	1.00	49.67	C
ATOM	566	C	LEU A 107	7.145	87.267	-0.066	1.00	46.90	C
ATOM	567	O	LEU A 107	6.793	87.686	-1.177	1.00	46.82	O
ATOM	568	N	ASP A 108	8.302	87.601	0.511	1.00	47.11	N
ATOM	569	CA	ASP A 108	9.241	88.537	-0.108	1.00	47.79	C
ATOM	570	CB	ASP A 108	8.543	89.875	-0.430	1.00	47.83	C
ATOM	571	CG	ASP A 108	9.311	90.725	-1.464	1.00	50.15	C
ATOM	572	OD1	ASP A 108	10.299	90.251	-2.085	1.00	50.90	O
ATOM	573	OD2	ASP A 108	8.978	91.903	-1.710	1.00	52.00	O
ATOM	574	C	ASP A 108	10.392	88.791	0.841	1.00	48.02	C
ATOM	575	O	ASP A 108	10.319	88.447	2.025	1.00	46.97	O
ATOM	576	N	TRP A 109	11.453	89.399	0.318	1.00	48.18	N
ATOM	577	CA	TRP A 109	12.613	89.748	1.114	1.00	48.85	C
ATOM	578	CB	TRP A 109	13.598	88.588	1.170	1.00	48.93	C
ATOM	579	CG	TRP A 109	14.148	88.237	-0.171	1.00	51.68	C
ATOM	580	CD1	TRP A 109	13.543	87.478	-1.137	1.00	52.64	C
ATOM	581	NE1	TRP A 109	14.354	87.383	-2.244	1.00	54.00	N
ATOM	582	CE2	TRP A 109	15.509	88.084	-2.013	1.00	54.40	C
ATOM	583	CD2	TRP A 109	15.407	88.645	-0.715	1.00	53.99	C
ATOM	584	CE3	TRP A 109	16.470	89.423	-0.236	1.00	55.22	C
ATOM	585	CZ3	TRP A 109	17.577	89.625	-1.056	1.00	56.91	C
ATOM	586	CH2	TRP A 109	17.641	89.061	-2.348	1.00	57.27	C
ATOM	587	CZ2	TRP A 109	16.621	88.288	-2.839	1.00	55.31	C
ATOM	588	C	TRP A 109	13.302	90.989	0.555	1.00	49.39	C
ATOM	589	O	TRP A 109	13.160	91.316	-0.638	1.00	49.52	O

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ATOM    590  N   PHE A 110      14.043  91.672   1.425  1.00 49.52           N
ATOM    591  CA  PHE A 110      14.737  92.912   1.077  1.00 50.21           C
ATOM    592  CB  PHE A 110      14.005  94.130   1.649  1.00 49.95           C
ATOM    593  CG  PHE A 110      12.583  94.259   1.182  1.00 51.89           C
ATOM    594  CD1 PHE A 110      12.268  95.026   0.061  1.00 53.85           C
ATOM    595  CE1 PHE A 110      10.950  95.139  -0.376  1.00 54.01           C
ATOM    596  CZ  PHE A 110       9.941  94.477   0.310  1.00 54.23           C
ATOM    597  CE2 PHE A 110      10.249  93.710   1.426  1.00 53.04           C
ATOM    598  CD2 PHE A 110      11.559  93.611   1.855  1.00 52.18           C
ATOM    599  C   PHE A 110      16.126  92.848   1.657  1.00 50.39           C
ATOM    600  O   PHE A 110      16.331  92.251   2.711  1.00 49.25           O
ATOM    601  N   GLU A 111      17.087  93.452   0.966  1.00 51.10           N
ATOM    602  CA  GLU A 111      18.440  93.541   1.494  1.00 52.22           C
ATOM    603  CB  GLU A 111      19.450  93.076   0.457  1.00 52.56           C
ATOM    604  CG  GLU A 111      20.896  93.340   0.835  1.00 54.50           C
ATOM    605  CD  GLU A 111      21.857  92.662  -0.109  1.00 57.61           C
ATOM    606  OE1 GLU A 111      21.513  92.561  -1.309  1.00 60.12           O
ATOM    607  OE2 GLU A 111      22.937  92.211   0.348  1.00 59.23           O
ATOM    608  C   GLU A 111      18.751  94.974   1.938  1.00 52.56           C
ATOM    609  O   GLU A 111      18.340  95.943   1.290  1.00 53.03           O
ATOM    610  N   ARG A 112      19.470  95.084   3.050  1.00 52.37           N
ATOM    611  CA  ARG A 112      19.880  96.362   3.605  1.00 52.15           C
ATOM    612  CB  ARG A 112      19.204  96.601   4.957  1.00 51.55           C
ATOM    613  CG  ARG A 112      17.795  97.170   4.862  1.00 50.03           C
ATOM    614  CD  ARG A 112      17.101  97.229   6.225  1.00 49.06           C
ATOM    615  NE  ARG A 112      15.825  97.939   6.172  1.00 47.63           N
ATOM    616  CZ  ARG A 112      15.036  98.135   7.223  1.00 48.41           C
ATOM    617  NH1 ARG A 112      15.379  97.664   8.420  1.00 47.11           N
ATOM    618  NH2 ARG A 112      13.895  98.797   7.078  1.00 48.44           N
ATOM    619  C   ARG A 112      21.380  96.312   3.789  1.00 52.90           C
ATOM    620  O   ARG A 112      21.972  95.227   3.727  1.00 52.95           O
ATOM    621  N   PRO A 113      22.008  97.466   4.027  1.00 53.80           N
ATOM    622  CA  PRO A 113      23.463  97.519   4.222  1.00 53.98           C
ATOM    623  CB  PRO A 113      23.696  98.958   4.718  1.00 54.67           C
ATOM    624  CG  PRO A 113      22.595  99.746   4.065  1.00 54.14           C
ATOM    625  CD  PRO A 113      21.396  98.811   4.112  1.00 54.32           C
ATOM    626  C   PRO A 113      23.998  96.489   5.220  1.00 54.07           C
ATOM    627  O   PRO A 113      24.980  95.812   4.914  1.00 54.49           O
ATOM    628  N   ASP A 114      23.373  96.342   6.382  1.00 54.16           N
ATOM    629  CA  ASP A 114      23.903  95.378   7.346  1.00 54.11           C
ATOM    630  CB  ASP A 114      24.430  96.112   8.575  1.00 55.71           C
ATOM    631  CG  ASP A 114      25.631  96.989   8.245  1.00 58.46           C
ATOM    632  OD1 ASP A 114      25.423  98.057   7.607  1.00 61.78           O
ATOM    633  OD2 ASP A 114      26.805  96.681   8.573  1.00 60.03           O
ATOM    634  C   ASP A 114      22.937  94.269   7.755  1.00 52.78           C
ATOM    635  O   ASP A 114      23.188  93.548   8.727  1.00 53.03           O
ATOM    636  N   SER A 115      21.852  94.111   6.999  1.00 50.98           N
ATOM    637  CA  SER A 115      20.856  93.105   7.331  1.00 48.41           C
ATOM    638  CB  SER A 115      19.960  93.649   8.439  1.00 48.04           C
ATOM    639  OG  SER A 115      18.997  94.528   7.893  1.00 45.84           O
ATOM    640  C   SER A 115      19.978  92.666   6.155  1.00 47.32           C
ATOM    641  O   SER A 115      19.987  93.285   5.096  1.00 46.92           O
ATOM    642  N   PHE A 116      19.198  91.609   6.381  1.00 45.66           N
ATOM    643  CA  PHE A 116      18.171  91.174   5.446  1.00 44.29           C
ATOM    644  CB  PHE A 116      18.457  89.746   4.994  1.00 44.76           C
ATOM    645  CG  PHE A 116      19.567  89.632   3.980  1.00 45.24           C
ATOM    646  CD1 PHE A 116      20.892  89.484   4.385  1.00 45.34           C
ATOM    647  CE1 PHE A 116      21.915  89.360   3.447  1.00 47.24           C
ATOM    648  CZ  PHE A 116      21.614  89.387   2.077  1.00 46.18           C
ATOM    649  CE2 PHE A 116      20.291  89.531   1.661  1.00 48.08           C
ATOM    650  CD2 PHE A 116      19.275  89.646   2.615  1.00 47.94           C
ATOM    651  C   PHE A 116      16.824  91.238   6.141  1.00 43.43           C
ATOM    652  O   PHE A 116      16.721  90.945   7.333  1.00 42.72           O
ATOM    653  N   VAL A 117      15.797  91.641   5.411  1.00 42.24           N
ATOM    654  CA  VAL A 117      14.450  91.681   5.945  1.00 41.74           C
ATOM    655  CB  VAL A 117      13.837  93.087   5.818  1.00 41.89           C
ATOM    656  CG1 VAL A 117      12.473  93.136   6.447  1.00 41.40           C
ATOM    657  CG2 VAL A 117      14.753  94.122   6.451  1.00 42.52           C
ATOM    658  C   VAL A 117      13.578  90.652   5.209  1.00 41.80           C
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ATOM	659	O	VAL	A 117	13.507	90.660	3.974	1.00 40.77	O
ATOM	660	N	LEU	A 118	12.934	89.765	5.974	1.00 41.04	N
ATOM	661	CA	LEU	A 118	12.094	88.693	5.410	1.00 40.22	C
ATOM	662	CB	LEU	A 118	12.520	87.337	5.977	1.00 39.98	C
ATOM	663	CG	LEU	A 118	13.795	86.695	5.423	1.00 40.10	C
ATOM	664	CD1	LEU	A 118	15.014	87.562	5.619	1.00 42.56	C
ATOM	665	CD2	LEU	A 118	14.032	85.325	6.063	1.00 39.40	C
ATOM	666	C	LEU	A 118	10.635	88.939	5.720	1.00 40.25	C
ATOM	667	O	LEU	A 118	10.275	89.223	6.861	1.00 39.35	O
ATOM	668	N	ILE	A 119	9.795	88.842	4.700	1.00 39.45	N
ATOM	669	CA	ILE	A 119	8.370	89.028	4.876	1.00 40.37	C
ATOM	670	CB	ILE	A 119	7.774	89.921	3.756	1.00 40.19	C
ATOM	671	CG1	ILE	A 119	8.555	91.248	3.612	1.00 41.49	C
ATOM	672	CD1	ILE	A 119	8.540	92.131	4.855	1.00 40.16	C
ATOM	673	CG2	ILE	A 119	6.296	90.136	3.989	1.00 39.40	C
ATOM	674	C	ILE	A 119	7.748	87.638	4.823	1.00 41.09	C
ATOM	675	O	ILE	A 119	7.793	86.966	3.788	1.00 40.59	O
ATOM	676	N	LEU	A 120	7.167	87.222	5.939	1.00 41.43	N
ATOM	677	CA	LEU	A 120	6.634	85.872	6.076	1.00 42.78	C
ATOM	678	CB	LEU	A 120	7.355	85.144	7.216	1.00 41.61	C
ATOM	679	CG	LEU	A 120	8.868	85.010	7.046	1.00 40.99	C
ATOM	680	CD1	LEU	A 120	9.558	84.928	8.402	1.00 43.47	C
ATOM	681	CD2	LEU	A 120	9.234	83.785	6.187	1.00 42.48	C
ATOM	682	C	LEU	A 120	5.138	85.922	6.330	1.00 44.08	C
ATOM	683	O	LEU	A 120	4.604	86.963	6.715	1.00 44.77	O
ATOM	684	N	GLU	A 121	4.449	84.808	6.109	1.00 45.28	N
ATOM	685	CA	GLU	A 121	3.026	84.738	6.436	1.00 47.09	C
ATOM	686	CB	GLU	A 121	2.430	83.409	5.985	1.00 47.99	C
ATOM	687	CG	GLU	A 121	2.534	83.123	4.497	1.00 49.97	C
ATOM	688	CD	GLU	A 121	1.959	81.759	4.170	1.00 53.32	C
ATOM	689	OE1	GLU	A 121	0.911	81.714	3.506	1.00 55.61	O
ATOM	690	OE2	GLU	A 121	2.548	80.735	4.586	1.00 52.97	O
ATOM	691	C	GLU	A 121	2.841	84.862	7.938	1.00 47.78	C
ATOM	692	O	GLU	A 121	3.753	84.550	8.711	1.00 47.35	O
ATOM	693	N	ARG	A 122	1.670	85.326	8.351	1.00 48.92	N
ATOM	694	CA	ARG	A 122	1.369	85.439	9.766	1.00 50.98	C
ATOM	695	CB	ARG	A 122	1.555	86.883	10.257	1.00 50.78	C
ATOM	696	CG	ARG	A 122	1.196	87.085	11.730	1.00 51.57	C
ATOM	697	CD	ARG	A 122	1.716	88.383	12.349	1.00 51.63	C
ATOM	698	NE	ARG	A 122	1.119	89.578	11.744	1.00 52.11	N
ATOM	699	CZ	ARG	A 122	-0.133	89.977	11.951	1.00 51.61	C
ATOM	700	NH1	ARG	A 122	-0.937	89.274	12.741	1.00 51.42	N
ATOM	701	NH2	ARG	A 122	-0.588	91.070	11.354	1.00 50.64	N
ATOM	702	C	ARG	A 122	-0.054	84.965	10.017	1.00 52.37	C
ATOM	703	O	ARG	A 122	-1.005	85.749	9.922	1.00 52.94	O
ATOM	704	N	PRO	A 123	-0.211	83.682	10.328	1.00 53.57	N
ATOM	705	CA	PRO	A 123	-1.529	83.141	10.672	1.00 54.00	C
ATOM	706	CB	PRO	A 123	-1.227	81.669	10.973	1.00 54.39	C
ATOM	707	CG	PRO	A 123	0.057	81.394	10.250	1.00 54.18	C
ATOM	708	CD	PRO	A 123	0.845	82.652	10.398	1.00 53.87	C
ATOM	709	C	PRO	A 123	-2.012	83.835	11.928	1.00 54.39	C
ATOM	710	O	PRO	A 123	-1.172	84.333	12.676	1.00 54.50	O
ATOM	711	N	GLU	A 124	-3.322	83.862	12.164	1.00 54.85	N
ATOM	712	CA	GLU	A 124	-3.859	84.533	13.348	1.00 55.63	C
ATOM	713	CB	GLU	A 124	-3.870	86.046	13.089	1.00 56.97	C
ATOM	714	CG	GLU	A 124	-3.856	86.946	14.335	1.00 62.93	C
ATOM	715	CD	GLU	A 124	-4.020	88.417	13.933	1.00 69.90	C
ATOM	716	OE1	GLU	A 124	-4.962	88.742	13.153	1.00 72.13	O
ATOM	717	OE2	GLU	A 124	-3.195	89.256	14.385	1.00 71.98	O
ATOM	718	C	GLU	A 124	-5.270	84.018	13.671	1.00 53.97	C
ATOM	719	O	GLU	A 124	-6.093	83.910	12.764	1.00 54.52	O
ATOM	720	N	PRO	A 125	-5.563	83.673	14.930	1.00 52.32	N
ATOM	721	CA	PRO	A 125	-4.601	83.673	16.040	1.00 51.14	C
ATOM	722	CB	PRO	A 125	-5.504	83.553	17.275	1.00 51.19	C
ATOM	723	CG	PRO	A 125	-6.689	82.766	16.783	1.00 50.94	C
ATOM	724	CD	PRO	A 125	-6.906	83.255	15.374	1.00 51.87	C
ATOM	725	C	PRO	A 125	-3.694	82.453	15.970	1.00 50.27	C
ATOM	726	O	PRO	A 125	-4.057	81.436	15.379	1.00 49.98	O
ATOM	727	N	VAL	A 126	-2.526	82.562	16.588	1.00 49.17	N

ATOM	728	CA	VAL	A	126	-1.525	81.526	16.500	1.00	48.07	C
ATOM	729	CB	VAL	A	126	-0.508	81.866	15.373	1.00	48.55	C
ATOM	730	CG1	VAL	A	126	0.307	83.104	15.726	1.00	49.90	C
ATOM	731	CG2	VAL	A	126	0.400	80.711	15.096	1.00	50.31	C
ATOM	732	C	VAL	A	126	-0.848	81.346	17.855	1.00	46.31	C
ATOM	733	O	VAL	A	126	-0.787	82.290	18.644	1.00	46.40	O
ATOM	734	N	GLN	A	127	-0.360	80.129	18.117	1.00	43.89	N
ATOM	735	CA	GLN	A	127	0.495	79.825	19.270	1.00	41.91	C
ATOM	736	CB	GLN	A	127	-0.356	79.311	20.438	1.00	41.96	C
ATOM	737	CG	GLN	A	127	0.414	79.085	21.751	1.00	41.25	C
ATOM	738	CD	GLN	A	127	-0.498	78.618	22.880	1.00	41.99	C
ATOM	739	OE1	GLN	A	127	-1.346	77.744	22.688	1.00	41.61	O
ATOM	740	NE2	GLN	A	127	-0.336	79.214	24.052	1.00	40.70	N
ATOM	741	C	GLN	A	127	1.500	78.750	18.868	1.00	41.00	C
ATOM	742	O	GLN	A	127	1.136	77.807	18.153	1.00	40.30	O
ATOM	743	N	ASP	A	128	2.755	78.874	19.307	1.00	40.28	N
ATOM	744	CA	ASP	A	128	3.719	77.829	18.995	1.00	39.77	C
ATOM	745	CB	ASP	A	128	5.174	78.319	19.018	1.00	40.70	C
ATOM	746	CG	ASP	A	128	5.670	78.691	20.390	1.00	42.88	C
ATOM	747	OD1	ASP	A	128	5.553	77.903	21.369	1.00	46.75	O
ATOM	748	OD2	ASP	A	128	6.231	79.788	20.562	1.00	48.33	O
ATOM	749	C	ASP	A	128	3.482	76.609	19.881	1.00	39.44	C
ATOM	750	O	ASP	A	128	2.898	76.723	20.978	1.00	38.51	O
ATOM	751	N	LEU	A	129	3.908	75.443	19.392	1.00	37.35	N
ATOM	752	CA	LEU	A	129	3.665	74.196	20.084	1.00	35.60	C
ATOM	753	CB	LEU	A	129	4.146	73.015	19.224	1.00	33.96	C
ATOM	754	CG	LEU	A	129	3.950	71.607	19.773	1.00	34.42	C
ATOM	755	CD1	LEU	A	129	2.485	71.352	20.108	1.00	29.98	C
ATOM	756	CD2	LEU	A	129	4.490	70.573	18.768	1.00	33.34	C
ATOM	757	C	LEU	A	129	4.281	74.165	21.489	1.00	35.69	C
ATOM	758	O	LEU	A	129	3.730	73.565	22.403	1.00	34.94	O
ATOM	759	N	PHE	A	130	5.422	74.804	21.659	1.00	36.83	N
ATOM	760	CA	PHE	A	130	6.047	74.850	22.976	1.00	38.88	C
ATOM	761	CB	PHE	A	130	7.342	75.665	22.930	1.00	39.30	C
ATOM	762	CG	PHE	A	130	8.070	75.714	24.254	1.00	42.49	C
ATOM	763	CD1	PHE	A	130	7.678	76.621	25.251	1.00	45.52	C
ATOM	764	CE1	PHE	A	130	8.349	76.680	26.489	1.00	46.12	C
ATOM	765	CZ	PHE	A	130	9.404	75.807	26.747	1.00	46.89	C
ATOM	766	CE2	PHE	A	130	9.806	74.886	25.758	1.00	47.58	C
ATOM	767	CD2	PHE	A	130	9.132	74.851	24.514	1.00	44.28	C
ATOM	768	C	PHE	A	130	5.099	75.492	23.989	1.00	39.51	C
ATOM	769	O	PHE	A	130	4.849	74.931	25.064	1.00	38.80	O
ATOM	770	N	ASP	A	131	4.596	76.679	23.657	1.00	40.69	N
ATOM	771	CA	ASP	A	131	3.719	77.401	24.583	1.00	42.23	C
ATOM	772	CB	ASP	A	131	3.418	78.805	24.088	1.00	43.13	C
ATOM	773	CG	ASP	A	131	4.620	79.699	24.113	1.00	44.46	C
ATOM	774	OD1	ASP	A	131	5.574	79.431	24.874	1.00	47.95	O
ATOM	775	OD2	ASP	A	131	4.702	80.700	23.375	1.00	49.81	O
ATOM	776	C	ASP	A	131	2.433	76.642	24.771	1.00	42.09	C
ATOM	777	O	ASP	A	131	1.888	76.600	25.877	1.00	42.20	O
ATOM	778	N	PHE	A	132	1.972	76.001	23.696	1.00	41.67	N
ATOM	779	CA	PHE	A	132	0.760	75.195	23.744	1.00	41.50	C
ATOM	780	CB	PHE	A	132	0.459	74.630	22.358	1.00	41.82	C
ATOM	781	CG	PHE	A	132	-0.854	73.909	22.263	1.00	40.63	C
ATOM	782	CD1	PHE	A	132	-2.039	74.618	22.148	1.00	40.87	C
ATOM	783	CE1	PHE	A	132	-3.251	73.965	22.053	1.00	41.37	C
ATOM	784	CZ	PHE	A	132	-3.297	72.581	22.062	1.00	41.96	C
ATOM	785	CE2	PHE	A	132	-2.123	71.855	22.173	1.00	40.31	C
ATOM	786	CD2	PHE	A	132	-0.910	72.524	22.281	1.00	42.21	C
ATOM	787	C	PHE	A	132	0.902	74.058	24.760	1.00	42.73	C
ATOM	788	O	PHE	A	132	-0.006	73.809	25.570	1.00	42.57	O
ATOM	789	N	ILE	A	133	2.040	73.369	24.718	1.00	42.81	N
ATOM	790	CA	ILE	A	133	2.286	72.247	25.630	1.00	43.91	C
ATOM	791	CB	ILE	A	133	3.487	71.395	25.138	1.00	42.90	C
ATOM	792	CG1	ILE	A	133	3.071	70.570	23.920	1.00	41.19	C
ATOM	793	CD1	ILE	A	133	4.220	69.961	23.174	1.00	41.52	C
ATOM	794	CG2	ILE	A	133	4.026	70.461	26.249	1.00	42.29	C
ATOM	795	C	ILE	A	133	2.514	72.780	27.054	1.00	46.10	C
ATOM	796	O	ILE	A	133	2.046	72.191	28.023	1.00	46.11	O

ATOM	797	N	THR	A	134	3.231	73.894	27.162	1.00 48.42	N
ATOM	798	CA	THR	A	134	3.487	74.529	28.453	1.00 51.23	C
ATOM	799	CB	THR	A	134	4.314	75.805	28.261	1.00 51.04	C
ATOM	800	OG1	THR	A	134	5.695	75.440	28.115	1.00 52.55	O
ATOM	801	CG2	THR	A	134	4.293	76.695	29.524	1.00 53.00	C
ATOM	802	C	THR	A	134	2.179	74.851	29.159	1.00 52.34	C
ATOM	803	O	THR	A	134	2.069	74.673	30.365	1.00 53.35	O
ATOM	804	N	GLU	A	135	1.188	75.303	28.400	1.00 53.42	N
ATOM	805	CA	GLU	A	135	-0.110	75.662	28.959	1.00 54.43	C
ATOM	806	CB	GLU	A	135	-0.840	76.644	28.038	1.00 55.03	C
ATOM	807	CG	GLU	A	135	-0.137	78.004	27.941	1.00 59.01	C
ATOM	808	CD	GLU	A	135	-0.981	79.054	27.234	1.00 62.58	C
ATOM	809	OE1	GLU	A	135	-1.942	78.685	26.505	1.00 64.20	O
ATOM	810	OE2	GLU	A	135	-0.675	80.254	27.412	1.00 63.63	O
ATOM	811	C	GLU	A	135	-1.009	74.468	29.215	1.00 53.96	C
ATOM	812	O	GLU	A	135	-1.743	74.440	30.206	1.00 54.61	O
ATOM	813	N	ARG	A	136	-0.975	73.490	28.318	1.00 52.83	N
ATOM	814	CA	ARG	A	136	-1.947	72.404	28.385	1.00 51.61	C
ATOM	815	CB	ARG	A	136	-2.646	72.261	27.036	1.00 52.42	C
ATOM	816	CG	ARG	A	136	-3.486	73.503	26.736	1.00 55.25	C
ATOM	817	CD	ARG	A	136	-4.130	73.538	25.378	1.00 58.99	C
ATOM	818	NE	ARG	A	136	-4.990	72.381	25.145	1.00 60.79	N
ATOM	819	CZ	ARG	A	136	-6.072	72.415	24.379	1.00 61.01	C
ATOM	820	NH1	ARG	A	136	-6.425	73.559	23.777	1.00 60.57	N
ATOM	821	NH2	ARG	A	136	-6.793	71.310	24.207	1.00 60.45	N
ATOM	822	C	ARG	A	136	-1.376	71.086	28.887	1.00 50.04	C
ATOM	823	O	ARG	A	136	-2.116	70.144	29.119	1.00 50.37	O
ATOM	824	N	GLY	A	137	-0.062	71.033	29.081	1.00 48.53	N
ATOM	825	CA	GLY	A	137	0.597	69.799	29.477	1.00 46.78	C
ATOM	826	C	GLY	A	137	0.532	68.744	28.381	1.00 44.89	C
ATOM	827	O	GLY	A	137	0.183	69.046	27.232	1.00 45.03	O
ATOM	828	N	ALA	A	138	0.849	67.509	28.748	1.00 43.07	N
ATOM	829	CA	ALA	A	138	0.841	66.374	27.833	1.00 41.43	C
ATOM	830	CB	ALA	A	138	1.023	65.083	28.602	1.00 41.46	C
ATOM	831	C	ALA	A	138	-0.433	66.321	26.990	1.00 40.58	C
ATOM	832	O	ALA	A	138	-1.533	66.476	27.491	1.00 40.85	O
ATOM	833	N	LEU	A	139	-0.274	66.108	25.693	1.00 38.87	N
ATOM	834	CA	LEU	A	139	-1.415	66.107	24.794	1.00 37.16	C
ATOM	835	CB	LEU	A	139	-0.994	66.557	23.392	1.00 34.91	C
ATOM	836	CG	LEU	A	139	-0.224	67.881	23.369	1.00 36.75	C
ATOM	837	CD1	LEU	A	139	0.082	68.270	21.920	1.00 35.15	C
ATOM	838	CD2	LEU	A	139	-1.002	68.999	24.124	1.00 35.61	C
ATOM	839	C	LEU	A	139	-2.039	64.741	24.731	1.00 36.86	C
ATOM	840	O	LEU	A	139	-1.338	63.733	24.761	1.00 37.14	O
ATOM	841	N	GLN	A	140	-3.362	64.714	24.626	1.00 37.15	N
ATOM	842	CA	GLN	A	140	-4.071	63.473	24.348	1.00 38.86	C
ATOM	843	CB	GLN	A	140	-5.566	63.726	24.208	1.00 39.38	C
ATOM	844	CG	GLN	A	140	-6.266	63.885	25.540	1.00 45.52	C
ATOM	845	CD	GLN	A	140	-7.649	64.493	25.395	1.00 52.38	C
ATOM	846	OE1	GLN	A	140	-8.442	64.070	24.534	1.00 54.06	O
ATOM	847	NE2	GLN	A	140	-7.949	65.488	26.234	1.00 55.44	N
ATOM	848	C	GLN	A	140	-3.532	62.890	23.062	1.00 37.84	C
ATOM	849	O	GLN	A	140	-3.192	63.643	22.141	1.00 37.63	O
ATOM	850	N	GLU	A	141	-3.449	61.559	22.996	1.00 37.43	N
ATOM	851	CA	GLU	A	141	-2.897	60.881	21.808	1.00 37.42	C
ATOM	852	CB	GLU	A	141	-2.849	59.373	22.030	1.00 37.84	C
ATOM	853	CG	GLU	A	141	-1.883	59.033	23.164	1.00 38.10	C
ATOM	854	CD	GLU	A	141	-1.571	57.568	23.263	1.00 36.74	C
ATOM	855	OE1	GLU	A	141	-1.639	56.867	22.233	1.00 35.36	O
ATOM	856	OE2	GLU	A	141	-1.261	57.117	24.383	1.00 37.15	O
ATOM	857	C	GLU	A	141	-3.596	61.227	20.498	1.00 36.95	C
ATOM	858	O	GLU	A	141	-2.958	61.254	19.443	1.00 36.70	O
ATOM	859	N	GLU	A	142	-4.900	61.497	20.566	1.00 36.62	N
ATOM	860	CA	GLU	A	142	-5.654	61.865	19.373	1.00 36.84	C
ATOM	861	CB	GLU	A	142	-7.151	62.019	19.677	1.00 37.69	C
ATOM	862	CG	GLU	A	142	-7.957	62.396	18.443	1.00 39.42	C
ATOM	863	CD	GLU	A	142	-9.440	62.567	18.730	1.00 43.91	C
ATOM	864	OE1	GLU	A	142	-9.809	63.542	19.421	1.00 44.11	O
ATOM	865	OE2	GLU	A	142	-10.233	61.727	18.254	1.00 45.16	O

ATOM	866	C	GLU	A	142	-5.127	63.181	18.814	1.00 35.87	C
ATOM	867	O	GLU	A	142	-4.975	63.336	17.601	1.00 35.78	O
ATOM	868	N	LEU	A	143	-4.857	64.120	19.709	1.00 34.68	N
ATOM	869	CA	LEU	A	143	-4.343	65.422	19.333	1.00 33.92	C
ATOM	870	CB	LEU	A	143	-4.434	66.378	20.526	1.00 33.86	C
ATOM	871	CG	LEU	A	143	-3.933	67.812	20.341	1.00 33.72	C
ATOM	872	CD1	LEU	A	143	-4.656	68.402	19.137	1.00 31.14	C
ATOM	873	CD2	LEU	A	143	-4.227	68.624	21.591	1.00 34.84	C
ATOM	874	C	LEU	A	143	-2.898	65.304	18.842	1.00 34.15	C
ATOM	875	O	LEU	A	143	-2.559	65.834	17.786	1.00 34.53	O
ATOM	876	N	ALA	A	144	-2.060	64.586	19.596	1.00 33.23	N
ATOM	877	CA	ALA	A	144	-0.669	64.366	19.204	1.00 32.59	C
ATOM	878	CB	ALA	A	144	0.046	63.540	20.247	1.00 32.52	C
ATOM	879	C	ALA	A	144	-0.598	63.676	17.844	1.00 32.09	C
ATOM	880	O	ALA	A	144	0.240	64.019	17.038	1.00 31.77	O
ATOM	881	N	ARG	A	145	-1.494	62.720	17.587	1.00 32.32	N
ATOM	882	CA	ARG	A	145	-1.545	62.050	16.293	1.00 32.91	C
ATOM	883	CB	ARG	A	145	-2.600	60.939	16.295	1.00 33.17	C
ATOM	884	CG	ARG	A	145	-2.769	60.208	14.961	1.00 35.72	C
ATOM	885	CD	ARG	A	145	-3.871	59.129	14.976	1.00 37.67	C
ATOM	886	NE	ARG	A	145	-3.583	58.127	15.993	1.00 39.30	N
ATOM	887	CZ	ARG	A	145	-4.264	57.978	17.127	1.00 41.07	C
ATOM	888	NH1	ARG	A	145	-5.331	58.736	17.399	1.00 41.09	N
ATOM	889	NH2	ARG	A	145	-3.884	57.050	17.987	1.00 40.07	N
ATOM	890	C	ARG	A	145	-1.789	63.044	15.155	1.00 33.07	C
ATOM	891	O	ARG	A	145	-1.063	63.050	14.158	1.00 32.72	O
ATOM	892	N	SER	A	146	-2.797	63.897	15.310	1.00 33.62	N
ATOM	893	CA	SER	A	146	-3.103	64.896	14.287	1.00 33.98	C
ATOM	894	CB	SER	A	146	-4.332	65.711	14.700	1.00 34.87	C
ATOM	895	OG	SER	A	146	-4.556	66.758	13.767	1.00 37.55	O
ATOM	896	C	SER	A	146	-1.920	65.837	14.058	1.00 34.16	C
ATOM	897	O	SER	A	146	-1.518	66.064	12.917	1.00 34.41	O
ATOM	898	N	PHE	A	147	-1.349	66.347	15.154	1.00 32.41	N
ATOM	899	CA	PHE	A	147	-0.235	67.278	15.088	1.00 32.56	C
ATOM	900	CB	PHE	A	147	0.117	67.793	16.481	1.00 32.83	C
ATOM	901	CG	PHE	A	147	-0.765	68.925	16.972	1.00 34.64	C
ATOM	902	CD1	PHE	A	147	-1.916	69.303	16.275	1.00 34.72	C
ATOM	903	CE1	PHE	A	147	-2.725	70.330	16.744	1.00 37.91	C
ATOM	904	CZ	PHE	A	147	-2.380	71.009	17.911	1.00 36.29	C
ATOM	905	CE2	PHE	A	147	-1.223	70.642	18.617	1.00 36.31	C
ATOM	906	CD2	PHE	A	147	-0.430	69.603	18.143	1.00 34.51	C
ATOM	907	C	PHE	A	147	1.005	66.617	14.491	1.00 32.09	C
ATOM	908	O	PHE	A	147	1.647	67.190	13.625	1.00 31.07	O
ATOM	909	N	PHE	A	148	1.357	65.436	14.992	1.00 32.05	N
ATOM	910	CA	PHE	A	148	2.516	64.706	14.486	1.00 32.29	C
ATOM	911	CB	PHE	A	148	2.701	63.391	15.247	1.00 32.29	C
ATOM	912	CG	PHE	A	148	4.061	62.783	15.070	1.00 32.26	C
ATOM	913	CD1	PHE	A	148	5.212	63.527	15.349	1.00 32.46	C
ATOM	914	CE1	PHE	A	148	6.477	62.979	15.206	1.00 29.15	C
ATOM	915	CZ	PHE	A	148	6.610	61.665	14.771	1.00 30.20	C
ATOM	916	CE2	PHE	A	148	5.465	60.909	14.475	1.00 30.97	C
ATOM	917	CD2	PHE	A	148	4.198	61.469	14.634	1.00 31.93	C
ATOM	918	C	PHE	A	148	2.385	64.405	12.990	1.00 32.02	C
ATOM	919	O	PHE	A	148	3.343	64.536	12.238	1.00 32.46	O
ATOM	920	N	TRP	A	149	1.196	64.006	12.571	1.00 31.64	N
ATOM	921	CA	TRP	A	149	0.960	63.687	11.169	1.00 32.22	C
ATOM	922	CB	TRP	A	149	-0.469	63.221	10.973	1.00 32.32	C
ATOM	923	CG	TRP	A	149	-0.814	62.851	9.562	1.00 33.58	C
ATOM	924	CD1	TRP	A	149	-1.276	63.695	8.583	1.00 35.97	C
ATOM	925	NE1	TRP	A	149	-1.497	62.992	7.422	1.00 38.04	N
ATOM	926	CE2	TRP	A	149	-1.201	61.670	7.635	1.00 35.85	C
ATOM	927	CD2	TRP	A	149	-0.773	61.542	8.978	1.00 32.84	C
ATOM	928	CE3	TRP	A	149	-0.396	60.273	9.445	1.00 32.94	C
ATOM	929	CZ3	TRP	A	149	-0.480	59.181	8.574	1.00 32.70	C
ATOM	930	CH2	TRP	A	149	-0.914	59.352	7.244	1.00 35.78	C
ATOM	931	CZ2	TRP	A	149	-1.279	60.584	6.763	1.00 35.70	C
ATOM	932	C	TRP	A	149	1.228	64.908	10.309	1.00 32.05	C
ATOM	933	O	TRP	A	149	1.926	64.810	9.309	1.00 31.43	O
ATOM	934	N	GLN	A	150	0.720	66.078	10.729	1.00 31.85	N

ATOM	935	CA	GLN	A	150	0.948	67.309	9.966	1.00 31.22	C
ATOM	936	CB	GLN	A	150	0.132	68.489	10.527	1.00 30.76	C
ATOM	937	CG	GLN	A	150	-1.376	68.335	10.336	1.00 32.09	C
ATOM	938	CD	GLN	A	150	-2.126	69.553	10.773	1.00 34.62	C
ATOM	939	OE1	GLN	A	150	-1.850	70.656	10.292	1.00 34.95	O
ATOM	940	NE2	GLN	A	150	-3.064	69.376	11.704	1.00 35.33	N
ATOM	941	C	GLN	A	150	2.414	67.686	9.932	1.00 31.38	C
ATOM	942	O	GLN	A	150	2.884	68.278	8.942	1.00 31.25	O
ATOM	943	N	VAL	A	151	3.143	67.400	11.014	1.00 30.59	N
ATOM	944	CA	VAL	A	151	4.576	67.691	11.006	1.00 31.25	C
ATOM	945	CB	VAL	A	151	5.222	67.562	12.407	1.00 31.59	C
ATOM	946	CG1	VAL	A	151	6.736	67.703	12.328	1.00 33.21	C
ATOM	947	CG2	VAL	A	151	4.661	68.652	13.325	1.00 31.32	C
ATOM	948	C	VAL	A	151	5.259	66.780	9.981	1.00 30.80	C
ATOM	949	O	VAL	A	151	6.140	67.215	9.239	1.00 30.84	O
ATOM	950	N	LEU	A	152	4.842	65.521	9.939	1.00 31.70	N
ATOM	951	CA	LEU	A	152	5.429	64.564	9.000	1.00 32.14	C
ATOM	952	CB	LEU	A	152	4.792	63.179	9.194	1.00 32.39	C
ATOM	953	CG	LEU	A	152	5.513	62.176	10.123	1.00 33.85	C
ATOM	954	CD1	LEU	A	152	6.723	61.611	9.411	1.00 35.80	C
ATOM	955	CD2	LEU	A	152	5.950	62.799	11.422	1.00 36.98	C
ATOM	956	C	LEU	A	152	5.215	65.052	7.567	1.00 31.63	C
ATOM	957	O	LEU	A	152	6.131	65.024	6.769	1.00 32.44	O
ATOM	958	N	GLU	A	153	3.997	65.471	7.252	1.00 31.63	N
ATOM	959	CA	GLU	A	153	3.671	65.980	5.907	1.00 32.26	C
ATOM	960	CB	GLU	A	153	2.177	66.330	5.780	1.00 32.59	C
ATOM	961	CG	GLU	A	153	1.233	65.126	5.736	1.00 33.60	C
ATOM	962	CD	GLU	A	153	1.423	64.215	4.510	1.00 35.47	C
ATOM	963	OE1	GLU	A	153	1.617	64.717	3.392	1.00 38.01	O
ATOM	964	OE2	GLU	A	153	1.380	62.991	4.659	1.00 34.71	O
ATOM	965	C	GLU	A	153	4.538	67.191	5.562	1.00 31.87	C
ATOM	966	O	GLU	A	153	5.076	67.281	4.449	1.00 30.83	O
ATOM	967	N	ALA	A	154	4.716	68.101	6.531	1.00 31.04	N
ATOM	968	CA	ALA	A	154	5.548	69.291	6.318	1.00 30.48	C
ATOM	969	CB	ALA	A	154	5.440	70.278	7.537	1.00 31.18	C
ATOM	970	C	ALA	A	154	7.002	68.933	6.082	1.00 31.22	C
ATOM	971	O	ALA	A	154	7.683	69.544	5.238	1.00 30.96	O
ATOM	972	N	VAL	A	155	7.504	67.967	6.842	1.00 31.29	N
ATOM	973	CA	VAL	A	155	8.898	67.580	6.704	1.00 32.75	C
ATOM	974	CB	VAL	A	155	9.335	66.651	7.856	1.00 32.61	C
ATOM	975	CG1	VAL	A	155	10.729	66.132	7.631	1.00 33.47	C
ATOM	976	CG2	VAL	A	155	9.292	67.439	9.189	1.00 35.41	C
ATOM	977	C	VAL	A	155	9.094	66.905	5.336	1.00 33.10	C
ATOM	978	O	VAL	A	155	10.092	67.155	4.648	1.00 33.39	O
ATOM	979	N	ARG	A	156	8.130	66.086	4.931	1.00 33.25	N
ATOM	980	CA	ARG	A	156	8.190	65.429	3.606	1.00 34.45	C
ATOM	981	CB	ARG	A	156	6.992	64.490	3.396	1.00 33.21	C
ATOM	982	CG	ARG	A	156	6.999	63.221	4.219	1.00 33.42	C
ATOM	983	CD	ARG	A	156	5.778	62.320	3.937	1.00 34.78	C
ATOM	984	NE	ARG	A	156	5.644	62.064	2.494	1.00 35.47	N
ATOM	985	CZ	ARG	A	156	4.533	61.636	1.903	1.00 33.43	C
ATOM	986	NH1	ARG	A	156	3.435	61.411	2.609	1.00 32.42	N
ATOM	987	NH2	ARG	A	156	4.525	61.437	0.594	1.00 34.38	N
ATOM	988	C	ARG	A	156	8.211	66.491	2.501	1.00 34.92	C
ATOM	989	O	ARG	A	156	8.986	66.414	1.542	1.00 35.22	O
ATOM	990	N	HIS	A	157	7.369	67.501	2.650	1.00 36.13	N
ATOM	991	CA	HIS	A	157	7.351	68.588	1.686	1.00 36.56	C
ATOM	992	CB	HIS	A	157	6.299	69.629	2.048	1.00 37.38	C
ATOM	993	CG	HIS	A	157	6.362	70.863	1.197	1.00 39.12	C
ATOM	994	ND1	HIS	A	157	7.005	72.014	1.608	1.00 41.07	N
ATOM	995	CE1	HIS	A	157	6.921	72.926	0.658	1.00 39.75	C
ATOM	996	NE2	HIS	A	157	6.249	72.407	-0.358	1.00 40.88	N
ATOM	997	CD2	HIS	A	157	5.873	71.124	-0.041	1.00 38.81	C
ATOM	998	C	HIS	A	157	8.710	69.238	1.555	1.00 36.34	C
ATOM	999	O	HIS	A	157	9.178	69.475	0.435	1.00 36.86	O
ATOM	1000	N	CYS	A	158	9.354	69.542	2.683	1.00 36.43	N
ATOM	1001	CA	CYS	A	158	10.664	70.184	2.649	1.00 36.33	C
ATOM	1002	CB	CYS	A	158	11.177	70.492	4.065	1.00 36.27	C
ATOM	1003	SG	CYS	A	158	10.201	71.754	4.924	1.00 37.34	S

ATOM	1004	C	CYS	A	158	11.663	69.290	1.937	1.00	37.14	C
ATOM	1005	O	CYS	A	158	12.431	69.751	1.069	1.00	36.89	O
ATOM	1006	N	HIS	A	159	11.678	68.019	2.334	1.00	36.70	N
ATOM	1007	CA	HIS	A	159	12.624	67.055	1.784	1.00	38.40	C
ATOM	1008	CB	HIS	A	159	12.521	65.732	2.551	1.00	38.71	C
ATOM	1009	CG	HIS	A	159	13.136	65.801	3.916	1.00	44.25	C
ATOM	1010	ND1	HIS	A	159	13.788	64.734	4.499	1.00	47.72	N
ATOM	1011	CE1	HIS	A	159	14.258	65.103	5.681	1.00	49.12	C
ATOM	1012	NE2	HIS	A	159	13.948	66.376	5.880	1.00	48.24	N
ATOM	1013	CD2	HIS	A	159	13.238	66.834	4.798	1.00	47.23	C
ATOM	1014	C	HIS	A	159	12.392	66.881	0.277	1.00	38.37	C
ATOM	1015	O	HIS	A	159	13.337	66.781	-0.481	1.00	36.82	O
ATOM	1016	N	ASN	A	160	11.128	66.926	-0.127	1.00	39.53	N
ATOM	1017	CA	ASN	A	160	10.742	66.927	-1.529	1.00	42.14	C
ATOM	1018	CB	ASN	A	160	9.239	67.045	-1.629	1.00	43.88	C
ATOM	1019	CG	ASN	A	160	8.602	65.778	-2.013	1.00	48.90	C
ATOM	1020	OD1	ASN	A	160	8.727	64.765	-1.312	1.00	53.59	O
ATOM	1021	ND2	ASN	A	160	7.913	65.795	-3.160	1.00	53.90	N
ATOM	1022	C	ASN	A	160	11.322	68.100	-2.286	1.00	42.07	C
ATOM	1023	O	ASN	A	160	11.668	67.978	-3.461	1.00	41.85	O
ATOM	1024	N	CYS	A	161	11.397	69.246	-1.616	1.00	40.47	N
ATOM	1025	CA	CYS	A	161	11.884	70.467	-2.225	1.00	39.41	C
ATOM	1026	CB	CYS	A	161	11.254	71.669	-1.529	1.00	39.11	C
ATOM	1027	SG	CYS	A	161	9.498	71.835	-1.845	1.00	40.42	S
ATOM	1028	C	CYS	A	161	13.391	70.551	-2.129	1.00	38.90	C
ATOM	1029	O	CYS	A	161	13.979	71.555	-2.518	1.00	39.21	O
ATOM	1030	N	GLY	A	162	14.022	69.510	-1.596	1.00	38.48	N
ATOM	1031	CA	GLY	A	162	15.474	69.511	-1.438	1.00	37.84	C
ATOM	1032	C	GLY	A	162	15.957	70.269	-0.221	1.00	37.83	C
ATOM	1033	O	GLY	A	162	17.122	70.693	-0.160	1.00	36.57	O
ATOM	1034	N	VAL	A	163	15.084	70.388	0.789	1.00	37.66	N
ATOM	1035	CA	VAL	A	163	15.420	71.145	2.007	1.00	37.08	C
ATOM	1036	CB	VAL	A	163	14.488	72.353	2.166	1.00	37.80	C
ATOM	1037	CG1	VAL	A	163	14.748	73.082	3.511	1.00	38.56	C
ATOM	1038	CG2	VAL	A	163	14.666	73.306	1.008	1.00	36.79	C
ATOM	1039	C	VAL	A	163	15.337	70.305	3.294	1.00	37.35	C
ATOM	1040	O	VAL	A	163	14.363	69.589	3.538	1.00	35.09	O
ATOM	1041	N	LEU	A	164	16.373	70.436	4.110	1.00	37.93	N
ATOM	1042	CA	LEU	A	164	16.468	69.790	5.405	1.00	38.78	C
ATOM	1043	CB	LEU	A	164	17.813	69.089	5.468	1.00	39.15	C
ATOM	1044	CG	LEU	A	164	18.083	68.153	6.625	1.00	41.81	C
ATOM	1045	CD1	LEU	A	164	17.260	66.866	6.466	1.00	42.67	C
ATOM	1046	CD2	LEU	A	164	19.553	67.843	6.711	1.00	43.27	C
ATOM	1047	C	LEU	A	164	16.382	70.911	6.472	1.00	38.81	C
ATOM	1048	O	LEU	A	164	17.209	71.834	6.474	1.00	38.57	O
ATOM	1049	N	HIS	A	165	15.387	70.830	7.357	1.00	38.45	N
ATOM	1050	CA	HIS	A	165	15.164	71.860	8.388	1.00	37.77	C
ATOM	1051	CB	HIS	A	165	13.758	71.731	8.991	1.00	37.59	C
ATOM	1052	CG	HIS	A	165	13.398	72.836	9.937	1.00	35.86	C
ATOM	1053	ND1	HIS	A	165	13.867	72.891	11.229	1.00	33.70	N
ATOM	1054	CE1	HIS	A	165	13.391	73.969	11.823	1.00	34.80	C
ATOM	1055	NE2	HIS	A	165	12.628	74.617	10.959	1.00	37.29	N
ATOM	1056	CD2	HIS	A	165	12.612	73.926	9.774	1.00	35.10	C
ATOM	1057	C	HIS	A	165	16.236	71.813	9.464	1.00	37.76	C
ATOM	1058	O	HIS	A	165	16.784	72.843	9.824	1.00	38.35	O
ATOM	1059	N	ARG	A	166	16.563	70.612	9.937	1.00	37.85	N
ATOM	1060	CA	ARG	A	166	17.615	70.390	10.933	1.00	38.53	C
ATOM	1061	CB	ARG	A	166	18.952	70.946	10.456	1.00	39.48	C
ATOM	1062	CG	ARG	A	166	19.500	70.338	9.178	1.00	42.23	C
ATOM	1063	CD	ARG	A	166	20.503	71.265	8.553	1.00	46.58	C
ATOM	1064	NE	ARG	A	166	21.839	70.788	8.808	1.00	50.91	N
ATOM	1065	CZ	ARG	A	166	22.933	71.523	8.743	1.00	50.31	C
ATOM	1066	NH1	ARG	A	166	22.882	72.821	8.466	1.00	50.71	N
ATOM	1067	NH2	ARG	A	166	24.091	70.941	8.972	1.00	50.70	N
ATOM	1068	C	ARG	A	166	17.370	70.951	12.331	1.00	38.67	C
ATOM	1069	O	ARG	A	166	18.243	70.839	13.184	1.00	39.30	O
ATOM	1070	N	ASP	A	167	16.222	71.567	12.569	1.00	38.24	N
ATOM	1071	CA	ASP	A	167	15.920	72.076	13.912	1.00	39.05	C
ATOM	1072	CB	ASP	A	167	16.297	73.567	13.972	1.00	40.02	C

ATOM	1073	CG	ASP	A	167	16.351	74.131	15.396	1.00	44.41	C
ATOM	1074	OD1	ASP	A	167	16.656	73.391	16.374	1.00	44.09	O
ATOM	1075	OD2	ASP	A	167	16.111	75.349	15.606	1.00	47.46	O
ATOM	1076	C	ASP	A	167	14.442	71.870	14.231	1.00	37.42	C
ATOM	1077	O	ASP	A	167	13.765	72.783	14.722	1.00	38.05	O
ATOM	1078	N	ILE	A	168	13.926	70.671	13.939	1.00	36.17	N
ATOM	1079	CA	ILE	A	168	12.516	70.380	14.201	1.00	34.82	C
ATOM	1080	CB	ILE	A	168	12.066	69.064	13.505	1.00	35.54	C
ATOM	1081	CG1	ILE	A	168	12.125	69.196	11.976	1.00	34.25	C
ATOM	1082	CD1	ILE	A	168	12.194	67.836	11.258	1.00	36.78	C
ATOM	1083	CG2	ILE	A	168	10.663	68.692	13.951	1.00	34.38	C
ATOM	1084	C	ILE	A	168	12.306	70.252	15.708	1.00	34.43	C
ATOM	1085	O	ILE	A	168	12.914	69.409	16.350	1.00	32.59	O
ATOM	1086	N	LYS	A	169	11.436	71.091	16.260	1.00	33.96	N
ATOM	1087	CA	LYS	A	169	11.122	71.056	17.701	1.00	33.91	C
ATOM	1088	CB	LYS	A	169	12.281	71.647	18.511	1.00	34.23	C
ATOM	1089	CG	LYS	A	169	12.644	73.064	18.140	1.00	35.79	C
ATOM	1090	CD	LYS	A	169	13.822	73.538	18.954	1.00	40.57	C
ATOM	1091	CE	LYS	A	169	14.137	75.024	18.631	1.00	44.31	C
ATOM	1092	NZ	LYS	A	169	15.134	75.616	19.597	1.00	47.28	N
ATOM	1093	C	LYS	A	169	9.862	71.860	17.947	1.00	33.20	C
ATOM	1094	O	LYS	A	169	9.444	72.619	17.065	1.00	32.12	O
ATOM	1095	N	ASP	A	170	9.272	71.731	19.138	1.00	33.18	N
ATOM	1096	CA	ASP	A	170	8.021	72.433	19.438	1.00	35.25	C
ATOM	1097	CB	ASP	A	170	7.517	72.132	20.839	1.00	36.00	C
ATOM	1098	CG	ASP	A	170	8.582	72.296	21.895	1.00	38.87	C
ATOM	1099	OD1	ASP	A	170	9.700	72.820	21.626	1.00	41.81	O
ATOM	1100	OD2	ASP	A	170	8.358	71.892	23.042	1.00	42.14	O
ATOM	1101	C	ASP	A	170	8.075	73.934	19.226	1.00	35.41	C
ATOM	1102	O	ASP	A	170	7.118	74.510	18.717	1.00	35.26	O
ATOM	1103	N	GLU	A	171	9.204	74.550	19.570	1.00	36.73	N
ATOM	1104	CA	GLU	A	171	9.370	76.005	19.446	1.00	38.95	C
ATOM	1105	CB	GLU	A	171	10.703	76.462	20.053	1.00	40.09	C
ATOM	1106	CG	GLU	A	171	10.892	76.109	21.523	1.00	46.32	C
ATOM	1107	CD	GLU	A	171	12.296	76.436	22.017	1.00	53.18	C
ATOM	1108	OE1	GLU	A	171	13.229	75.621	21.798	1.00	56.05	O
ATOM	1109	OE2	GLU	A	171	12.474	77.511	22.636	1.00	57.82	O
ATOM	1110	C	GLU	A	171	9.340	76.438	17.983	1.00	38.68	C
ATOM	1111	O	GLU	A	171	9.000	77.583	17.678	1.00	38.39	O
ATOM	1112	N	ASN	A	172	9.716	75.531	17.080	1.00	37.88	N
ATOM	1113	CA	ASN	A	172	9.752	75.848	15.653	1.00	37.39	C
ATOM	1114	CB	ASN	A	172	11.022	75.288	15.019	1.00	37.23	C
ATOM	1115	CG	ASN	A	172	12.270	76.063	15.433	1.00	38.63	C
ATOM	1116	OD1	ASN	A	172	12.195	77.241	15.769	1.00	38.90	O
ATOM	1117	ND2	ASN	A	172	13.421	75.407	15.390	1.00	36.90	N
ATOM	1118	C	ASN	A	172	8.519	75.353	14.917	1.00	36.59	C
ATOM	1119	O	ASN	A	172	8.567	75.150	13.710	1.00	36.84	O
ATOM	1120	N	ILE	A	173	7.430	75.141	15.653	1.00	35.61	N
ATOM	1121	CA	ILE	A	173	6.143	74.742	15.085	1.00	35.39	C
ATOM	1122	CB	ILE	A	173	5.797	73.292	15.516	1.00	35.63	C
ATOM	1123	CG1	ILE	A	173	6.798	72.283	14.897	1.00	36.07	C
ATOM	1124	CD1	ILE	A	173	6.648	70.871	15.388	1.00	33.90	C
ATOM	1125	CG2	ILE	A	173	4.356	72.954	15.161	1.00	35.62	C
ATOM	1126	C	ILE	A	173	5.023	75.691	15.548	1.00	36.51	C
ATOM	1127	O	ILE	A	173	4.796	75.863	16.767	1.00	35.35	O
ATOM	1128	N	LEU	A	174	4.319	76.286	14.588	1.00	36.38	N
ATOM	1129	CA	LEU	A	174	3.223	77.192	14.900	1.00	37.97	C
ATOM	1130	CB	LEU	A	174	3.307	78.506	14.107	1.00	38.37	C
ATOM	1131	CG	LEU	A	174	4.444	79.472	14.437	1.00	41.65	C
ATOM	1132	CD1	LEU	A	174	4.357	80.715	13.531	1.00	44.42	C
ATOM	1133	CD2	LEU	A	174	4.399	79.905	15.882	1.00	42.22	C
ATOM	1134	C	LEU	A	174	1.891	76.518	14.642	1.00	38.02	C
ATOM	1135	O	LEU	A	174	1.711	75.822	13.642	1.00	37.64	O
ATOM	1136	N	ILE	A	175	0.963	76.721	15.567	1.00	37.87	N
ATOM	1137	CA	ILE	A	175	-0.379	76.199	15.417	1.00	38.43	C
ATOM	1138	CB	ILE	A	175	-0.845	75.563	16.744	1.00	38.70	C
ATOM	1139	CG1	ILE	A	175	0.148	74.510	17.228	1.00	38.66	C
ATOM	1140	CD1	ILE	A	175	-0.025	74.200	18.722	1.00	41.58	C
ATOM	1141	CG2	ILE	A	175	-2.241	74.971	16.609	1.00	36.19	C

ATOM	1142	C	ILE	A	175	-1.342	77.313	14.997	1.00	40.30	C
ATOM	1143	O	ILE	A	175	-1.522	78.307	15.716	1.00	41.15	O
ATOM	1144	N	ASP	A	176	-1.969	77.144	13.840	1.00	41.47	N
ATOM	1145	CA	ASP	A	176	-3.092	77.991	13.438	1.00	42.38	C
ATOM	1146	CB	ASP	A	176	-3.337	77.853	11.926	1.00	42.29	C
ATOM	1147	CG	ASP	A	176	-4.437	78.782	11.401	1.00	44.69	C
ATOM	1148	OD1	ASP	A	176	-5.440	79.033	12.113	1.00	46.71	O
ATOM	1149	OD2	ASP	A	176	-4.382	79.271	10.250	1.00	43.65	O
ATOM	1150	C	ASP	A	176	-4.279	77.497	14.235	1.00	43.24	C
ATOM	1151	O	ASP	A	176	-4.904	76.483	13.882	1.00	42.40	O
ATOM	1152	N	LEU	A	177	-4.582	78.214	15.319	1.00	44.51	N
ATOM	1153	CA	LEU	A	177	-5.612	77.803	16.281	1.00	45.60	C
ATOM	1154	CB	LEU	A	177	-5.611	78.719	17.518	1.00	45.31	C
ATOM	1155	CG	LEU	A	177	-4.338	78.689	18.362	1.00	45.46	C
ATOM	1156	CD1	LEU	A	177	-4.275	79.850	19.374	1.00	44.16	C
ATOM	1157	CD2	LEU	A	177	-4.247	77.335	19.066	1.00	44.99	C
ATOM	1158	C	LEU	A	177	-7.019	77.691	15.708	1.00	46.83	C
ATOM	1159	O	LEU	A	177	-7.793	76.840	16.145	1.00	47.74	O
ATOM	1160	N	ASN	A	178	-7.348	78.535	14.737	1.00	47.91	N
ATOM	1161	CA	ASN	A	178	-8.664	78.512	14.104	1.00	48.63	C
ATOM	1162	CB	ASN	A	178	-8.886	79.810	13.316	1.00	49.80	C
ATOM	1163	CG	ASN	A	178	-9.487	80.939	14.169	1.00	52.87	C
ATOM	1164	OD1	ASN	A	178	-9.966	80.712	15.287	1.00	55.06	O
ATOM	1165	ND2	ASN	A	178	-9.463	82.166	13.628	1.00	54.84	N
ATOM	1166	C	ASN	A	178	-8.843	77.332	13.154	1.00	48.41	C
ATOM	1167	O	ASN	A	178	-9.892	76.686	13.132	1.00	49.39	O
ATOM	1168	N	ARG	A	179	-7.821	77.061	12.348	1.00	47.30	N
ATOM	1169	CA	ARG	A	179	-7.907	75.998	11.353	1.00	45.90	C
ATOM	1170	CB	ARG	A	179	-7.183	76.420	10.088	1.00	46.22	C
ATOM	1171	CG	ARG	A	179	-7.790	77.611	9.403	1.00	47.89	C
ATOM	1172	CD	ARG	A	179	-7.036	77.967	8.138	1.00	50.30	C
ATOM	1173	NE	ARG	A	179	-7.672	79.037	7.378	1.00	54.18	N
ATOM	1174	CZ	ARG	A	179	-8.825	78.919	6.715	1.00	56.15	C
ATOM	1175	NH1	ARG	A	179	-9.498	77.773	6.717	1.00	55.19	N
ATOM	1176	NH2	ARG	A	179	-9.309	79.958	6.042	1.00	57.24	N
ATOM	1177	C	ARG	A	179	-7.356	74.653	11.839	1.00	44.78	C
ATOM	1178	O	ARG	A	179	-7.604	73.614	11.208	1.00	44.31	O
ATOM	1179	N	GLY	A	180	-6.612	74.667	12.946	1.00	42.54	N
ATOM	1180	CA	GLY	A	180	-6.001	73.448	13.448	1.00	41.77	C
ATOM	1181	C	GLY	A	180	-4.862	72.972	12.551	1.00	41.19	C
ATOM	1182	O	GLY	A	180	-4.609	71.776	12.440	1.00	40.99	O
ATOM	1183	N	GLU	A	181	-4.172	73.908	11.909	1.00	39.77	N
ATOM	1184	CA	GLU	A	181	-3.105	73.549	10.986	1.00	39.51	C
ATOM	1185	CB	GLU	A	181	-3.335	74.241	9.641	1.00	38.79	C
ATOM	1186	CG	GLU	A	181	-4.438	73.608	8.809	1.00	39.75	C
ATOM	1187	CD	GLU	A	181	-4.919	74.501	7.676	1.00	40.13	C
ATOM	1188	OE1	GLU	A	181	-4.195	75.443	7.326	1.00	42.55	O
ATOM	1189	OE2	GLU	A	181	-6.018	74.264	7.151	1.00	38.74	O
ATOM	1190	C	GLU	A	181	-1.761	73.957	11.553	1.00	39.26	C
ATOM	1191	O	GLU	A	181	-1.617	75.074	12.048	1.00	39.89	O
ATOM	1192	N	LEU	A	182	-0.783	73.051	11.482	1.00	38.44	N
ATOM	1193	CA	LEU	A	182	0.567	73.323	11.966	1.00	37.99	C
ATOM	1194	CB	LEU	A	182	1.201	72.066	12.588	1.00	37.43	C
ATOM	1195	CG	LEU	A	182	0.947	71.895	14.094	1.00	38.02	C
ATOM	1196	CD1	LEU	A	182	-0.528	71.939	14.378	1.00	39.25	C
ATOM	1197	CD2	LEU	A	182	1.546	70.567	14.578	1.00	35.43	C
ATOM	1198	C	LEU	A	182	1.448	73.854	10.857	1.00	37.83	C
ATOM	1199	O	LEU	A	182	1.256	73.519	9.688	1.00	37.14	O
ATOM	1200	N	LYS	A	183	2.417	74.681	11.235	1.00	37.37	N
ATOM	1201	CA	LYS	A	183	3.280	75.320	10.269	1.00	38.66	C
ATOM	1202	CB	LYS	A	183	2.756	76.721	9.919	1.00	39.51	C
ATOM	1203	CG	LYS	A	183	1.723	76.691	8.799	1.00	44.32	C
ATOM	1204	CD	LYS	A	183	1.157	78.081	8.560	1.00	50.71	C
ATOM	1205	CE	LYS	A	183	0.426	78.195	7.226	1.00	53.19	C
ATOM	1206	NZ	LYS	A	183	-0.586	77.117	6.989	1.00	52.77	N
ATOM	1207	C	LYS	A	183	4.697	75.373	10.797	1.00	37.98	C
ATOM	1208	O	LYS	A	183	4.954	75.805	11.923	1.00	37.88	O
ATOM	1209	N	LEU	A	184	5.617	74.918	9.969	1.00	37.28	N
ATOM	1210	CA	LEU	A	184	7.015	74.830	10.333	1.00	37.45	C

ATOM	1211	CB	LEU	A	184	7.658	73.726	9.494	1.00	38.41	C
ATOM	1212	CG	LEU	A	184	9.013	73.126	9.811	1.00	42.44	C
ATOM	1213	CD1	LEU	A	184	9.162	72.736	11.300	1.00	44.98	C
ATOM	1214	CD2	LEU	A	184	9.156	71.900	8.895	1.00	44.78	C
ATOM	1215	C	LEU	A	184	7.689	76.195	10.135	1.00	37.17	C
ATOM	1216	O	LEU	A	184	7.411	76.886	9.159	1.00	34.75	O
ATOM	1217	N	ILE	A	185	8.546	76.590	11.085	1.00	37.08	N
ATOM	1218	CA	ILE	A	185	9.233	77.882	11.007	1.00	38.22	C
ATOM	1219	CB	ILE	A	185	8.589	78.967	11.964	1.00	38.24	C
ATOM	1220	CG1	ILE	A	185	8.676	78.523	13.428	1.00	38.15	C
ATOM	1221	CD1	ILE	A	185	8.508	79.649	14.460	1.00	40.09	C
ATOM	1222	CG2	ILE	A	185	7.180	79.280	11.555	1.00	37.83	C
ATOM	1223	C	ILE	A	185	10.678	77.766	11.365	1.00	38.83	C
ATOM	1224	O	ILE	A	185	11.105	76.792	12.000	1.00	38.96	O
ATOM	1225	N	ASP	A	186	11.419	78.807	10.980	1.00	39.40	N
ATOM	1226	CA	ASP	A	186	12.822	78.985	11.315	1.00	40.27	C
ATOM	1227	CB	ASP	A	186	13.046	79.073	12.830	1.00	41.48	C
ATOM	1228	CG	ASP	A	186	14.441	79.582	13.178	1.00	45.31	C
ATOM	1229	OD1	ASP	A	186	15.190	79.992	12.255	1.00	47.25	O
ATOM	1230	OD2	ASP	A	186	14.885	79.588	14.351	1.00	50.71	O
ATOM	1231	C	ASP	A	186	13.803	78.013	10.648	1.00	40.90	C
ATOM	1232	O	ASP	A	186	14.343	77.096	11.285	1.00	40.21	O
ATOM	1233	N	PHE	A	187	14.087	78.292	9.378	1.00	40.98	N
ATOM	1234	CA	PHE	A	187	15.042	77.522	8.591	1.00	42.42	C
ATOM	1235	CB	PHE	A	187	14.602	77.517	7.140	1.00	41.27	C
ATOM	1236	CG	PHE	A	187	13.394	76.662	6.891	1.00	41.11	C
ATOM	1237	CD1	PHE	A	187	12.129	77.128	7.202	1.00	40.65	C
ATOM	1238	CE1	PHE	A	187	11.000	76.342	6.977	1.00	39.93	C
ATOM	1239	CZ	PHE	A	187	11.131	75.078	6.444	1.00	40.45	C
ATOM	1240	CE2	PHE	A	187	12.398	74.586	6.128	1.00	38.34	C
ATOM	1241	CD2	PHE	A	187	13.522	75.373	6.349	1.00	40.39	C
ATOM	1242	C	PHE	A	187	16.476	78.031	8.711	1.00	43.76	C
ATOM	1243	O	PHE	A	187	17.346	77.647	7.927	1.00	44.80	O
ATOM	1244	N	GLY	A	188	16.723	78.868	9.716	1.00	44.55	N
ATOM	1245	CA	GLY	A	188	18.034	79.449	9.940	1.00	45.36	C
ATOM	1246	C	GLY	A	188	19.156	78.493	10.252	1.00	45.97	C
ATOM	1247	O	GLY	A	188	20.320	78.870	10.168	1.00	46.90	O
ATOM	1248	N	SER	A	189	18.830	77.260	10.631	1.00	46.13	N
ATOM	1249	CA	SER	A	189	19.853	76.240	10.866	1.00	45.91	C
ATOM	1250	CB	SER	A	189	19.725	75.652	12.280	1.00	46.57	C
ATOM	1251	OG	SER	A	189	19.539	76.674	13.258	1.00	51.43	O
ATOM	1252	C	SER	A	189	19.742	75.111	9.825	1.00	44.92	C
ATOM	1253	O	SER	A	189	20.356	74.051	9.977	1.00	43.79	O
ATOM	1254	N	GLY	A	190	18.948	75.337	8.784	1.00	44.05	N
ATOM	1255	CA	GLY	A	190	18.720	74.310	7.784	1.00	43.67	C
ATOM	1256	C	GLY	A	190	19.851	74.120	6.783	1.00	43.35	C
ATOM	1257	O	GLY	A	190	20.908	74.764	6.862	1.00	41.72	O
ATOM	1258	N	ALA	A	191	19.614	73.222	5.825	1.00	42.84	N
ATOM	1259	CA	ALA	A	191	20.584	72.942	4.769	1.00	41.99	C
ATOM	1260	CB	ALA	A	191	21.722	72.067	5.294	1.00	41.84	C
ATOM	1261	C	ALA	A	191	19.927	72.305	3.551	1.00	42.18	C
ATOM	1262	O	ALA	A	191	18.779	71.813	3.608	1.00	41.24	O
ATOM	1263	N	LEU	A	192	20.637	72.347	2.428	1.00	42.32	N
ATOM	1264	CA	LEU	A	192	20.170	71.649	1.236	1.00	42.24	C
ATOM	1265	CB	LEU	A	192	21.059	71.977	0.031	1.00	43.21	C
ATOM	1266	CG	LEU	A	192	21.088	73.455	-0.389	1.00	46.28	C
ATOM	1267	CD1	LEU	A	192	22.271	73.763	-1.328	1.00	49.62	C
ATOM	1268	CD2	LEU	A	192	19.778	73.889	-1.025	1.00	46.71	C
ATOM	1269	C	LEU	A	192	20.244	70.179	1.589	1.00	41.12	C
ATOM	1270	O	LEU	A	192	21.187	69.742	2.270	1.00	39.72	O
ATOM	1271	N	LEU	A	193	19.227	69.428	1.190	1.00	41.80	N
ATOM	1272	CA	LEU	A	193	19.237	67.983	1.401	1.00	43.29	C
ATOM	1273	CB	LEU	A	193	17.870	67.405	1.066	1.00	43.47	C
ATOM	1274	CG	LEU	A	193	17.658	65.896	1.213	1.00	45.93	C
ATOM	1275	CD1	LEU	A	193	17.805	65.456	2.671	1.00	45.54	C
ATOM	1276	CD2	LEU	A	193	16.279	65.518	0.652	1.00	46.41	C
ATOM	1277	C	LEU	A	193	20.306	67.331	0.512	1.00	43.97	C
ATOM	1278	O	LEU	A	193	20.386	67.649	-0.667	1.00	44.14	O
ATOM	1279	N	LYS	A	194	21.110	66.434	1.084	1.00	44.53	N

ATOM	1280	CA	LYS A 194	22.106	65.663	0.340	1.00	45.14	C
ATOM	1281	CB	LYS A 194	23.500	66.291	0.450	1.00	45.29	C
ATOM	1282	CG	LYS A 194	24.054	66.305	1.860	1.00	44.80	C
ATOM	1283	CD	LYS A 194	25.300	67.144	1.961	1.00	45.08	C
ATOM	1284	CE	LYS A 194	25.991	66.854	3.284	1.00	46.87	C
ATOM	1285	NZ	LYS A 194	27.243	67.643	3.464	1.00	48.08	N
ATOM	1286	C	LYS A 194	22.134	64.272	0.920	1.00	45.51	C
ATOM	1287	O	LYS A 194	21.615	64.054	2.026	1.00	45.00	O
ATOM	1288	N	ASP A 195	22.745	63.335	0.188	1.00	45.31	N
ATOM	1289	CA	ASP A 195	22.779	61.933	0.609	1.00	45.82	C
ATOM	1290	CB	ASP A 195	22.653	60.999	-0.601	1.00	46.48	C
ATOM	1291	CG	ASP A 195	21.330	61.124	-1.303	1.00	47.68	C
ATOM	1292	OD1	ASP A 195	20.279	60.858	-0.678	1.00	50.02	O
ATOM	1293	OD2	ASP A 195	21.243	61.469	-2.499	1.00	49.94	O
ATOM	1294	C	ASP A 195	24.038	61.607	1.384	1.00	45.41	C
ATOM	1295	O	ASP A 195	24.161	60.519	1.950	1.00	46.43	O
ATOM	1296	N	THR A 196	24.984	62.538	1.385	1.00	45.63	N
ATOM	1297	CA	THR A 196	26.259	62.371	2.083	1.00	46.00	C
ATOM	1298	CB	THR A 196	27.394	63.091	1.322	1.00	45.69	C
ATOM	1299	OG1	THR A 196	26.951	64.387	0.899	1.00	44.12	O
ATOM	1300	CG2	THR A 196	27.728	62.348	0.026	1.00	46.47	C
ATOM	1301	C	THR A 196	26.211	62.902	3.518	1.00	46.75	C
ATOM	1302	O	THR A 196	25.283	63.616	3.886	1.00	46.70	O
ATOM	1303	N	VAL A 197	27.237	62.569	4.302	1.00	47.32	N
ATOM	1304	CA	VAL A 197	27.294	62.912	5.713	1.00	48.22	C
ATOM	1305	CB	VAL A 197	28.440	62.174	6.437	1.00	48.78	C
ATOM	1306	CG1	VAL A 197	29.801	62.699	6.003	1.00	50.58	C
ATOM	1307	CG2	VAL A 197	28.282	62.289	7.956	1.00	49.66	C
ATOM	1308	C	VAL A 197	27.366	64.409	5.965	1.00	48.10	C
ATOM	1309	O	VAL A 197	27.949	65.152	5.182	1.00	47.85	O
ATOM	1310	N	TYR A 198	26.717	64.842	7.046	1.00	47.69	N
ATOM	1311	CA	TYR A 198	26.810	66.212	7.531	1.00	47.39	C
ATOM	1312	CB	TYR A 198	25.437	66.722	7.984	1.00	46.27	C
ATOM	1313	CG	TYR A 198	24.412	66.951	6.891	1.00	43.05	C
ATOM	1314	CD1	TYR A 198	23.574	65.924	6.464	1.00	40.17	C
ATOM	1315	CE1	TYR A 198	22.631	66.123	5.466	1.00	39.03	C
ATOM	1316	CZ	TYR A 198	22.490	67.368	4.904	1.00	38.13	C
ATOM	1317	OH	TYR A 198	21.539	67.577	3.933	1.00	36.97	O
ATOM	1318	CE2	TYR A 198	23.293	68.421	5.317	1.00	39.95	C
ATOM	1319	CD2	TYR A 198	24.256	68.204	6.312	1.00	41.73	C
ATOM	1320	C	TYR A 198	27.753	66.211	8.729	1.00	48.60	C
ATOM	1321	O	TYR A 198	27.657	65.349	9.597	1.00	48.27	O
ATOM	1322	N	THR A 199	28.658	67.183	8.775	1.00	50.37	N
ATOM	1323	CA	THR A 199	29.619	67.304	9.875	1.00	52.48	C
ATOM	1324	CB	THR A 199	31.079	67.267	9.364	1.00	52.38	C
ATOM	1325	OG1	THR A 199	31.242	68.240	8.318	1.00	53.03	O
ATOM	1326	CG2	THR A 199	31.393	65.936	8.714	1.00	53.00	C
ATOM	1327	C	THR A 199	29.409	68.606	10.636	1.00	53.92	C
ATOM	1328	O	THR A 199	30.172	68.924	11.545	1.00	53.86	O
ATOM	1329	N	ASP A 200	28.381	69.359	10.253	1.00	56.06	N
ATOM	1330	CA	ASP A 200	28.005	70.568	10.977	1.00	58.11	C
ATOM	1331	CB	ASP A 200	28.067	71.798	10.062	1.00	58.64	C
ATOM	1332	CG	ASP A 200	26.971	71.802	9.017	1.00	59.95	C
ATOM	1333	OD1	ASP A 200	26.266	72.826	8.884	1.00	61.08	O
ATOM	1334	OD2	ASP A 200	26.739	70.813	8.279	1.00	63.15	O
ATOM	1335	C	ASP A 200	26.602	70.424	11.539	1.00	59.05	C
ATOM	1336	O	ASP A 200	25.751	69.737	10.957	1.00	58.97	O
ATOM	1337	N	PHE A 201	26.365	71.091	12.664	1.00	60.22	N
ATOM	1338	CA	PHE A 201	25.061	71.089	13.315	1.00	61.47	C
ATOM	1339	CB	PHE A 201	24.847	69.790	14.094	1.00	61.39	C
ATOM	1340	CG	PHE A 201	23.526	69.717	14.805	1.00	61.76	C
ATOM	1341	CD1	PHE A 201	22.342	69.550	14.085	1.00	62.43	C
ATOM	1342	CE1	PHE A 201	21.110	69.475	14.741	1.00	62.41	C
ATOM	1343	CZ	PHE A 201	21.064	69.560	16.131	1.00	62.12	C
ATOM	1344	CE2	PHE A 201	22.242	69.727	16.856	1.00	61.55	C
ATOM	1345	CD2	PHE A 201	23.464	69.804	16.190	1.00	61.34	C
ATOM	1346	C	PHE A 201	24.957	72.286	14.245	1.00	62.42	C
ATOM	1347	O	PHE A 201	25.712	72.411	15.214	1.00	62.75	O
ATOM	1348	N	ASP A 202	24.012	73.158	13.934	1.00	63.58	N

ATOM	1349	CA	ASP	A	202	23.820	74.406	14.651	1.00	64.74	C
ATOM	1350	CB	ASP	A	202	24.100	75.583	13.704	1.00	65.58	C
ATOM	1351	CG	ASP	A	202	23.966	76.930	14.388	1.00	69.34	C
ATOM	1352	OD1	ASP	A	202	24.626	77.141	15.440	1.00	71.91	O
ATOM	1353	OD2	ASP	A	202	23.207	77.831	13.950	1.00	72.83	O
ATOM	1354	C	ASP	A	202	22.397	74.467	15.198	1.00	64.11	C
ATOM	1355	O	ASP	A	202	21.920	75.524	15.600	1.00	64.30	O
ATOM	1356	N	GLY	A	203	21.716	73.324	15.202	1.00	63.47	N
ATOM	1357	CA	GLY	A	203	20.358	73.250	15.712	1.00	62.03	C
ATOM	1358	C	GLY	A	203	20.346	72.947	17.200	1.00	60.94	C
ATOM	1359	O	GLY	A	203	21.392	72.972	17.854	1.00	61.08	O
ATOM	1360	N	THR	A	204	19.158	72.643	17.727	1.00	59.86	N
ATOM	1361	CA	THR	A	204	18.975	72.364	19.158	1.00	58.03	C
ATOM	1362	CB	THR	A	204	17.481	72.402	19.547	1.00	57.90	C
ATOM	1363	OG1	THR	A	204	16.900	73.630	19.090	1.00	56.77	O
ATOM	1364	CG2	THR	A	204	17.332	72.488	21.079	1.00	57.65	C
ATOM	1365	C	THR	A	204	19.574	71.032	19.575	1.00	57.57	C
ATOM	1366	O	THR	A	204	19.196	69.966	19.047	1.00	56.94	O
ATOM	1367	N	ARG	A	205	20.487	71.106	20.545	1.00	56.60	N
ATOM	1368	CA	ARG	A	205	21.238	69.959	21.022	1.00	56.09	C
ATOM	1369	CB	ARG	A	205	22.204	70.417	22.124	1.00	56.67	C
ATOM	1370	CG	ARG	A	205	22.870	69.291	22.879	1.00	59.97	C
ATOM	1371	CD	ARG	A	205	24.127	69.719	23.631	1.00	63.64	C
ATOM	1372	NE	ARG	A	205	25.317	69.608	22.785	1.00	64.42	N
ATOM	1373	CZ	ARG	A	205	26.049	68.501	22.667	1.00	65.48	C
ATOM	1374	NH1	ARG	A	205	25.712	67.410	23.340	1.00	65.75	N
ATOM	1375	NH2	ARG	A	205	27.114	68.476	21.872	1.00	64.31	N
ATOM	1376	C	ARG	A	205	20.360	68.784	21.503	1.00	55.41	C
ATOM	1377	O	ARG	A	205	20.536	67.630	21.069	1.00	55.27	O
ATOM	1378	N	VAL	A	206	19.420	69.077	22.400	1.00	54.06	N
ATOM	1379	CA	VAL	A	206	18.634	68.037	23.067	1.00	52.40	C
ATOM	1380	CB	VAL	A	206	17.704	68.640	24.178	1.00	52.71	C
ATOM	1381	CG1	VAL	A	206	18.516	69.018	25.416	1.00	50.99	C
ATOM	1382	CG2	VAL	A	206	16.919	69.844	23.636	1.00	51.73	C
ATOM	1383	C	VAL	A	206	17.799	67.291	22.048	1.00	51.99	C
ATOM	1384	O	VAL	A	206	17.219	66.257	22.363	1.00	52.27	O
ATOM	1385	N	TYR	A	207	17.731	67.834	20.830	1.00	50.50	N
ATOM	1386	CA	TYR	A	207	17.001	67.202	19.738	1.00	49.94	C
ATOM	1387	CB	TYR	A	207	16.126	68.236	19.021	1.00	49.34	C
ATOM	1388	CG	TYR	A	207	14.759	68.542	19.600	1.00	48.61	C
ATOM	1389	CD1	TYR	A	207	14.604	69.438	20.679	1.00	49.28	C
ATOM	1390	CE1	TYR	A	207	13.314	69.753	21.194	1.00	48.65	C
ATOM	1391	CZ	TYR	A	207	12.182	69.164	20.590	1.00	50.59	C
ATOM	1392	OH	TYR	A	207	10.901	69.447	21.042	1.00	47.38	O
ATOM	1393	CE2	TYR	A	207	12.332	68.284	19.488	1.00	48.14	C
ATOM	1394	CD2	TYR	A	207	13.605	67.999	19.007	1.00	48.95	C
ATOM	1395	C	TYR	A	207	17.982	66.571	18.718	1.00	49.22	C
ATOM	1396	O	TYR	A	207	17.560	66.165	17.621	1.00	48.88	O
ATOM	1397	N	SER	A	208	19.269	66.529	19.085	1.00	48.13	N
ATOM	1398	CA	SER	A	208	20.361	66.030	18.231	1.00	47.87	C
ATOM	1399	CB	SER	A	208	21.667	66.791	18.496	1.00	48.10	C
ATOM	1400	OG	SER	A	208	22.280	66.316	19.688	1.00	49.78	O
ATOM	1401	C	SER	A	208	20.620	64.566	18.503	1.00	46.42	C
ATOM	1402	O	SER	A	208	20.531	64.110	19.656	1.00	46.94	O
ATOM	1403	N	PRO	A	209	20.941	63.826	17.449	1.00	44.93	N
ATOM	1404	CA	PRO	A	209	21.043	62.374	17.545	1.00	43.05	C
ATOM	1405	CB	PRO	A	209	20.979	61.948	16.083	1.00	43.11	C
ATOM	1406	CG	PRO	A	209	21.596	63.062	15.366	1.00	43.72	C
ATOM	1407	CD	PRO	A	209	21.165	64.293	16.070	1.00	45.04	C
ATOM	1408	C	PRO	A	209	22.334	61.918	18.200	1.00	42.08	C
ATOM	1409	O	PRO	A	209	23.303	62.675	18.235	1.00	40.92	O
ATOM	1410	N	PRO	A	210	22.355	60.685	18.705	1.00	41.24	N
ATOM	1411	CA	PRO	A	210	23.546	60.167	19.374	1.00	42.13	C
ATOM	1412	CB	PRO	A	210	23.117	58.762	19.830	1.00	41.13	C
ATOM	1413	CG	PRO	A	210	21.980	58.403	18.942	1.00	41.77	C
ATOM	1414	CD	PRO	A	210	21.270	59.693	18.669	1.00	40.59	C
ATOM	1415	C	PRO	A	210	24.768	60.119	18.442	1.00	43.19	C
ATOM	1416	O	PRO	A	210	25.884	60.302	18.942	1.00	42.91	O
ATOM	1417	N	GLU	A	211	24.567	59.901	17.138	1.00	43.80	N

ATOM	1418	CA	GLU	A	211	25.683	59.896	16.184	1.00 45.23	C
ATOM	1419	CB	GLU	A	211	25.253	59.400	14.780	1.00 44.59	C
ATOM	1420	CG	GLU	A	211	24.227	60.279	14.079	1.00 42.32	C
ATOM	1421	CD	GLU	A	211	22.796	59.821	14.334	1.00 41.06	C
ATOM	1422	OE1	GLU	A	211	22.529	59.217	15.394	1.00 38.90	O
ATOM	1423	OE2	GLU	A	211	21.940	60.065	13.460	1.00 38.76	O
ATOM	1424	C	GLU	A	211	26.354	61.263	16.095	1.00 46.56	C
ATOM	1425	O	GLU	A	211	27.563	61.353	15.883	1.00 46.98	O
ATOM	1426	N	TRP	A	212	25.585	62.331	16.284	1.00 48.34	N
ATOM	1427	CA	TRP	A	212	26.184	63.658	16.339	1.00 50.36	C
ATOM	1428	CB	TRP	A	212	25.147	64.769	16.186	1.00 50.50	C
ATOM	1429	CG	TRP	A	212	25.742	66.114	16.495	1.00 52.39	C
ATOM	1430	CD1	TRP	A	212	25.599	66.830	17.652	1.00 53.01	C
ATOM	1431	NE1	TRP	A	212	26.318	67.999	17.579	1.00 53.68	N
ATOM	1432	CE2	TRP	A	212	26.962	68.052	16.368	1.00 53.34	C
ATOM	1433	CD2	TRP	A	212	26.626	66.877	15.661	1.00 52.72	C
ATOM	1434	CE3	TRP	A	212	27.159	66.692	14.373	1.00 52.54	C
ATOM	1435	CZ3	TRP	A	212	27.992	67.675	13.842	1.00 52.69	C
ATOM	1436	CH2	TRP	A	212	28.306	68.832	14.575	1.00 52.71	C
ATOM	1437	CZ2	TRP	A	212	27.802	69.040	15.833	1.00 53.56	C
ATOM	1438	C	TRP	A	212	26.996	63.835	17.622	1.00 51.79	C
ATOM	1439	O	TRP	A	212	28.118	64.342	17.588	1.00 52.13	O
ATOM	1440	N	ILE	A	213	26.435	63.388	18.743	1.00 53.62	N
ATOM	1441	CA	ILE	A	213	27.095	63.496	20.048	1.00 55.72	C
ATOM	1442	CB	ILE	A	213	26.195	62.917	21.183	1.00 55.41	C
ATOM	1443	CG1	ILE	A	213	24.804	63.568	21.202	1.00 56.07	C
ATOM	1444	CD1	ILE	A	213	24.816	65.083	21.258	1.00 57.43	C
ATOM	1445	CG2	ILE	A	213	26.874	63.055	22.525	1.00 56.33	C
ATOM	1446	C	ILE	A	213	28.440	62.771	20.050	1.00 57.10	C
ATOM	1447	O	ILE	A	213	29.461	63.335	20.447	1.00 57.22	O
ATOM	1448	N	ARG	A	214	28.416	61.524	19.591	1.00 58.27	N
ATOM	1449	CA	ARG	A	214	29.559	60.635	19.650	1.00 59.99	C
ATOM	1450	CB	ARG	A	214	29.083	59.190	19.585	1.00 60.48	C
ATOM	1451	CG	ARG	A	214	28.391	58.721	20.837	1.00 64.19	C
ATOM	1452	CD	ARG	A	214	28.138	57.237	20.844	1.00 68.93	C
ATOM	1453	NE	ARG	A	214	29.398	56.501	20.865	1.00 73.42	N
ATOM	1454	CZ	ARG	A	214	29.499	55.185	21.015	1.00 76.10	C
ATOM	1455	NH1	ARG	A	214	28.405	54.439	21.161	1.00 76.91	N
ATOM	1456	NH2	ARG	A	214	30.697	54.609	21.013	1.00 76.26	N
ATOM	1457	C	ARG	A	214	30.579	60.864	18.546	1.00 59.96	C
ATOM	1458	O	ARG	A	214	31.774	60.803	18.812	1.00 60.37	O
ATOM	1459	N	TYR	A	215	30.116	61.106	17.318	1.00 59.65	N
ATOM	1460	CA	TYR	A	215	31.018	61.161	16.159	1.00 59.46	C
ATOM	1461	CB	TYR	A	215	30.751	59.997	15.196	1.00 59.78	C
ATOM	1462	CG	TYR	A	215	30.624	58.648	15.858	1.00 61.91	C
ATOM	1463	CD1	TYR	A	215	31.657	58.120	16.639	1.00 63.80	C
ATOM	1464	CE1	TYR	A	215	31.532	56.877	17.247	1.00 64.01	C
ATOM	1465	CZ	TYR	A	215	30.370	56.151	17.070	1.00 65.13	C
ATOM	1466	OH	TYR	A	215	30.228	54.910	17.657	1.00 66.40	O
ATOM	1467	CE2	TYR	A	215	29.346	56.647	16.288	1.00 64.30	C
ATOM	1468	CD2	TYR	A	215	29.475	57.885	15.692	1.00 63.31	C
ATOM	1469	C	TYR	A	215	30.984	62.453	15.364	1.00 58.84	C
ATOM	1470	O	TYR	A	215	31.672	62.556	14.356	1.00 58.96	O
ATOM	1471	N	HIS	A	216	30.189	63.431	15.791	1.00 57.99	N
ATOM	1472	CA	HIS	A	216	30.018	64.666	15.020	1.00 57.44	C
ATOM	1473	CB	HIS	A	216	31.238	65.583	15.198	1.00 58.54	C
ATOM	1474	CG	HIS	A	216	31.302	66.231	16.547	1.00 62.71	C
ATOM	1475	ND1	HIS	A	216	30.780	67.486	16.793	1.00 65.61	N
ATOM	1476	CE1	HIS	A	216	30.965	67.796	18.065	1.00 67.49	C
ATOM	1477	NE2	HIS	A	216	31.591	66.788	18.655	1.00 67.79	N
ATOM	1478	CD2	HIS	A	216	31.808	65.793	17.730	1.00 65.96	C
ATOM	1479	C	HIS	A	216	29.721	64.415	13.524	1.00 55.81	C
ATOM	1480	O	HIS	A	216	30.212	65.135	12.653	1.00 55.97	O
ATOM	1481	N	ARG	A	217	28.910	63.395	13.243	1.00 53.48	N
ATOM	1482	CA	ARG	A	217	28.502	63.041	11.881	1.00 51.48	C
ATOM	1483	CB	ARG	A	217	29.335	61.864	11.347	1.00 51.91	C
ATOM	1484	CG	ARG	A	217	30.818	62.132	11.121	1.00 54.97	C
ATOM	1485	CD	ARG	A	217	31.688	60.860	11.180	1.00 59.48	C
ATOM	1486	NE	ARG	A	217	31.581	60.059	9.957	1.00 63.43	N

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ATOM   1487  CZ  ARG A 217      32.061  60.411   8.751  1.00 64.73           C
ATOM   1488  NH1 ARG A 217      32.700  61.569   8.577  1.00 66.07           N
ATOM   1489  NH2 ARG A 217      31.892  59.602   7.709  1.00 63.46           N
ATOM   1490  C   ARG A 217      27.054  62.581  11.923  1.00 48.94           C
ATOM   1491  O   ARG A 217      26.641  61.939  12.884  1.00 48.53           O
ATOM   1492  N   TYR A 218      26.300  62.893  10.875  1.00 45.99           N
ATOM   1493  CA  TYR A 218      24.938  62.394  10.722  1.00 43.71           C
ATOM   1494  CB  TYR A 218      23.976  63.126  11.694  1.00 42.32           C
ATOM   1495  CG  TYR A 218      23.830  64.587  11.395  1.00 40.14           C
ATOM   1496  CD1 TYR A 218      24.708  65.529  11.937  1.00 39.79           C
ATOM   1497  CE1 TYR A 218      24.574  66.882  11.628  1.00 42.32           C
ATOM   1498  CZ  TYR A 218      23.562  67.298  10.770  1.00 41.14           C
ATOM   1499  OH  TYR A 218      23.412  68.630  10.464  1.00 43.32           O
ATOM   1500  CE2 TYR A 218      22.680  66.375  10.224  1.00 39.68           C
ATOM   1501  CD2 TYR A 218      22.828  65.031  10.539  1.00 39.80           C
ATOM   1502  C   TYR A 218      24.448  62.520   9.279  1.00 42.58           C
ATOM   1503  O   TYR A 218      24.959  63.323   8.492  1.00 42.66           O
ATOM   1504  N   HIS A 219      23.434  61.732   8.947  1.00 41.95           N
ATOM   1505  CA  HIS A 219      22.769  61.849   7.658  1.00 40.52           C
ATOM   1506  CB  HIS A 219      22.655  60.465   7.030  1.00 41.07           C
ATOM   1507  CG  HIS A 219      23.984  59.906   6.614  1.00 42.12           C
ATOM   1508  ND1 HIS A 219      24.497  60.080   5.344  1.00 43.99           N
ATOM   1509  CE1 HIS A 219      25.692  59.523   5.273  1.00 42.45           C
ATOM   1510  NE2 HIS A 219      25.982  59.010   6.455  1.00 43.76           N
ATOM   1511  CD2 HIS A 219      24.935  59.246   7.317  1.00 41.90           C
ATOM   1512  C   HIS A 219      21.404  62.521   7.843  1.00 39.33           C
ATOM   1513  O   HIS A 219      20.779  62.370   8.889  1.00 38.64           O
ATOM   1514  N   GLY A 220      20.965  63.270   6.836  1.00 38.11           N
ATOM   1515  CA  GLY A 220      19.784  64.103   6.950  1.00 37.81           C
ATOM   1516  C   GLY A 220      18.527  63.394   7.405  1.00 38.27           C
ATOM   1517  O   GLY A 220      17.931  63.745   8.429  1.00 37.53           O
ATOM   1518  N   ARG A 221      18.122  62.386   6.647  1.00 38.11           N
ATOM   1519  CA  ARG A 221      16.855  61.717   6.895  1.00 38.50           C
ATOM   1520  CB  ARG A 221      16.542  60.729   5.767  1.00 40.47           C
ATOM   1521  CG  ARG A 221      16.585  61.401   4.388  1.00 45.37           C
ATOM   1522  CD  ARG A 221      16.575  60.448   3.185  1.00 51.09           C
ATOM   1523  NE  ARG A 221      16.584  61.200   1.919  1.00 53.82           N
ATOM   1524  CZ  ARG A 221      17.690  61.495   1.222  1.00 55.73           C
ATOM   1525  NH1 ARG A 221      18.894  61.099   1.646  1.00 56.00           N
ATOM   1526  NH2 ARG A 221      17.594  62.164   0.075  1.00 55.14           N
ATOM   1527  C   ARG A 221      16.824  61.050   8.256  1.00 37.41           C
ATOM   1528  O   ARG A 221      15.873  61.254   9.013  1.00 37.16           O
ATOM   1529  N   SER A 222      17.858  60.290   8.597  1.00 36.13           N
ATOM   1530  CA  SER A 222      17.836  59.563   9.863  1.00 35.73           C
ATOM   1531  CB  SER A 222      18.900  58.448   9.890  1.00 34.73           C
ATOM   1532  OG  SER A 222      20.215  58.968   9.772  1.00 36.77           O
ATOM   1533  C   SER A 222      17.941  60.519  11.069  1.00 35.26           C
ATOM   1534  O   SER A 222      17.365  60.250  12.137  1.00 35.32           O
ATOM   1535  N   ALA A 223      18.647  61.633  10.899  1.00 34.89           N
ATOM   1536  CA  ALA A 223      18.743  62.643  11.958  1.00 34.34           C
ATOM   1537  CB  ALA A 223      19.847  63.660  11.666  1.00 32.42           C
ATOM   1538  C   ALA A 223      17.399  63.350  12.101  1.00 34.25           C
ATOM   1539  O   ALA A 223      16.992  63.726  13.214  1.00 33.94           O
ATOM   1540  N   ALA A 224      16.699  63.523  10.983  1.00 33.64           N
ATOM   1541  CA  ALA A 224      15.384  64.152  11.033  1.00 32.93           C
ATOM   1542  CB  ALA A 224      14.862  64.456   9.651  1.00 33.29           C
ATOM   1543  C   ALA A 224      14.410  63.269  11.812  1.00 33.44           C
ATOM   1544  O   ALA A 224      13.645  63.770  12.651  1.00 33.58           O
ATOM   1545  N   VAL A 225      14.455  61.962  11.562  1.00 32.40           N
ATOM   1546  CA  VAL A 225      13.569  61.003  12.228  1.00 31.69           C
ATOM   1547  CB  VAL A 225      13.724  59.574  11.622  1.00 32.53           C
ATOM   1548  CG1 VAL A 225      13.083  58.504  12.507  1.00 30.93           C
ATOM   1549  CG2 VAL A 225      13.123  59.544  10.219  1.00 32.75           C
ATOM   1550  C   VAL A 225      13.856  60.988  13.740  1.00 32.12           C
ATOM   1551  O   VAL A 225      12.943  60.876  14.552  1.00 31.44           O
ATOM   1552  N   TRP A 226      15.125  61.117  14.110  1.00 31.95           N
ATOM   1553  CA  TRP A 226      15.476  61.173  15.530  1.00 32.47           C
ATOM   1554  CB  TRP A 226      16.990  61.279  15.721  1.00 33.06           C
ATOM   1555  CG  TRP A 226      17.322  61.494  17.183  1.00 32.56           C
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ATOM   1556  CD1 TRP A 226      17.334  62.682  17.851  1.00 32.49           C
ATOM   1557  NE1 TRP A 226      17.660  62.479  19.173  1.00 32.64           N
ATOM   1558  CE2 TRP A 226      17.834  61.134  19.383  1.00 31.73           C
ATOM   1559  CD2 TRP A 226      17.631  60.485  18.148  1.00 31.24           C
ATOM   1560  CE3 TRP A 226      17.757  59.089  18.094  1.00 32.89           C
ATOM   1561  CZ3 TRP A 226      18.096  58.391  19.261  1.00 32.32           C
ATOM   1562  CH2 TRP A 226      18.286  59.080  20.478  1.00 33.34           C
ATOM   1563  CZ2 TRP A 226      18.157  60.444  20.552  1.00 32.43           C
ATOM   1564  C   TRP A 226      14.754  62.372  16.178  1.00 32.00           C
ATOM   1565  O   TRP A 226      14.071  62.224  17.192  1.00 31.94           O
ATOM   1566  N   SER A 227      14.872  63.546  15.558  1.00 31.65           N
ATOM   1567  CA  SER A 227      14.217  64.752  16.073  1.00 31.57           C
ATOM   1568  CB  SER A 227      14.611  65.982  15.259  1.00 31.61           C
ATOM   1569  OG  SER A 227      13.916  66.048  14.016  1.00 33.45           O
ATOM   1570  C   SER A 227      12.695  64.599  16.161  1.00 31.31           C
ATOM   1571  O   SER A 227      12.052  65.151  17.072  1.00 30.56           O
ATOM   1572  N   LEU A 228      12.124  63.841  15.229  1.00 30.36           N
ATOM   1573  CA  LEU A 228      10.701  63.545  15.217  1.00 30.48           C
ATOM   1574  CB  LEU A 228      10.300  62.865  13.901  1.00 30.69           C
ATOM   1575  CG  LEU A 228      10.325  63.767  12.661  1.00 31.45           C
ATOM   1576  CD1 LEU A 228      10.069  62.947  11.389  1.00 30.81           C
ATOM   1577  CD2 LEU A 228       9.321  64.917  12.784  1.00 30.15           C
ATOM   1578  C   LEU A 228      10.315  62.661  16.394  1.00 29.84           C
ATOM   1579  O   LEU A 228       9.227  62.815  16.958  1.00 30.50           O
ATOM   1580  N   GLY A 229      11.206  61.751  16.765  1.00 29.67           N
ATOM   1581  CA  GLY A 229      11.008  60.895  17.920  1.00 29.67           C
ATOM   1582  C   GLY A 229      10.994  61.723  19.208  1.00 30.52           C
ATOM   1583  O   GLY A 229      10.169  61.486  20.105  1.00 28.98           O
ATOM   1584  N   ILE A 230      11.920  62.670  19.307  1.00 30.54           N
ATOM   1585  CA  ILE A 230      11.986  63.587  20.459  1.00 31.11           C
ATOM   1586  CB  ILE A 230      13.199  64.564  20.334  1.00 31.68           C
ATOM   1587  CG1 ILE A 230      14.526  63.792  20.281  1.00 30.92           C
ATOM   1588  CD1 ILE A 230      14.824  62.992  21.546  1.00 30.66           C
ATOM   1589  CG2 ILE A 230      13.229  65.553  21.533  1.00 30.61           C
ATOM   1590  C   ILE A 230      10.693  64.397  20.532  1.00 31.56           C
ATOM   1591  O   ILE A 230      10.050  64.488  21.596  1.00 31.09           O
ATOM   1592  N   LEU A 231      10.289  64.928  19.373  1.00 30.97           N
ATOM   1593  CA  LEU A 231       9.050  65.711  19.257  1.00 30.14           C
ATOM   1594  CB  LEU A 231       8.894  66.239  17.828  1.00 30.10           C
ATOM   1595  CG  LEU A 231       7.627  67.043  17.556  1.00 32.25           C
ATOM   1596  CD1 LEU A 231       7.733  68.372  18.310  1.00 30.47           C
ATOM   1597  CD2 LEU A 231       7.419  67.246  16.065  1.00 30.92           C
ATOM   1598  C   LEU A 231       7.798  64.950  19.689  1.00 30.59           C
ATOM   1599  O   LEU A 231       6.949  65.484  20.439  1.00 30.81           O
ATOM   1600  N   LEU A 232       7.655  63.721  19.210  1.00 29.58           N
ATOM   1601  CA  LEU A 232       6.499  62.916  19.552  1.00 30.41           C
ATOM   1602  CB  LEU A 232       6.470  61.609  18.745  1.00 30.17           C
ATOM   1603  CG  LEU A 232       5.301  60.642  19.033  1.00 30.99           C
ATOM   1604  CD1 LEU A 232       3.947  61.346  18.919  1.00 33.55           C
ATOM   1605  CD2 LEU A 232       5.359  59.465  18.073  1.00 31.95           C
ATOM   1606  C   LEU A 232       6.439  62.630  21.062  1.00 30.78           C
ATOM   1607  O   LEU A 232       5.371  62.721  21.667  1.00 31.42           O
ATOM   1608  N   TYR A 233       7.571  62.272  21.650  1.00 30.02           N
ATOM   1609  CA  TYR A 233       7.646  62.042  23.103  1.00 30.55           C
ATOM   1610  CB  TYR A 233       9.068  61.662  23.526  1.00 30.26           C
ATOM   1611  CG  TYR A 233       9.209  61.373  25.008  1.00 28.93           C
ATOM   1612  CD1 TYR A 233       9.255  62.416  25.930  1.00 29.15           C
ATOM   1613  CE1 TYR A 233       9.353  62.171  27.311  1.00 28.65           C
ATOM   1614  CZ  TYR A 233       9.407  60.882  27.769  1.00 31.81           C
ATOM   1615  OH  TYR A 233       9.505  60.681  29.132  1.00 36.02           O
ATOM   1616  CE2 TYR A 233       9.365  59.801  26.878  1.00 30.59           C
ATOM   1617  CD2 TYR A 233       9.267  60.058  25.486  1.00 28.47           C
ATOM   1618  C   TYR A 233       7.216  63.306  23.834  1.00 31.37           C
ATOM   1619  O   TYR A 233       6.416  63.250  24.769  1.00 32.79           O
ATOM   1620  N   ASP A 234       7.762  64.434  23.407  1.00 31.52           N
ATOM   1621  CA  ASP A 234       7.411  65.750  23.934  1.00 33.52           C
ATOM   1622  CB  ASP A 234       8.156  66.833  23.162  1.00 34.26           C
ATOM   1623  CG  ASP A 234       7.951  68.224  23.745  1.00 37.82           C
ATOM   1624  OD1 ASP A 234       8.206  68.450  24.956  1.00 39.31           O
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ATOM	1625	OD2	ASP	A	234	7.531	69.156	23.030	1.00	39.97	O
ATOM	1626	C	ASP	A	234	5.923	66.023	23.923	1.00	34.29	C
ATOM	1627	O	ASP	A	234	5.368	66.524	24.931	1.00	35.28	O
ATOM	1628	N	MET	A	235	5.258	65.695	22.810	1.00	33.03	N
ATOM	1629	CA	MET	A	235	3.819	65.904	22.713	1.00	33.96	C
ATOM	1630	CB	MET	A	235	3.293	65.625	21.305	1.00	33.12	C
ATOM	1631	CG	MET	A	235	3.641	66.708	20.286	1.00	36.42	C
ATOM	1632	SD	MET	A	235	2.965	66.246	18.692	1.00	39.55	S
ATOM	1633	CE	MET	A	235	4.174	65.260	18.147	1.00	43.23	C
ATOM	1634	C	MET	A	235	3.020	65.078	23.703	1.00	33.96	C
ATOM	1635	O	MET	A	235	2.133	65.607	24.337	1.00	35.00	O
ATOM	1636	N	VAL	A	236	3.322	63.787	23.816	1.00	34.07	N
ATOM	1637	CA	VAL	A	236	2.518	62.893	24.660	1.00	35.02	C
ATOM	1638	CB	VAL	A	236	2.405	61.476	24.055	1.00	35.33	C
ATOM	1639	CG1	VAL	A	236	1.757	61.562	22.673	1.00	34.30	C
ATOM	1640	CG2	VAL	A	236	3.763	60.805	23.937	1.00	33.11	C
ATOM	1641	C	VAL	A	236	2.955	62.843	26.129	1.00	35.63	C
ATOM	1642	O	VAL	A	236	2.225	62.326	26.970	1.00	35.58	O
ATOM	1643	N	CYS	A	237	4.131	63.389	26.432	1.00	36.11	N
ATOM	1644	CA	CYS	A	237	4.642	63.383	27.814	1.00	36.98	C
ATOM	1645	CB	CYS	A	237	5.972	62.630	27.909	1.00	36.35	C
ATOM	1646	SG	CYS	A	237	5.796	60.844	27.757	1.00	38.34	S
ATOM	1647	C	CYS	A	237	4.790	64.778	28.416	1.00	37.40	C
ATOM	1648	O	CYS	A	237	4.983	64.907	29.628	1.00	38.17	O
ATOM	1649	N	GLY	A	238	4.722	65.812	27.576	1.00	36.49	N
ATOM	1650	CA	GLY	A	238	4.791	67.183	28.045	1.00	36.34	C
ATOM	1651	C	GLY	A	238	6.186	67.717	28.259	1.00	37.64	C
ATOM	1652	O	GLY	A	238	6.353	68.842	28.719	1.00	37.75	O
ATOM	1653	N	ASP	A	239	7.198	66.916	27.939	1.00	38.11	N
ATOM	1654	CA	ASP	A	239	8.580	67.369	28.009	1.00	39.21	C
ATOM	1655	CB	ASP	A	239	9.056	67.339	29.458	1.00	40.74	C
ATOM	1656	CG	ASP	A	239	10.214	68.302	29.735	1.00	45.40	C
ATOM	1657	OD1	ASP	A	239	10.586	69.135	28.867	1.00	49.01	O
ATOM	1658	OD2	ASP	A	239	10.822	68.274	30.828	1.00	50.33	O
ATOM	1659	C	ASP	A	239	9.418	66.434	27.142	1.00	39.28	C
ATOM	1660	O	ASP	A	239	8.957	65.354	26.769	1.00	39.18	O
ATOM	1661	N	ILE	A	240	10.630	66.856	26.809	1.00	39.54	N
ATOM	1662	CA	ILE	A	240	11.529	66.066	25.983	1.00	39.95	C
ATOM	1663	CB	ILE	A	240	12.641	66.964	25.440	1.00	40.83	C
ATOM	1664	CG1	ILE	A	240	13.306	67.740	26.578	1.00	41.83	C
ATOM	1665	CD1	ILE	A	240	14.455	68.627	26.125	1.00	44.95	C
ATOM	1666	CG2	ILE	A	240	12.092	67.911	24.344	1.00	39.77	C
ATOM	1667	C	ILE	A	240	12.106	64.916	26.827	1.00	40.26	C
ATOM	1668	O	ILE	A	240	12.187	65.046	28.049	1.00	40.89	O
ATOM	1669	N	PRO	A	241	12.470	63.791	26.210	1.00	40.14	N
ATOM	1670	CA	PRO	A	241	12.941	62.620	26.971	1.00	41.03	C
ATOM	1671	CB	PRO	A	241	12.879	61.494	25.932	1.00	40.79	C
ATOM	1672	CG	PRO	A	241	13.150	62.187	24.622	1.00	39.44	C
ATOM	1673	CD	PRO	A	241	12.444	63.518	24.757	1.00	39.54	C
ATOM	1674	C	PRO	A	241	14.361	62.737	27.548	1.00	42.89	C
ATOM	1675	O	PRO	A	241	14.639	62.109	28.571	1.00	42.98	O
ATOM	1676	N	PHE	A	242	15.243	63.508	26.912	1.00	44.80	N
ATOM	1677	CA	PHE	A	242	16.644	63.555	27.340	1.00	46.51	C
ATOM	1678	CB	PHE	A	242	17.589	62.944	26.285	1.00	45.41	C
ATOM	1679	CG	PHE	A	242	17.145	61.617	25.735	1.00	43.12	C
ATOM	1680	CD1	PHE	A	242	16.885	60.545	26.578	1.00	42.42	C
ATOM	1681	CE1	PHE	A	242	16.496	59.313	26.068	1.00	41.08	C
ATOM	1682	CZ	PHE	A	242	16.367	59.148	24.676	1.00	43.10	C
ATOM	1683	CE2	PHE	A	242	16.618	60.222	23.824	1.00	40.87	C
ATOM	1684	CD2	PHE	A	242	17.012	61.438	24.350	1.00	42.39	C
ATOM	1685	C	PHE	A	242	17.104	64.973	27.639	1.00	48.94	C
ATOM	1686	O	PHE	A	242	16.783	65.913	26.903	1.00	48.57	O
ATOM	1687	N	GLU	A	243	17.884	65.112	28.714	1.00	52.57	N
ATOM	1688	CA	GLU	A	243	18.514	66.391	29.046	1.00	55.94	C
ATOM	1689	CB	GLU	A	243	18.204	66.793	30.496	1.00	57.25	C
ATOM	1690	CG	GLU	A	243	16.930	67.634	30.664	1.00	62.51	C
ATOM	1691	CD	GLU	A	243	16.911	68.912	29.814	1.00	68.14	C
ATOM	1692	OE1	GLU	A	243	17.901	69.697	29.854	1.00	69.83	O
ATOM	1693	OE2	GLU	A	243	15.894	69.140	29.104	1.00	69.55	O

ATOM	1694	C	GLU	A	243	20.022	66.364	28.813	1.00	56.70	C
ATOM	1695	O	GLU	A	243	20.596	67.329	28.291	1.00	57.61	O
ATOM	1696	N	HIS	A	244	20.654	65.250	29.169	1.00	57.00	N
ATOM	1697	CA	HIS	A	244	22.111	65.145	29.128	1.00	57.57	C
ATOM	1698	CB	HIS	A	244	22.634	64.653	30.484	1.00	57.93	C
ATOM	1699	CG	HIS	A	244	22.177	65.491	31.641	1.00	60.15	C
ATOM	1700	ND1	HIS	A	244	21.243	65.040	32.563	1.00	61.46	N
ATOM	1701	CE1	HIS	A	244	21.021	65.986	33.459	1.00	61.53	C
ATOM	1702	NE2	HIS	A	244	21.772	67.040	33.145	1.00	61.93	N
ATOM	1703	CD2	HIS	A	244	22.501	66.761	32.008	1.00	60.89	C
ATOM	1704	C	HIS	A	244	22.632	64.251	27.999	1.00	57.12	C
ATOM	1705	O	HIS	A	244	21.946	63.321	27.564	1.00	56.42	O
ATOM	1706	N	ASP	A	245	23.850	64.550	27.542	1.00	56.65	N
ATOM	1707	CA	ASP	A	245	24.536	63.778	26.508	1.00	56.51	C
ATOM	1708	CB	ASP	A	245	25.982	64.254	26.364	1.00	56.84	C
ATOM	1709	CG	ASP	A	245	26.093	65.551	25.602	1.00	58.28	C
ATOM	1710	OD1	ASP	A	245	25.109	66.322	25.555	1.00	60.57	O
ATOM	1711	OD2	ASP	A	245	27.132	65.889	25.003	1.00	61.68	O
ATOM	1712	C	ASP	A	245	24.520	62.289	26.792	1.00	55.85	C
ATOM	1713	O	ASP	A	245	24.240	61.487	25.902	1.00	55.84	O
ATOM	1714	N	GLU	A	246	24.807	61.926	28.038	1.00	55.12	N
ATOM	1715	CA	GLU	A	246	24.814	60.528	28.473	1.00	54.57	C
ATOM	1716	CB	GLU	A	246	25.227	60.414	29.948	1.00	55.49	C
ATOM	1717	CG	GLU	A	246	26.247	61.439	30.419	1.00	59.92	C
ATOM	1718	CD	GLU	A	246	25.601	62.745	30.853	1.00	64.57	C
ATOM	1719	OE1	GLU	A	246	24.864	62.732	31.873	1.00	66.43	O
ATOM	1720	OE2	GLU	A	246	25.824	63.779	30.165	1.00	66.00	O
ATOM	1721	C	GLU	A	246	23.464	59.838	28.284	1.00	52.76	C
ATOM	1722	O	GLU	A	246	23.405	58.637	27.998	1.00	51.94	O
ATOM	1723	N	GLU	A	247	22.381	60.583	28.491	1.00	51.08	N
ATOM	1724	CA	GLU	A	247	21.037	60.031	28.289	1.00	50.00	C
ATOM	1725	CB	GLU	A	247	19.982	60.949	28.888	1.00	50.91	C
ATOM	1726	CG	GLU	A	247	20.048	61.069	30.398	1.00	54.76	C
ATOM	1727	CD	GLU	A	247	19.070	62.089	30.919	1.00	59.14	C
ATOM	1728	OE1	GLU	A	247	19.189	63.281	30.568	1.00	61.88	O
ATOM	1729	OE2	GLU	A	247	18.172	61.693	31.672	1.00	63.68	O
ATOM	1730	C	GLU	A	247	20.734	59.785	26.810	1.00	47.56	C
ATOM	1731	O	GLU	A	247	20.177	58.757	26.463	1.00	46.72	O
ATOM	1732	N	ILE	A	248	21.102	60.738	25.957	1.00	46.28	N
ATOM	1733	CA	ILE	A	248	20.964	60.598	24.498	1.00	46.12	C
ATOM	1734	CB	ILE	A	248	21.446	61.876	23.754	1.00	45.90	C
ATOM	1735	CG1	ILE	A	248	20.599	63.092	24.141	1.00	44.91	C
ATOM	1736	CD1	ILE	A	248	21.110	64.419	23.588	1.00	44.29	C
ATOM	1737	CG2	ILE	A	248	21.444	61.658	22.233	1.00	45.48	C
ATOM	1738	C	ILE	A	248	21.741	59.390	23.988	1.00	46.47	C
ATOM	1739	O	ILE	A	248	21.221	58.613	23.199	1.00	46.50	O
ATOM	1740	N	ILE	A	249	22.977	59.223	24.462	1.00	46.70	N
ATOM	1741	CA	ILE	A	249	23.845	58.119	24.021	1.00	47.73	C
ATOM	1742	CB	ILE	A	249	25.315	58.342	24.516	1.00	48.27	C
ATOM	1743	CG1	ILE	A	249	25.882	59.634	23.929	1.00	50.01	C
ATOM	1744	CD1	ILE	A	249	27.162	60.114	24.638	1.00	54.07	C
ATOM	1745	CG2	ILE	A	249	26.208	57.167	24.127	1.00	49.80	C
ATOM	1746	C	ILE	A	249	23.344	56.752	24.463	1.00	47.21	C
ATOM	1747	O	ILE	A	249	23.473	55.754	23.735	1.00	47.14	O
ATOM	1748	N	ARG	A	250	22.798	56.697	25.671	1.00	46.59	N
ATOM	1749	CA	ARG	A	250	22.259	55.454	26.197	1.00	46.70	C
ATOM	1750	CB	ARG	A	250	22.052	55.573	27.712	1.00	46.73	C
ATOM	1751	CG	ARG	A	250	21.612	54.297	28.415	1.00	47.47	C
ATOM	1752	CD	ARG	A	250	21.702	54.415	29.942	1.00	49.11	C
ATOM	1753	NE	ARG	A	250	21.290	53.191	30.631	1.00	50.87	N
ATOM	1754	CZ	ARG	A	250	20.217	53.076	31.429	1.00	50.66	C
ATOM	1755	NH1	ARG	A	250	19.412	54.117	31.656	1.00	46.65	N
ATOM	1756	NH2	ARG	A	250	19.955	51.909	32.006	1.00	50.26	N
ATOM	1757	C	ARG	A	250	20.949	55.097	25.483	1.00	46.42	C
ATOM	1758	O	ARG	A	250	20.617	53.922	25.352	1.00	47.00	O
ATOM	1759	N	GLY	A	251	20.224	56.113	25.018	1.00	46.84	N
ATOM	1760	CA	GLY	A	251	18.982	55.936	24.269	1.00	47.26	C
ATOM	1761	C	GLY	A	251	17.855	55.180	24.968	1.00	47.36	C
ATOM	1762	O	GLY	A	251	16.936	54.702	24.318	1.00	47.71	O

ATOM	1763	N	GLN	A	252	17.921	55.067	26.290	1.00	46.77	N
ATOM	1764	CA	GLN	A	252	16.872	54.400	27.058	1.00	46.61	C
ATOM	1765	CB	GLN	A	252	17.438	53.965	28.410	1.00	47.77	C
ATOM	1766	CG	GLN	A	252	16.745	52.797	29.034	1.00	53.27	C
ATOM	1767	CD	GLN	A	252	17.362	51.495	28.593	1.00	58.82	C
ATOM	1768	OE1	GLN	A	252	16.922	50.902	27.587	1.00	62.58	O
ATOM	1769	NE2	GLN	A	252	18.381	51.040	29.328	1.00	59.71	N
ATOM	1770	C	GLN	A	252	15.720	55.388	27.264	1.00	44.36	C
ATOM	1771	O	GLN	A	252	15.914	56.458	27.842	1.00	43.90	O
ATOM	1772	N	VAL	A	253	14.534	55.036	26.789	1.00	42.26	N
ATOM	1773	CA	VAL	A	253	13.366	55.917	26.887	1.00	41.30	C
ATOM	1774	CB	VAL	A	253	12.515	55.900	25.574	1.00	40.85	C
ATOM	1775	CG1	VAL	A	253	11.398	56.917	25.657	1.00	41.13	C
ATOM	1776	CG2	VAL	A	253	13.386	56.184	24.330	1.00	41.05	C
ATOM	1777	C	VAL	A	253	12.452	55.558	28.080	1.00	40.21	C
ATOM	1778	O	VAL	A	253	11.870	54.475	28.128	1.00	39.18	O
ATOM	1779	N	PHE	A	254	12.312	56.494	29.004	1.00	40.53	N
ATOM	1780	CA	PHE	A	254	11.415	56.340	30.147	1.00	41.30	C
ATOM	1781	CB	PHE	A	254	12.125	56.749	31.446	1.00	42.46	C
ATOM	1782	CG	PHE	A	254	11.181	56.979	32.597	1.00	45.89	C
ATOM	1783	CD1	PHE	A	254	10.698	55.890	33.354	1.00	48.15	C
ATOM	1784	CE1	PHE	A	254	9.794	56.087	34.453	1.00	46.65	C
ATOM	1785	CZ	PHE	A	254	9.368	57.391	34.762	1.00	47.61	C
ATOM	1786	CE2	PHE	A	254	9.840	58.499	33.990	1.00	48.28	C
ATOM	1787	CD2	PHE	A	254	10.742	58.287	32.922	1.00	47.87	C
ATOM	1788	C	PHE	A	254	10.192	57.216	29.960	1.00	40.77	C
ATOM	1789	O	PHE	A	254	10.324	58.388	29.630	1.00	40.62	O
ATOM	1790	N	PHE	A	255	9.011	56.656	30.202	1.00	39.76	N
ATOM	1791	CA	PHE	A	255	7.772	57.377	30.041	1.00	40.05	C
ATOM	1792	CB	PHE	A	255	6.744	56.512	29.293	1.00	38.87	C
ATOM	1793	CG	PHE	A	255	7.047	56.408	27.844	1.00	38.12	C
ATOM	1794	CD1	PHE	A	255	6.520	57.332	26.945	1.00	37.51	C
ATOM	1795	CE1	PHE	A	255	6.834	57.267	25.588	1.00	37.08	C
ATOM	1796	CZ	PHE	A	255	7.715	56.277	25.126	1.00	38.31	C
ATOM	1797	CE2	PHE	A	255	8.251	55.353	26.034	1.00	37.42	C
ATOM	1798	CD2	PHE	A	255	7.917	55.429	27.379	1.00	36.49	C
ATOM	1799	C	PHE	A	255	7.233	57.901	31.355	1.00	40.75	C
ATOM	1800	O	PHE	A	255	6.974	57.139	32.280	1.00	41.63	O
ATOM	1801	N	ARG	A	256	7.078	59.214	31.414	1.00	42.10	N
ATOM	1802	CA	ARG	A	256	6.613	59.911	32.614	1.00	43.68	C
ATOM	1803	CB	ARG	A	256	7.284	61.291	32.722	1.00	44.33	C
ATOM	1804	CG	ARG	A	256	7.050	62.233	31.549	1.00	46.48	C
ATOM	1805	CD	ARG	A	256	7.915	63.508	31.606	1.00	49.15	C
ATOM	1806	NE	ARG	A	256	9.248	63.277	31.034	1.00	53.26	N
ATOM	1807	CZ	ARG	A	256	10.334	64.018	31.293	1.00	54.62	C
ATOM	1808	NH1	ARG	A	256	10.260	65.060	32.133	1.00	55.57	N
ATOM	1809	NH2	ARG	A	256	11.502	63.720	30.716	1.00	52.61	N
ATOM	1810	C	ARG	A	256	5.096	60.051	32.658	1.00	43.59	C
ATOM	1811	O	ARG	A	256	4.525	60.251	33.724	1.00	44.72	O
ATOM	1812	N	GLN	A	257	4.454	59.930	31.498	1.00	42.63	N
ATOM	1813	CA	GLN	A	257	3.001	59.949	31.403	1.00	41.06	C
ATOM	1814	CB	GLN	A	257	2.538	61.061	30.445	1.00	42.46	C
ATOM	1815	CG	GLN	A	257	2.890	62.451	30.901	1.00	46.35	C
ATOM	1816	CD	GLN	A	257	1.908	62.984	31.916	1.00	51.18	C
ATOM	1817	OE1	GLN	A	257	0.693	62.917	31.711	1.00	52.75	O
ATOM	1818	NE2	GLN	A	257	2.428	63.504	33.020	1.00	55.05	N
ATOM	1819	C	GLN	A	257	2.510	58.618	30.872	1.00	38.68	C
ATOM	1820	O	GLN	A	257	3.267	57.849	30.300	1.00	38.45	O
ATOM	1821	N	ARG	A	258	1.226	58.353	31.047	1.00	36.14	N
ATOM	1822	CA	ARG	A	258	0.614	57.177	30.479	1.00	36.06	C
ATOM	1823	CB	ARG	A	258	-0.820	57.048	30.997	1.00	34.77	C
ATOM	1824	CG	ARG	A	258	-1.402	55.659	30.847	1.00	39.04	C
ATOM	1825	CD	ARG	A	258	-1.624	55.230	29.442	1.00	40.99	C
ATOM	1826	NE	ARG	A	258	-1.799	53.789	29.300	1.00	40.39	N
ATOM	1827	CZ	ARG	A	258	-2.327	53.219	28.215	1.00	43.89	C
ATOM	1828	NH1	ARG	A	258	-2.730	53.966	27.158	1.00	45.06	N
ATOM	1829	NH2	ARG	A	258	-2.444	51.899	28.162	1.00	40.81	N
ATOM	1830	C	ARG	A	258	0.599	57.345	28.950	1.00	35.62	C
ATOM	1831	O	ARG	A	258	0.071	58.325	28.463	1.00	35.32	O

ATOM	1832	N	VAL	A	259	1.159	56.385	28.221	1.00	34.94	N
ATOM	1833	CA	VAL	A	259	1.223	56.440	26.755	1.00	34.87	C
ATOM	1834	CB	VAL	A	259	2.629	56.926	26.277	1.00	35.54	C
ATOM	1835	CG1	VAL	A	259	2.782	56.824	24.747	1.00	34.21	C
ATOM	1836	CG2	VAL	A	259	2.902	58.365	26.752	1.00	33.65	C
ATOM	1837	C	VAL	A	259	0.967	55.033	26.235	1.00	35.77	C
ATOM	1838	O	VAL	A	259	1.579	54.062	26.728	1.00	35.74	O
ATOM	1839	N	SER	A	260	0.055	54.901	25.267	1.00	35.24	N
ATOM	1840	CA	SER	A	260	-0.269	53.601	24.698	1.00	36.49	C
ATOM	1841	CB	SER	A	260	-1.247	53.749	23.525	1.00	36.47	C
ATOM	1842	OG	SER	A	260	-0.608	54.285	22.377	1.00	37.04	O
ATOM	1843	C	SER	A	260	0.973	52.855	24.226	1.00	37.15	C
ATOM	1844	O	SER	A	260	1.981	53.465	23.874	1.00	37.30	O
ATOM	1845	N	SER	A	261	0.876	51.533	24.178	1.00	37.42	N
ATOM	1846	CA	SER	A	261	2.000	50.701	23.767	1.00	37.73	C
ATOM	1847	CB	SER	A	261	1.659	49.225	23.941	1.00	38.27	C
ATOM	1848	OG	SER	A	261	1.475	48.939	25.316	1.00	42.42	O
ATOM	1849	C	SER	A	261	2.399	50.965	22.325	1.00	37.68	C
ATOM	1850	O	SER	A	261	3.578	50.914	21.997	1.00	36.60	O
ATOM	1851	N	GLU	A	262	1.413	51.260	21.478	1.00	37.69	N
ATOM	1852	CA	GLU	A	262	1.662	51.578	20.080	1.00	38.33	C
ATOM	1853	CB	GLU	A	262	0.343	51.655	19.307	1.00	40.07	C
ATOM	1854	CG	GLU	A	262	-0.522	50.401	19.444	1.00	47.46	C
ATOM	1855	CD	GLU	A	262	-1.138	49.954	18.125	1.00	55.14	C
ATOM	1856	OE1	GLU	A	262	-1.716	50.811	17.407	1.00	58.98	O
ATOM	1857	OE2	GLU	A	262	-1.058	48.740	17.799	1.00	59.70	O
ATOM	1858	C	GLU	A	262	2.469	52.878	19.945	1.00	36.65	C
ATOM	1859	O	GLU	A	262	3.442	52.911	19.227	1.00	36.27	O
ATOM	1860	N	CYS	A	263	2.073	53.931	20.651	1.00	35.34	N
ATOM	1861	CA	CYS	A	263	2.822	55.188	20.621	1.00	34.46	C
ATOM	1862	CB	CYS	A	263	2.051	56.272	21.363	1.00	34.30	C
ATOM	1863	SG	CYS	A	263	2.728	57.931	21.207	1.00	34.38	S
ATOM	1864	C	CYS	A	263	4.250	55.021	21.181	1.00	34.46	C
ATOM	1865	O	CYS	A	263	5.221	55.477	20.556	1.00	32.45	O
ATOM	1866	N	GLN	A	264	4.385	54.325	22.321	1.00	33.42	N
ATOM	1867	CA	GLN	A	264	5.715	54.008	22.859	1.00	33.11	C
ATOM	1868	CB	GLN	A	264	5.629	53.110	24.097	1.00	33.38	C
ATOM	1869	CG	GLN	A	264	5.022	53.781	25.364	1.00	35.44	C
ATOM	1870	CD	GLN	A	264	5.296	52.968	26.647	1.00	37.59	C
ATOM	1871	OE1	GLN	A	264	6.162	52.098	26.655	1.00	39.41	O
ATOM	1872	NE2	GLN	A	264	4.566	53.262	27.717	1.00	33.63	N
ATOM	1873	C	GLN	A	264	6.578	53.314	21.795	1.00	33.15	C
ATOM	1874	O	GLN	A	264	7.753	53.689	21.606	1.00	32.43	O
ATOM	1875	N	HIS	A	265	6.001	52.322	21.110	1.00	32.53	N
ATOM	1876	CA	HIS	A	265	6.710	51.575	20.068	1.00	34.99	C
ATOM	1877	CB	HIS	A	265	5.836	50.455	19.469	1.00	36.23	C
ATOM	1878	CG	HIS	A	265	6.515	49.687	18.369	1.00	39.71	C
ATOM	1879	ND1	HIS	A	265	6.481	50.086	17.050	1.00	40.80	N
ATOM	1880	CE1	HIS	A	265	7.189	49.244	16.314	1.00	42.05	C
ATOM	1881	NE2	HIS	A	265	7.687	48.312	17.110	1.00	42.46	N
ATOM	1882	CD2	HIS	A	265	7.286	48.570	18.402	1.00	42.81	C
ATOM	1883	C	HIS	A	265	7.226	52.508	18.968	1.00	34.14	C
ATOM	1884	O	HIS	A	265	8.410	52.463	18.613	1.00	34.55	O
ATOM	1885	N	LEU	A	266	6.355	53.372	18.445	1.00	32.99	N
ATOM	1886	CA	LEU	A	266	6.778	54.306	17.394	1.00	32.41	C
ATOM	1887	CB	LEU	A	266	5.587	55.147	16.896	1.00	32.45	C
ATOM	1888	CG	LEU	A	266	5.863	56.209	15.818	1.00	33.18	C
ATOM	1889	CD1	LEU	A	266	6.584	55.619	14.605	1.00	30.32	C
ATOM	1890	CD2	LEU	A	266	4.511	56.820	15.367	1.00	30.03	C
ATOM	1891	C	LEU	A	266	7.885	55.211	17.904	1.00	31.79	C
ATOM	1892	O	LEU	A	266	8.907	55.417	17.231	1.00	31.14	O
ATOM	1893	N	ILE	A	267	7.706	55.750	19.112	1.00	31.36	N
ATOM	1894	CA	ILE	A	267	8.702	56.661	19.666	1.00	30.41	C
ATOM	1895	CB	ILE	A	267	8.273	57.184	21.052	1.00	29.95	C
ATOM	1896	CG1	ILE	A	267	7.134	58.210	20.924	1.00	30.35	C
ATOM	1897	CD1	ILE	A	267	6.410	58.513	22.271	1.00	30.22	C
ATOM	1898	CG2	ILE	A	267	9.472	57.849	21.751	1.00	28.77	C
ATOM	1899	C	ILE	A	267	10.052	55.956	19.782	1.00	31.85	C
ATOM	1900	O	ILE	A	267	11.093	56.485	19.340	1.00	32.22	O

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ATOM   1901  N   ARG A 268      10.034  54.774  20.388  1.00 32.17           N
ATOM   1902  CA  ARG A 268      11.248  53.988  20.594  1.00 34.65           C
ATOM   1903  CB  ARG A 268      10.927  52.713  21.369  1.00 35.11           C
ATOM   1904  CG  ARG A 268      10.707  52.931  22.864  1.00 39.57           C
ATOM   1905  CD  ARG A 268      10.398  51.637  23.600  1.00 45.10           C
ATOM   1906  NE  ARG A 268       9.725  51.866  24.890  1.00 48.08           N
ATOM   1907  CZ  ARG A 268      10.370  52.338  25.935  1.00 49.97           C
ATOM   1908  NH1 ARG A 268      11.663  52.609  25.806  1.00 53.48           N
ATOM   1909  NH2 ARG A 268       9.753  52.551  27.093  1.00 48.54           N
ATOM   1910  C   ARG A 268      11.921  53.622  19.278  1.00 34.22           C
ATOM   1911  O   ARG A 268      13.140  53.491  19.223  1.00 34.73           O
ATOM   1912  N   TRP A 269      11.124  53.464  18.225  1.00 34.43           N
ATOM   1913  CA  TRP A 269      11.649  53.135  16.889  1.00 34.10           C
ATOM   1914  CB  TRP A 269      10.503  52.657  15.992  1.00 34.69           C
ATOM   1915  CG  TRP A 269      10.921  52.008  14.716  1.00 36.80           C
ATOM   1916  CD1 TRP A 269      12.191  51.632  14.352  1.00 39.30           C
ATOM   1917  NE1 TRP A 269      12.182  51.081  13.090  1.00 38.76           N
ATOM   1918  CE2 TRP A 269      10.895  51.071  12.618  1.00 37.50           C
ATOM   1919  CD2 TRP A 269      10.074  51.669  13.609  1.00 36.90           C
ATOM   1920  CE3 TRP A 269       8.703  51.787  13.359  1.00 35.95           C
ATOM   1921  CZ3 TRP A 269       8.197  51.332  12.136  1.00 37.55           C
ATOM   1922  CH2 TRP A 269       9.047  50.765  11.172  1.00 36.64           C
ATOM   1923  CZ2 TRP A 269      10.392  50.618  11.401  1.00 36.32           C
ATOM   1924  C   TRP A 269      12.346  54.351  16.279  1.00 34.12           C
ATOM   1925  O   TRP A 269      13.461  54.248  15.766  1.00 34.65           O
ATOM   1926  N   CYS A 270      11.704  55.514  16.347  1.00 33.89           N
ATOM   1927  CA  CYS A 270      12.315  56.762  15.881  1.00 33.18           C
ATOM   1928  CB  CYS A 270      11.364  57.958  16.030  1.00 32.73           C
ATOM   1929  SG  CYS A 270       9.894  57.933  14.980  1.00 34.78           S
ATOM   1930  C   CYS A 270      13.593  57.085  16.627  1.00 33.31           C
ATOM   1931  O   CYS A 270      14.471  57.759  16.085  1.00 33.37           O
ATOM   1932  N   LEU A 271      13.686  56.635  17.879  1.00 32.81           N
ATOM   1933  CA  LEU A 271      14.835  56.934  18.711  1.00 33.61           C
ATOM   1934  CB  LEU A 271      14.405  57.342  20.143  1.00 33.79           C
ATOM   1935  CG  LEU A 271      13.573  58.649  20.223  1.00 33.39           C
ATOM   1936  CD1 LEU A 271      13.178  58.971  21.668  1.00 32.58           C
ATOM   1937  CD2 LEU A 271      14.330  59.820  19.602  1.00 29.30           C
ATOM   1938  C   LEU A 271      15.805  55.766  18.761  1.00 34.83           C
ATOM   1939  O   LEU A 271      16.536  55.613  19.727  1.00 34.16           O
ATOM   1940  N   ALA A 272      15.836  54.958  17.705  1.00 35.68           N
ATOM   1941  CA  ALA A 272      16.796  53.853  17.658  1.00 37.00           C
ATOM   1942  CB  ALA A 272      16.563  52.994  16.429  1.00 37.89           C
ATOM   1943  C   ALA A 272      18.191  54.460  17.658  1.00 37.13           C
ATOM   1944  O   ALA A 272      18.436  55.466  16.996  1.00 36.83           O
ATOM   1945  N   LEU A 273      19.087  53.886  18.447  1.00 38.00           N
ATOM   1946  CA  LEU A 273      20.464  54.378  18.537  1.00 39.46           C
ATOM   1947  CB  LEU A 273      21.266  53.531  19.532  1.00 39.79           C
ATOM   1948  CG  LEU A 273      20.990  53.795  21.011  1.00 40.61           C
ATOM   1949  CD1 LEU A 273      21.923  52.966  21.914  1.00 40.75           C
ATOM   1950  CD2 LEU A 273      21.174  55.277  21.304  1.00 39.54           C
ATOM   1951  C   LEU A 273      21.146  54.350  17.168  1.00 40.47           C
ATOM   1952  O   LEU A 273      21.742  55.331  16.747  1.00 40.46           O
ATOM   1953  N   ARG A 274      21.051  53.225  16.470  1.00 41.49           N
ATOM   1954  CA  ARG A 274      21.670  53.138  15.151  1.00 43.63           C
ATOM   1955  CB  ARG A 274      21.929  51.683  14.753  1.00 44.96           C
ATOM   1956  CG  ARG A 274      22.917  50.943  15.665  1.00 51.46           C
ATOM   1957  CD  ARG A 274      23.145  49.470  15.275  1.00 60.47           C
ATOM   1958  NE  ARG A 274      23.426  49.354  13.842  1.00 66.38           N
ATOM   1959  CZ  ARG A 274      23.511  48.212  13.172  1.00 69.93           C
ATOM   1960  NH1 ARG A 274      23.344  47.048  13.792  1.00 71.16           N
ATOM   1961  NH2 ARG A 274      23.775  48.239  11.868  1.00 72.00           N
ATOM   1962  C   ARG A 274      20.784  53.826  14.117  1.00 42.18           C
ATOM   1963  O   ARG A 274      19.632  53.469  13.959  1.00 42.54           O
ATOM   1964  N   PRO A 275      21.325  54.807  13.409  1.00 41.48           N
ATOM   1965  CA  PRO A 275      20.566  55.529  12.383  1.00 41.53           C
ATOM   1966  CB  PRO A 275      21.655  56.302  11.648  1.00 41.70           C
ATOM   1967  CG  PRO A 275      22.618  56.629  12.745  1.00 41.06           C
ATOM   1968  CD  PRO A 275      22.693  55.340  13.546  1.00 41.06           C
ATOM   1969  C   PRO A 275      19.784  54.624  11.429  1.00 41.71           C
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ATOM   1970  O   PRO A 275      18.633  54.932  11.132  1.00 39.61           O
ATOM   1971  N   SER A 276      20.393  53.516  10.993  1.00 41.90           N
ATOM   1972  CA  SER A 276      19.774  52.587  10.040  1.00 42.57           C
ATOM   1973  CB  SER A 276      20.831  51.624   9.446  1.00 43.08           C
ATOM   1974  OG  SER A 276      21.290  50.683  10.419  1.00 45.84           O
ATOM   1975  C   SER A 276      18.597  51.799  10.613  1.00 41.74           C
ATOM   1976  O   SER A 276      17.786  51.287   9.845  1.00 42.39           O
ATOM   1977  N   ASP A 277      18.497  51.696  11.942  1.00 40.48           N
ATOM   1978  CA  ASP A 277      17.344  51.038  12.575  1.00 39.45           C
ATOM   1979  CB  ASP A 277      17.676  50.520  13.981  1.00 40.14           C
ATOM   1980  CG  ASP A 277      18.671  49.374  13.974  1.00 41.45           C
ATOM   1981  OD1 ASP A 277      18.697  48.577  13.010  1.00 43.47           O
ATOM   1982  OD2 ASP A 277      19.471  49.221  14.915  1.00 43.49           O
ATOM   1983  C   ASP A 277      16.102  51.946  12.676  1.00 38.59           C
ATOM   1984  O   ASP A 277      15.010  51.486  13.014  1.00 37.61           O
ATOM   1985  N   ARG A 278      16.269  53.227  12.364  1.00 37.09           N
ATOM   1986  CA  ARG A 278      15.145  54.159  12.448  1.00 35.81           C
ATOM   1987  CB  ARG A 278      15.657  55.598  12.545  1.00 34.54           C
ATOM   1988  CG  ARG A 278      16.407  55.836  13.836  1.00 34.40           C
ATOM   1989  CD  ARG A 278      17.017  57.225  13.957  1.00 35.33           C
ATOM   1990  NE  ARG A 278      18.119  57.186  14.913  1.00 35.31           N
ATOM   1991  CZ  ARG A 278      19.163  57.996  14.913  1.00 36.13           C
ATOM   1992  NH1 ARG A 278      19.286  58.971  14.010  1.00 34.75           N
ATOM   1993  NH2 ARG A 278      20.103  57.815  15.829  1.00 36.28           N
ATOM   1994  C   ARG A 278      14.223  53.983  11.243  1.00 36.08           C
ATOM   1995  O   ARG A 278      14.687  53.610  10.156  1.00 36.69           O
ATOM   1996  N   PRO A 279      12.936  54.275  11.421  1.00 35.45           N
ATOM   1997  CA  PRO A 279      11.984  54.193  10.314  1.00 35.56           C
ATOM   1998  CB  PRO A 279      10.627  54.303  11.004  1.00 35.57           C
ATOM   1999  CG  PRO A 279      10.915  55.147  12.224  1.00 35.53           C
ATOM   2000  CD  PRO A 279      12.284  54.710  12.677  1.00 35.37           C
ATOM   2001  C   PRO A 279      12.174  55.322   9.311  1.00 35.53           C
ATOM   2002  O   PRO A 279      12.784  56.354   9.626  1.00 35.63           O
ATOM   2003  N   THR A 280      11.661  55.107   8.101  1.00 34.85           N
ATOM   2004  CA  THR A 280      11.618  56.145   7.079  1.00 34.43           C
ATOM   2005  CB  THR A 280      11.509  55.513   5.683  1.00 34.63           C
ATOM   2006  OG1 THR A 280      10.344  54.690   5.655  1.00 34.43           O
ATOM   2007  CG2 THR A 280      12.712  54.555   5.379  1.00 35.88           C
ATOM   2008  C   THR A 280      10.334  56.900   7.337  1.00 34.28           C
ATOM   2009  O   THR A 280       9.501  56.458   8.120  1.00 33.22           O
ATOM   2010  N   PHE A 281      10.129  58.012   6.637  1.00 35.30           N
ATOM   2011  CA  PHE A 281       8.893  58.771   6.797  1.00 35.82           C
ATOM   2012  CB  PHE A 281       8.892  60.020   5.907  1.00 36.90           C
ATOM   2013  CG  PHE A 281       9.984  61.009   6.223  1.00 38.29           C
ATOM   2014  CD1 PHE A 281      10.332  61.300   7.536  1.00 39.19           C
ATOM   2015  CE1 PHE A 281      11.320  62.234   7.823  1.00 39.73           C
ATOM   2016  CZ  PHE A 281      11.968  62.874   6.810  1.00 41.57           C
ATOM   2017  CE2 PHE A 281      11.621  62.608   5.483  1.00 43.04           C
ATOM   2018  CD2 PHE A 281      10.633  61.681   5.200  1.00 41.16           C
ATOM   2019  C   PHE A 281       7.690  57.894   6.477  1.00 36.17           C
ATOM   2020  O   PHE A 281       6.671  57.924   7.179  1.00 35.36           O
ATOM   2021  N   GLU A 282       7.815  57.101   5.414  1.00 35.33           N
ATOM   2022  CA  GLU A 282       6.741  56.194   4.992  1.00 35.04           C
ATOM   2023  CB  GLU A 282       7.154  55.461   3.700  1.00 35.95           C
ATOM   2024  CG  GLU A 282       6.092  54.530   3.141  1.00 38.88           C
ATOM   2025  CD  GLU A 282       6.504  53.872   1.819  1.00 42.76           C
ATOM   2026  OE1 GLU A 282       7.654  54.056   1.362  1.00 43.67           O
ATOM   2027  OE2 GLU A 282       5.654  53.182   1.233  1.00 43.19           O
ATOM   2028  C   GLU A 282       6.385  55.199   6.084  1.00 34.27           C
ATOM   2029  O   GLU A 282       5.209  54.986   6.378  1.00 34.51           O
ATOM   2030  N   GLU A 283       7.397  54.594   6.693  1.00 34.18           N
ATOM   2031  CA  GLU A 283       7.194  53.640   7.795  1.00 34.58           C
ATOM   2032  CB  GLU A 283       8.512  53.012   8.208  1.00 35.26           C
ATOM   2033  CG  GLU A 283       9.077  52.096   7.131  1.00 38.60           C
ATOM   2034  CD  GLU A 283      10.406  51.501   7.502  1.00 40.02           C
ATOM   2035  OE1 GLU A 283      11.340  52.257   7.832  1.00 41.52           O
ATOM   2036  OE2 GLU A 283      10.517  50.266   7.435  1.00 44.14           O
ATOM   2037  C   GLU A 283       6.524  54.259   9.014  1.00 33.96           C
ATOM   2038  O   GLU A 283       5.700  53.614   9.674  1.00 33.93           O
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ATOM	2039	N	ILE	A	284	6.859	55.517	9.298	1.00 33.26	N
ATOM	2040	CA	ILE	A	284	6.204	56.233	10.401	1.00 31.63	C
ATOM	2041	CB	ILE	A	284	6.889	57.590	10.650	1.00 31.52	C
ATOM	2042	CG1	ILE	A	284	8.282	57.373	11.252	1.00 29.17	C
ATOM	2043	CD1	ILE	A	284	9.195	58.585	11.190	1.00 32.09	C
ATOM	2044	CG2	ILE	A	284	6.002	58.489	11.602	1.00 29.23	C
ATOM	2045	C	ILE	A	284	4.732	56.430	10.089	1.00 31.80	C
ATOM	2046	O	ILE	A	284	3.856	56.165	10.917	1.00 31.97	O
ATOM	2047	N	GLN	A	285	4.451	56.917	8.886	1.00 32.64	N
ATOM	2048	CA	GLN	A	285	3.070	57.204	8.515	1.00 32.77	C
ATOM	2049	CB	GLN	A	285	3.022	58.099	7.280	1.00 32.86	C
ATOM	2050	CG	GLN	A	285	3.373	59.566	7.613	1.00 32.93	C
ATOM	2051	CD	GLN	A	285	3.056	60.507	6.485	1.00 35.30	C
ATOM	2052	OE1	GLN	A	285	3.637	60.401	5.395	1.00 34.32	O
ATOM	2053	NE2	GLN	A	285	2.122	61.423	6.725	1.00 33.69	N
ATOM	2054	C	GLN	A	285	2.239	55.948	8.334	1.00 33.74	C
ATOM	2055	O	GLN	A	285	1.021	55.996	8.454	1.00 34.52	O
ATOM	2056	N	ASN	A	286	2.889	54.816	8.084	1.00 34.59	N
ATOM	2057	CA	ASN	A	286	2.165	53.533	8.016	1.00 36.22	C
ATOM	2058	CB	ASN	A	286	2.770	52.607	6.966	1.00 35.90	C
ATOM	2059	CG	ASN	A	286	2.450	53.042	5.553	1.00 37.57	C
ATOM	2060	OD1	ASN	A	286	1.397	53.611	5.283	1.00 37.74	O
ATOM	2061	ND2	ASN	A	286	3.373	52.785	4.642	1.00 39.91	N
ATOM	2062	C	ASN	A	286	2.079	52.805	9.360	1.00 36.58	C
ATOM	2063	O	ASN	A	286	1.432	51.767	9.466	1.00 37.11	O
ATOM	2064	N	HIS	A	287	2.723	53.356	10.384	1.00 36.48	N
ATOM	2065	CA	HIS	A	287	2.677	52.771	11.717	1.00 36.00	C
ATOM	2066	CB	HIS	A	287	3.525	53.596	12.697	1.00 35.69	C
ATOM	2067	CG	HIS	A	287	3.703	52.938	14.029	1.00 33.97	C
ATOM	2068	ND1	HIS	A	287	4.826	52.211	14.359	1.00 35.79	N
ATOM	2069	CE1	HIS	A	287	4.706	51.749	15.592	1.00 34.10	C
ATOM	2070	NE2	HIS	A	287	3.537	52.138	16.066	1.00 36.32	N
ATOM	2071	CD2	HIS	A	287	2.888	52.875	15.103	1.00 33.02	C
ATOM	2072	C	HIS	A	287	1.238	52.724	12.223	1.00 36.98	C
ATOM	2073	O	HIS	A	287	0.475	53.663	11.985	1.00 36.67	O
ATOM	2074	N	PRO	A	288	0.870	51.638	12.909	1.00 37.63	N
ATOM	2075	CA	PRO	A	288	-0.465	51.480	13.468	1.00 38.40	C
ATOM	2076	CB	PRO	A	288	-0.318	50.203	14.315	1.00 39.46	C
ATOM	2077	CG	PRO	A	288	0.684	49.420	13.576	1.00 40.31	C
ATOM	2078	CD	PRO	A	288	1.699	50.447	13.174	1.00 38.01	C
ATOM	2079	C	PRO	A	288	-0.936	52.652	14.325	1.00 37.78	C
ATOM	2080	O	PRO	A	288	-2.096	53.024	14.227	1.00 38.92	O
ATOM	2081	N	TRP	A	289	-0.062	53.231	15.143	1.00 37.99	N
ATOM	2082	CA	TRP	A	289	-0.459	54.387	15.951	1.00 36.84	C
ATOM	2083	CB	TRP	A	289	0.642	54.779	16.932	1.00 37.43	C
ATOM	2084	CG	TRP	A	289	0.197	55.892	17.862	1.00 36.44	C
ATOM	2085	CD1	TRP	A	289	-0.601	55.776	18.969	1.00 36.79	C
ATOM	2086	NE1	TRP	A	289	-0.800	57.014	19.542	1.00 35.91	N
ATOM	2087	CE2	TRP	A	289	-0.136	57.956	18.795	1.00 35.04	C
ATOM	2088	CD2	TRP	A	289	0.500	57.281	17.730	1.00 35.44	C
ATOM	2089	CE3	TRP	A	289	1.275	58.034	16.822	1.00 34.75	C
ATOM	2090	CZ3	TRP	A	289	1.365	59.412	17.000	1.00 33.10	C
ATOM	2091	CH2	TRP	A	289	0.719	60.046	18.072	1.00 32.65	C
ATOM	2092	CZ2	TRP	A	289	-0.024	59.337	18.980	1.00 35.41	C
ATOM	2093	C	TRP	A	289	-0.886	55.598	15.102	1.00 37.02	C
ATOM	2094	O	TRP	A	289	-1.703	56.402	15.551	1.00 36.85	O
ATOM	2095	N	MET	A	290	-0.375	55.704	13.875	1.00 37.67	N
ATOM	2096	CA	MET	A	290	-0.681	56.857	13.002	1.00 39.50	C
ATOM	2097	CB	MET	A	290	0.475	57.119	12.038	1.00 38.69	C
ATOM	2098	CG	MET	A	290	1.770	57.552	12.737	1.00 39.97	C
ATOM	2099	SD	MET	A	290	2.026	59.340	12.660	1.00 43.39	S
ATOM	2100	CE	MET	A	290	0.826	59.826	13.609	1.00 36.57	C
ATOM	2101	C	MET	A	290	-1.973	56.787	12.186	1.00 41.20	C
ATOM	2102	O	MET	A	290	-2.269	57.703	11.397	1.00 40.58	O
ATOM	2103	N	GLN	A	291	-2.735	55.709	12.338	1.00 43.28	N
ATOM	2104	CA	GLN	A	291	-3.928	55.516	11.504	1.00 45.49	C
ATOM	2105	CB	GLN	A	291	-4.294	54.031	11.420	1.00 46.70	C
ATOM	2106	CG	GLN	A	291	-3.169	53.163	10.863	1.00 52.12	C
ATOM	2107	CD	GLN	A	291	-2.989	53.257	9.330	1.00 58.53	C

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ATOM   2108  OE1 GLN A 291      -3.107  54.339   8.723  1.00 59.20           O
ATOM   2109  NE2 GLN A 291      -2.674  52.113   8.708  1.00 62.36           N
ATOM   2110  C   GLN A 291      -5.112  56.329  12.001  1.00 45.68           C
ATOM   2111  O   GLN A 291      -5.165  56.708  13.177  1.00 45.87           O
ATOM   2112  N   ASP A 292      -6.064  56.590  11.100  1.00 46.07           N
ATOM   2113  CA  ASP A 292      -7.305  57.331  11.410  1.00 46.57           C
ATOM   2114  CB  ASP A 292      -8.195  56.556  12.391  1.00 47.72           C
ATOM   2115  CG  ASP A 292      -8.324  55.099  12.018  1.00 52.03           C
ATOM   2116  OD1 ASP A 292      -8.714  54.836  10.858  1.00 54.96           O
ATOM   2117  OD2 ASP A 292      -8.031  54.164  12.805  1.00 56.19           O
ATOM   2118  C   ASP A 292      -7.071  58.739  11.961  1.00 45.48           C
ATOM   2119  O   ASP A 292      -7.779  59.181  12.880  1.00 44.34           O
ATOM   2120  N   VAL A 293      -6.067  59.433  11.424  1.00 44.87           N
ATOM   2121  CA  VAL A 293      -5.750  60.787  11.882  1.00 44.61           C
ATOM   2122  CB  VAL A 293      -4.495  61.338  11.181  1.00 44.85           C
ATOM   2123  CG1 VAL A 293      -4.791  61.662   9.735  1.00 44.77           C
ATOM   2124  CG2 VAL A 293      -3.989  62.568  11.896  1.00 43.11           C
ATOM   2125  C   VAL A 293      -6.935  61.709  11.640  1.00 44.94           C
ATOM   2126  O   VAL A 293      -7.658  61.532  10.653  1.00 45.74           O
ATOM   2127  N   LEU A 294      -7.149  62.668  12.538  1.00 44.60           N
ATOM   2128  CA  LEU A 294      -8.209  63.650  12.354  1.00 44.83           C
ATOM   2129  CB  LEU A 294      -8.489  64.416  13.641  1.00 43.88           C
ATOM   2130  CG  LEU A 294      -9.009  63.721  14.886  1.00 44.35           C
ATOM   2131  CD1 LEU A 294      -9.118  64.760  15.972  1.00 42.61           C
ATOM   2132  CD2 LEU A 294     -10.337  63.036  14.632  1.00 45.06           C
ATOM   2133  C   LEU A 294      -7.763  64.655  11.312  1.00 45.35           C
ATOM   2134  O   LEU A 294      -6.570  64.888  11.142  1.00 45.48           O
ATOM   2135  N   LEU A 295      -8.728  65.266  10.629  1.00 46.10           N
ATOM   2136  CA  LEU A 295      -8.444  66.358   9.712  1.00 46.34           C
ATOM   2137  CB  LEU A 295      -9.645  66.586   8.790  1.00 47.42           C
ATOM   2138  CG  LEU A 295      -9.552  65.968   7.380  1.00 50.24           C
ATOM   2139  CD1 LEU A 295      -9.352  64.460   7.415  1.00 51.66           C
ATOM   2140  CD2 LEU A 295     -10.812  66.288   6.595  1.00 54.37           C
ATOM   2141  C   LEU A 295      -8.123  67.612  10.527  1.00 46.02           C
ATOM   2142  O   LEU A 295      -8.531  67.723  11.693  1.00 44.80           O
ATOM   2143  N   PRO A 296      -7.366  68.544   9.955  1.00 46.46           N
ATOM   2144  CA  PRO A 296      -7.048  69.790  10.658  1.00 47.09           C
ATOM   2145  CB  PRO A 296      -6.405  70.633   9.561  1.00 46.93           C
ATOM   2146  CG  PRO A 296      -5.698  69.609   8.741  1.00 45.84           C
ATOM   2147  CD  PRO A 296      -6.708  68.496   8.638  1.00 46.93           C
ATOM   2148  C   PRO A 296      -8.282  70.465  11.266  1.00 48.28           C
ATOM   2149  O   PRO A 296      -8.280  70.739  12.474  1.00 47.68           O
ATOM   2150  N   GLN A 297      -9.335  70.684  10.480  1.00 50.01           N
ATOM   2151  CA  GLN A 297     -10.537  71.328  11.022  1.00 51.78           C
ATOM   2152  CB  GLN A 297     -11.572  71.636   9.933  1.00 52.87           C
ATOM   2153  CG  GLN A 297     -12.552  72.781  10.298  1.00 55.96           C
ATOM   2154  CD  GLN A 297     -11.858  74.122  10.632  1.00 60.05           C
ATOM   2155  OE1 GLN A 297     -11.221  74.739   9.765  1.00 62.29           O
ATOM   2156  NE2 GLN A 297     -11.992  74.570  11.884  1.00 60.16           N
ATOM   2157  C   GLN A 297     -11.175  70.550  12.181  1.00 51.71           C
ATOM   2158  O   GLN A 297     -11.536  71.140  13.201  1.00 52.21           O
ATOM   2159  N   GLU A 298     -11.292  69.234  12.034  1.00 51.63           N
ATOM   2160  CA  GLU A 298     -11.819  68.391  13.108  1.00 51.67           C
ATOM   2161  CB  GLU A 298     -11.714  66.922  12.736  1.00 52.61           C
ATOM   2162  CG  GLU A 298     -12.716  66.406  11.732  1.00 56.45           C
ATOM   2163  CD  GLU A 298     -12.568  64.908  11.552  1.00 60.37           C
ATOM   2164  OE1 GLU A 298     -11.606  64.480  10.874  1.00 61.21           O
ATOM   2165  OE2 GLU A 298     -13.403  64.160  12.112  1.00 63.66           O
ATOM   2166  C   GLU A 298     -10.991  68.586  14.372  1.00 50.78           C
ATOM   2167  O   GLU A 298     -11.523  68.666  15.490  1.00 50.03           O
ATOM   2168  N   THR A 299      -9.676  68.624  14.186  1.00 49.28           N
ATOM   2169  CA  THR A 299      -8.756  68.812  15.291  1.00 48.32           C
ATOM   2170  CB  THR A 299      -7.310  68.855  14.781  1.00 48.02           C
ATOM   2171  OG1 THR A 299      -7.007  67.636  14.096  1.00 45.02           O
ATOM   2172  CG2 THR A 299      -6.324  68.910  15.951  1.00 47.18           C
ATOM   2173  C   THR A 299      -9.072  70.095  16.040  1.00 48.76           C
ATOM   2174  O   THR A 299      -9.135  70.101  17.268  1.00 47.62           O
ATOM   2175  N   ALA A 300      -9.252  71.181  15.293  1.00 49.46           N
ATOM   2176  CA  ALA A 300      -9.540  72.468  15.887  1.00 50.94           C
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ATOM   2177  CB  ALA A 300      -9.541  73.556  14.820  1.00 50.83           C
ATOM   2178  C   ALA A 300     -10.875  72.438  16.664  1.00 51.99           C
ATOM   2179  O   ALA A 300     -10.961  72.940  17.793  1.00 51.96           O
ATOM   2180  N   GLU A 301     -11.896  71.832  16.064  1.00 53.05           N
ATOM   2181  CA  GLU A 301     -13.218  71.757  16.689  1.00 54.49           C
ATOM   2182  CB  GLU A 301     -14.220  71.094  15.754  1.00 55.03           C
ATOM   2183  CG  GLU A 301     -14.926  72.073  14.831  1.00 58.47           C
ATOM   2184  CD  GLU A 301     -15.129  71.518  13.429  1.00 61.94           C
ATOM   2185  OE1 GLU A 301     -15.418  70.303  13.287  1.00 62.49           O
ATOM   2186  OE2 GLU A 301     -15.006  72.306  12.459  1.00 64.87           O
ATOM   2187  C   GLU A 301     -13.177  71.018  18.026  1.00 54.40           C
ATOM   2188  O   GLU A 301     -13.652  71.536  19.048  1.00 54.62           O
ATOM   2189  N   ILE A 302     -12.581  69.826  18.011  1.00 54.14           N
ATOM   2190  CA  ILE A 302     -12.487  68.970  19.196  1.00 53.52           C
ATOM   2191  CB  ILE A 302     -12.124  67.529  18.791  1.00 53.66           C
ATOM   2192  CG1 ILE A 302     -13.150  66.981  17.795  1.00 53.26           C
ATOM   2193  CD1 ILE A 302     -12.813  65.609  17.254  1.00 52.59           C
ATOM   2194  CG2 ILE A 302     -12.047  66.624  20.026  1.00 53.65           C
ATOM   2195  C   ILE A 302     -11.496  69.462  20.246  1.00 53.50           C
ATOM   2196  O   ILE A 302     -11.800  69.422  21.440  1.00 53.33           O
ATOM   2197  N   HIS A 303     -10.322  69.937  19.822  1.00 53.16           N
ATOM   2198  CA  HIS A 303      -9.258  70.220  20.793  1.00 53.02           C
ATOM   2199  CB  HIS A 303      -8.018  69.390  20.459  1.00 51.63           C
ATOM   2200  CG  HIS A 303      -8.212  67.926  20.680  1.00 47.34           C
ATOM   2201  ND1 HIS A 303      -8.396  67.043  19.640  1.00 45.24           N
ATOM   2202  CE1 HIS A 303      -8.540  65.822  20.119  1.00 42.60           C
ATOM   2203  NE2 HIS A 303      -8.456  65.883  21.437  1.00 42.67           N
ATOM   2204  CD2 HIS A 303      -8.251  67.188  21.815  1.00 43.90           C
ATOM   2205  C   HIS A 303      -8.861  71.671  20.960  1.00 54.55           C
ATOM   2206  O   HIS A 303      -8.265  72.036  21.979  1.00 54.31           O
ATOM   2207  N   LEU A 304      -9.168  72.500  19.966  1.00 56.55           N
ATOM   2208  CA  LEU A 304      -8.696  73.876  19.999  1.00 59.36           C
ATOM   2209  CB  LEU A 304      -7.967  74.211  18.701  1.00 58.46           C
ATOM   2210  CG  LEU A 304      -6.479  73.870  18.549  1.00 58.16           C
ATOM   2211  CD1 LEU A 304      -6.026  72.669  19.390  1.00 55.35           C
ATOM   2212  CD2 LEU A 304      -6.160  73.653  17.061  1.00 56.12           C
ATOM   2213  C   LEU A 304      -9.832  74.873  20.273  1.00 62.12           C
ATOM   2214  O   LEU A 304      -9.586  76.067  20.431  1.00 62.18           O
ATOM   2215  N   HIS A 305     -11.061  74.361  20.340  1.00 65.89           N
ATOM   2216  CA  HIS A 305     -12.278  75.150  20.571  1.00 69.84           C
ATOM   2217  CB  HIS A 305     -12.201  75.963  21.884  1.00 70.73           C
ATOM   2218  CG  HIS A 305     -11.780  75.138  23.069  1.00 74.80           C
ATOM   2219  ND1 HIS A 305     -12.611  74.206  23.664  1.00 77.77           N
ATOM   2220  CE1 HIS A 305     -11.976  73.629  24.674  1.00 78.93           C
ATOM   2221  NE2 HIS A 305     -10.760  74.149  24.753  1.00 79.02           N
ATOM   2222  CD2 HIS A 305     -10.611  75.093  23.760  1.00 77.72           C
ATOM   2223  C   HIS A 305     -12.591  76.047  19.382  1.00 71.35           C
ATOM   2224  O   HIS A 305     -12.458  77.272  19.463  1.00 72.07           O
ATOM   2225  N   SER A 306     -12.998  75.426  18.275  1.00 73.04           N
ATOM   2226  CA  SER A 306     -13.372  76.161  17.066  1.00 74.54           C
ATOM   2227  CB  SER A 306     -12.563  75.685  15.850  1.00 74.28           C
ATOM   2228  OG  SER A 306     -11.270  76.309  15.843  1.00 74.68           O
ATOM   2229  C   SER A 306     -14.878  76.061  16.804  1.00 75.41           C
ATOM   2230  O   SER A 306     -15.588  77.080  16.858  1.00 76.03           O
ATOM   2231  OXT SER A 306     -15.397  74.966  16.542  1.00 75.98           O
ATOM   2232  N3  IMD I   1       8.128  71.298  26.439  1.00 62.13           N
ATOM   2233  C4  IMD I   1       8.441  71.428  27.755  1.00 62.64           C
ATOM   2234  C5  IMD I   1       7.731  72.513  28.267  1.00 61.10           C
ATOM   2235  C2  IMD I   1       7.245  72.276  26.125  1.00 61.77           C
ATOM   2236  N1  IMD I   1       7.001  73.016  27.242  1.00 61.00           N
ATOM   2237  O   HOH W   1      -0.732  54.528   9.728  1.00 45.36           O
ATOM   2238  O   HOH W   2      19.630  58.716   6.576  1.00 43.01           O
ATOM   2239  O   HOH W   3       0.310  61.264   2.849  1.00 32.73           O
ATOM   2240  O   HOH W   4      18.440  64.206  21.527  1.00 32.96           O
ATOM   2241  O   HOH W   5      12.988  80.668   8.424  1.00 39.01           O
ATOM   2242  O   HOH W   6      -1.368  51.617  30.489  1.00 40.35           O
ATOM   2243  O   HOH W   7      16.488  75.633  10.896  1.00 39.22           O
ATOM   2244  O   HOH W   8      22.715  62.695   4.286  1.00 41.65           O
ATOM   2245  O   HOH W   9      15.546  67.975   9.969  1.00 34.80           O
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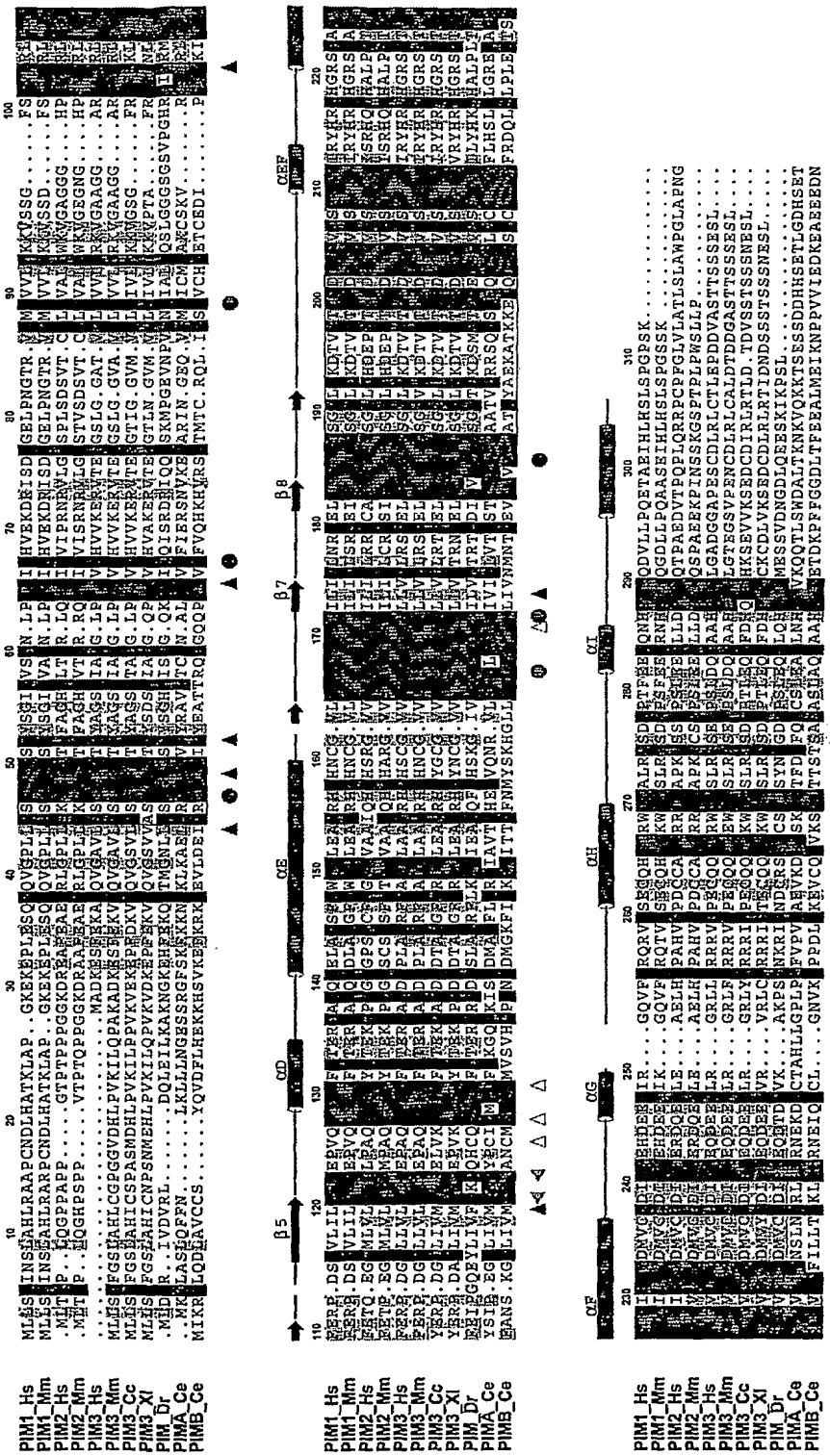
ATOM	2246	O	HOH	W	10	9.873	57.733	3.200	1.00	34.66	O
ATOM	2247	O	HOH	W	11	22.041	77.197	8.223	1.00	59.58	O
ATOM	2248	O	HOH	W	12	13.921	68.295	7.801	1.00	43.48	O
ATOM	2249	O	HOH	W	13	-2.001	49.454	29.335	1.00	40.96	O
ATOM	2250	O	HOH	W	14	22.261	59.914	10.882	1.00	37.32	O
ATOM	2251	O	HOH	W	15	19.419	50.734	16.966	1.00	40.82	O
ATOM	2252	O	HOH	W	16	15.338	57.159	9.022	1.00	39.03	O
ATOM	2253	O	HOH	W	17	17.961	66.549	9.882	1.00	39.50	O
ATOM	2254	O	HOH	W	18	4.818	76.341	0.545	1.00	44.94	O
ATOM	2255	O	HOH	W	19	8.855	79.196	7.518	1.00	39.17	O
ATOM	2256	O	HOH	W	20	17.072	54.130	21.844	1.00	43.20	O
ATOM	2257	O	HOH	W	21	1.325	69.587	7.110	1.00	36.36	O
ATOM	2258	O	HOH	W	22	8.150	61.656	1.220	1.00	40.26	O
ATOM	2259	O	HOH	W	23	-4.435	66.666	10.979	1.00	43.16	O
ATOM	2260	O	HOH	W	24	10.513	80.713	9.117	1.00	42.28	O
ATOM	2261	O	HOH	W	25	15.497	65.164	24.557	1.00	34.79	O
ATOM	2262	O	HOH	W	26	9.900	52.831	3.589	1.00	42.40	O
ATOM	2263	O	HOH	W	27	-0.200	71.719	8.387	1.00	41.34	O
ATOM	2264	O	HOH	W	28	-7.398	59.982	15.551	1.00	40.20	O
ATOM	2265	O	HOH	W	29	3.492	81.322	21.013	1.00	47.98	O
ATOM	2266	O	HOH	W	30	-4.714	67.425	25.026	1.00	43.45	O
ATOM	2267	O	HOH	W	31	15.251	68.122	12.673	1.00	36.68	O
ATOM	2268	O	HOH	W	32	-5.709	62.260	15.119	1.00	39.90	O
ATOM	2269	O	HOH	W	33	4.553	83.955	11.446	1.00	45.99	O
ATOM	2270	O	HOH	W	34	18.791	57.169	28.057	1.00	43.68	O
ATOM	2271	O	HOH	W	35	18.231	65.464	14.872	1.00	37.87	O
ATOM	2272	O	HOH	W	36	8.971	53.789	30.860	1.00	43.70	O
ATOM	2273	O	HOH	W	37	5.180	50.983	9.900	1.00	39.96	O
ATOM	2274	O	HOH	W	38	-4.081	60.211	25.479	1.00	43.04	O
ATOM	2275	O	HOH	W	39	-1.650	50.298	24.953	1.00	50.05	O
ATOM	2276	O	HOH	W	40	-0.323	79.686	2.181	1.00	64.08	O
ATOM	2277	O	HOH	W	41	-4.014	58.332	9.232	1.00	45.77	O
ATOM	2278	O	HOH	W	42	10.273	50.306	18.899	1.00	43.91	O
ATOM	2279	O	HOH	W	43	16.890	54.883	8.955	1.00	43.73	O
ATOM	2280	O	HOH	W	44	3.730	65.993	2.097	1.00	44.04	O
ATOM	2281	O	HOH	W	45	23.972	70.563	2.275	1.00	40.95	O
ATOM	2282	O	HOH	W	46	24.633	58.602	10.052	1.00	42.68	O
ATOM	2283	O	HOH	W	47	19.828	61.618	4.358	1.00	51.38	O
ATOM	2284	O	HOH	W	48	22.517	90.823	15.952	1.00	70.96	O
ATOM	2285	O	HOH	W	49	29.354	60.921	3.167	1.00	57.58	O
ATOM	2286	O	HOH	W	50	11.468	82.369	12.289	1.00	50.02	O
ATOM	2287	O	HOH	W	51	24.772	62.519	-4.121	1.00	45.22	O
ATOM	2288	O	HOH	W	52	3.211	68.554	31.582	1.00	69.57	O
ATOM	2289	O	HOH	W	53	7.936	50.002	23.124	1.00	47.40	O
ATOM	2290	O	HOH	W	54	15.587	71.212	17.046	1.00	52.35	O
ATOM	2291	O	HOH	W	55	15.884	79.008	-3.580	1.00	56.72	O
ATOM	2292	O	HOH	W	56	25.279	56.110	10.230	1.00	44.21	O
ATOM	2293	O	HOH	W	57	12.514	58.767	4.837	1.00	52.23	O
ATOM	2294	O	HOH	W	58	1.688	78.234	4.543	1.00	43.74	O
ATOM	2295	O	HOH	W	59	9.018	82.803	11.168	1.00	50.76	O
ATOM	2296	O	HOH	W	60	-0.217	85.742	6.096	1.00	53.93	O
ATOM	2297	O	HOH	W	61	-2.930	82.309	21.772	1.00	58.06	O
ATOM	2298	O	HOH	W	62	5.504	51.225	5.130	1.00	48.90	O
ATOM	2299	O	HOH	W	63	20.076	54.469	7.350	1.00	61.18	O
ATOM	2300	O	HOH	W	64	5.722	68.809	-1.934	1.00	59.42	O
ATOM	2301	O	HOH	W	65	27.882	66.292	-1.512	1.00	65.79	O
ATOM	2302	O	HOH	W	66	19.676	72.153	23.229	1.00	61.17	O
ATOM	2303	O	HOH	W	67	-5.501	71.414	5.301	1.00	61.16	O
ATOM	2304	O	HOH	W	68	15.016	58.056	6.473	1.00	49.90	O
ATOM	2305	O	HOH	W	69	-2.012	55.730	6.130	1.00	56.99	O
ATOM	2306	O	HOH	W	70	-9.447	70.188	7.682	1.00	57.22	O
ATOM	2307	O	HOH	W	71	2.484	55.120	-0.038	1.00	49.25	O
ATOM	2308	O	HOH	W	72	-7.908	59.237	8.479	1.00	65.73	O
ATOM	2309	O	HOH	W	73	22.353	73.255	11.764	1.00	60.74	O
ATOM	2310	O	HOH	W	74	19.477	67.324	11.857	1.00	50.67	O
ATOM	2311	O	HOH	W	75	14.506	47.970	13.280	1.00	62.36	O
ATOM	2312	O	HOH	W	76	16.862	47.807	8.768	1.00	52.55	O
ATOM	2313	O	HOH	W	77	13.313	53.083	32.098	1.00	54.43	O
ATOM	2314	O	HOH	W	78	17.503	50.798	19.041	1.00	55.72	O

ATOM	2315	O	HOH W	79	-12.736	62.094	18.189	1.00 53.56	O
ATOM	2316	O	HOH W	80	33.908	62.979	10.712	1.00 63.79	O
ATOM	2317	O	HOH W	81	-6.870	60.605	22.628	1.00 49.67	O
ATOM	2318	O	HOH W	82	9.987	47.582	14.046	1.00 66.52	O
ATOM	2319	O	HOH W	83	23.183	73.287	2.510	1.00 52.15	O
ATOM	2320	O	HOH W	84	27.578	55.770	9.060	1.00 63.00	O
ATOM	2321	O	HOH W	85	5.576	82.970	-1.748	1.00 62.58	O
ATOM	2322	O	HOH W	86	-0.509	84.330	3.857	1.00 59.32	O
ATOM	2323	O	HOH W	87	13.665	91.473	-3.552	1.00 61.08	O
ATOM	2324	O	HOH W	88	-2.861	75.397	-2.038	1.00 63.22	O
ATOM	2325	O	HOH W	89	10.204	73.979	29.790	1.00 66.32	O
ATOM	2326	O	HOH W	90	20.070	78.983	6.971	1.00 67.67	O
ATOM	2327	O	HOH W	91	17.169	77.347	21.910	1.00 65.17	O
ATOM	2328	O	HOH W	92	-2.870	53.045	18.163	1.00 59.47	O
ATOM	2329	O	HOH W	93	11.627	71.628	23.440	1.00 63.19	O
ATOM	2330	O	HOH W	94	8.310	74.960	-2.678	1.00 55.47	O
ATOM	2331	O	HOH W	95	-12.002	78.851	4.304	1.00 58.94	O
ATOM	2332	O	HOH W	96	5.566	49.157	22.796	1.00 51.78	O
ATOM	2333	O	HOH W	97	31.358	61.478	0.597	1.00 66.61	O
ATOM	2334	O	HOH W	98	24.035	64.093	-2.091	1.00 47.25	O
ATOM	2335	O	HOH W	99	11.294	69.111	34.295	1.00 70.13	O
ATOM	2336	O	HOH W	100	18.999	64.123	-2.168	1.00 62.14	O
ATOM	2337	O	HOH W	101	-9.739	61.493	7.698	1.00 82.68	O
ATOM	2338	O	HOH W	102	22.435	52.025	25.439	1.00 54.62	O
ATOM	2339	O	HOH W	103	5.045	49.276	12.114	1.00 55.83	O
ATOM	2340	O	HOH W	104	-3.965	50.524	12.224	1.00 62.13	O
ATOM	2341	O	HOH W	105	13.472	75.945	26.250	1.00 61.94	O
ATOM	2342	O	HOH W	106	15.560	72.156	26.297	1.00 58.39	O
ATOM	2343	O	HOH W	107	-0.195	96.034	19.635	1.00 69.60	O
ATOM	2344	O	HOH W	108	1.243	88.090	-4.031	1.00 62.22	O
ATOM	2345	O	HOH W	109	19.973	83.759	20.581	1.00 71.41	O
ATOM	2346	O	HOH W	110	-8.152	73.486	8.288	1.00 53.47	O
ATOM	2347	O	HOH W	111	23.420	81.722	9.233	1.00 71.36	O
ATOM	2348	O	HOH W	112	1.596	82.691	-0.096	1.00 71.76	O
ATOM	2349	O	HOH W	113	5.657	56.059	-1.336	1.00 61.94	O
ATOM	2350	O	HOH W	114	13.967	51.575	8.374	1.00 5 .56	O
ATOM	2351	O	HOH W	115	12.416	78.389	25.200	1.00 60.19	O
ATOM	2352	O	HOH W	116	17.235	83.392	11.447	1.00 52.25	O
ATOM	2353	O	HOH W	117	14.767	52.852	21.314	1.00 47.79	O
ATOM	2354	O	HOH W	118	19.075	60.231	-4.028	1.00 64.58	O
ATOM	2355	O	HOH W	119	25.476	66.800	28.823	1.00 55.96	O
ATOM	2356	O	HOH W	120	4.473	70.021	30.020	1.00 56.80	O
ATOM	2357	O	HOH W	121	8.400	80.051	18.580	1.00 47.86	O
ATOM	2358	O	HOH W	122	-0.274	81.374	6.467	1.00 70.59	O
ATOM	2359	O	HOH W	123	8.016	51.083	3.826	1.00 50.11	O
ATOM	2360	O	HOH W	124	-5.762	55.323	8.603	1.00 59.77	O
ATOM	2361	O	HOH W	125	24.801	94.210	-1.115	1.00 67.33	O
ATOM	2362	O	HOH W	126	9.710	48.669	26.328	1.00 63.06	O
ATOM	2363	O	HOH W	127	8.684	99.063	14.167	1.00 63.47	O
ATOM	2364	O	HOH W	128	19.451	83.648	8.511	1.00 51.41	O
ATOM	2365	O	HOH W	129	-10.889	61.955	10.215	1.00 55.28	O
ATOM	2366	O	HOH W	130	-4.253	61.866	27.652	1.00 61.67	O
ATOM	2367	O	HOH W	131	27.030	90.340	3.848	1.00 80.85	O
ATOM	2368	O	HOH W	132	10.977	87.131	22.623	1.00 65.06	O
ATOM	2369	O	HOH W	133	14.634	65.394	-2.521	1.00 56.18	O
ATOM	2370	O	HOH W	134	-3.405	52.808	20.692	1.00 57.93	O
ATOM	2371	O	HOH W	135	-5.420	55.451	15.525	1.00 51.90	O
ATOM	2372	O	HOH W	136	8.056	79.671	22.675	1.00 59.54	O
ATOM	2373	O	HOH W	137	28.392	57.786	4.755	1.00 78.57	O
ATOM	2374	O	HOH W	138	18.312	99.689	9.767	1.00 61.28	O
ATOM	2375	O	HOH W	139	33.446	63.253	17.723	1.00 59.53	O
ATOM	2376	O	HOH W	140	24.283	56.206	17.474	1.00 54.00	O
ATOM	2377	O	HOH W	141	16.808	50.392	32.500	1.00 57.59	O
ATOM	2378	O	HOH W	142	15.746	83.812	-7.461	1.00 64.85	O
ATOM	2379	O	HOH W	143	-7.082	94.424	-2.169	1.00 67.76	O
ATOM	2380	O	HOH W	144	13.631	49.312	10.749	1.00 54.19	O
ATOM	2381	O	HOH W	145	30.247	61.193	23.440	1.00 71.27	O
ATOM	2382	O	HOH W	146	13.010	80.075	-6.528	1.00 68.99	O



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                                   β1        β2                   β3                     αC
                          10        20         30  40            50         60           70        80
PHKG1:2phk_            ........TRDAALPGSHSTHGFYENYE.PKEILGRGVSSVVRRCIHKP..........TCKEYAVKIIDVTGGGSFSAEEV..........QELREATLKEVDILRKVSG.
CAMK1:1a06_            .......MPGAVEGPRWKQAEDIRDIYD.FRDVLGTGAFSEVILAEDKR..........TQKLVAIKCIAKKAL...........EGKEGSMENEIAVLHKIK..
CDK2:1e1xA_            ......................MENFQ.KVEKIGEGTYGVVYKARNKL..........TGEVVALKKIRLDTET...........EGVPSTAIREISLLKELN..
CDK6:1blxA             ............MEKDGLCRADQQYE.CVAEIGEGAYGKVFKARDLKN..........GGRFVALKRVRVQTGE...........EGMPLSTIREVAVLRHLETF
MAPK12:1cm8A           ..MSSPPPARSGFYRQEVTKTAWEVRAVYRDL.QPVGSGAYGAVCSAVDGR..........TGAKVAIKKLYRPFQS...........ELFAKRAYRELRLLKHMR..
MAPK14:1p38_           ...SQERPTFYRQELNKTIWEVPERYQNL.SPVGSGAYGSVCAAFDTK..........TGHRVAVKKLSRPFQS...........IIHAKRTYRELRLLKHMK..
MAPK10:1jnk_           PTLDVKIAFCQGFDKQVDVSYIAKHYNMSKSKVDNQFYSVEVGDSTFTVLKRYQNL.KPIGSGAQGIVCAAYDAV..........LDRNVAIKKLSRPFQN...........QTHAKRAYRELVLMKCVN..
MAPK1:3erk_            .......AAAAGPEMVRGQVFDVGPRYTNL.SYIGEGAYGMVCSAYDNL..........NKVRVAIKKISPFEH...........QTYCQRTLREIKILLRFR..
HCK:1qcfA              SPRSTFSTLQELVDHYKKGNDGLCQKLSVPCMSSKPQK.PWEKDAWEIPRESLK.LEKKLGAGQFGEVWMATYNK..........HTKVAVKTMKPG...........SMSVEAFLAEANVMKTLQ..
LCK:1qpcA              ..........KPWWEDEWEVPRETLK.LVERLGAGQFGEVWMGYYNG..........HTKVAVKSLKQG...........SMSPDAFLAEANLMKQLQ..
SRC:2src_              TSRTQFNSLQQLVAYYSKHADGLCHRLTTVCPTSKPQTQGLAKDAWEIPRESLR.LEVKLGQGCFGEVWMGTWNG..........TTRVAIKTLKPG...........TMSPEAFLQEAQVMKKLR..
ABL1:1iepA             ........GAMDPSSPNYDKWEMERTDIT.MKHKLGGGQYGEVYEGVWKK..........YSLTVAVKTLKED...........TMEVEEFLKEAAVMKEIK .
EPHB2:1jpaA            ......GHMTPGMKIFIDPFTFEDPNEAVREFAKEIDISCVK IEQVIGAGEFGEVCSGHLKLPG..........KREIFVAIKTLKSGYT...........EKQRRDFLSEASIMGQFD..
CSK:1bygA              ........MGGSVAAQDEFYRSGWALNMKELK.LLQTIGKGEFGDVMLGDYR..........GNKVAVKCIKN...........DATAQAFLAEASVMTQLR..
KDR:1vr2A              ......MDPDELPLDEHCERLPYDASKWEFPRDRLK.LGKPLGRGAFGQVIEADAFGIDK..........TATCRTVAVKMLKEGAT...........HSEHRALMSELKILIHIGH.
FGFR1:1agwA            ........MVAGVSEYELPEDPRWELPRDRLV.LGKPLGEGAFGQVVLAEAIGLDKD..........KPNRVTKVAVKMLKSDAT...........EKDLSDLISEMEMMKMIGK.
TEK:1fvrA              ..MKKHHHHHHGKNNPDPTIYPVLDWNDIK.FQDVIGEGNFGQVLKARIKKD..........GLRMDAAIKRMKEYAS...........KDDHRDFAGELEVLCKLGH.
IGF1R:1k3aA            ........VPDEWEVAREKIT.MSRELGQGSFGMVYEGVAKGVVK..........DEPETRVAIKTVNEAAS...........MRERIEFLNEASVMKEFN..
INSR:1lr3A             ......VFPSSVFVPDEWEVSREKIT.LLRELGQGSFGMVYEGNARDIIK..........GEAETRVAVKTVNESAS...........LRERIEFLNEASVMKGFT..
GSK3B:1h8fA            ....SKVTTVVATPGQGPDRPQEVSYTDT.KVIGNGSFGVVYQAKLCD..........SGELVAIKKVLQ...........GKAFKNRELQIMRKLD..
TTN:1tklA              ........KELYEKYM.IAEDLGRGEFGIVHRCVETS..........SKKTYMAKFVKVK...........GTDQVLVKKEISILNIAR..
CSNK2A1:1dawA          ......SKARVYADVNVLRPKEYWDYEALTVQWGEQDDYE.VVRKVGRGKYSEVFEGINVN..........NNEKCIIKILKP...........VKKKKIKREIKILQNLCGG
PAK1:1f3mC             ........SDEEILEKLRSIVSVGDPKKKYTRF.EKIGQGASGTVYTAMDVA..........TGQEVAIRQMNLQQ...........QPKKELIINEILVMRENK.
SRPK2:1howA            ........DYRPGGFHPAFKGEPYKDARYI.LVRKLGWGHFSTVWLAKDMV..........NNTHVAMKIVRGD...........KVYTEAAEDEIKLLQRVNDA
PRKACA:1cdkA          ....GNAAAAKKGSEQESVKEFLAKAKEDFLKKWENPAQNTAHLDQFE.RIKTLGTGSFGRVMLVKHKE..........TGNHFAMKILDKQKVVK...........LKQIEHTLNEKRILQAVN..
TGFBR1:1b6cB           .......EDPSLDRPFISEGTTLKDLIYDMTTSGSGSGLPLLVQRTIARTIV.LQESIGKGRFGEVWRGKWR..........GEEVAVKIFSS...........REERSWFREAEIYQTVMLR
CSNK1P:1ckjA          ........MELRVGNRYR.LGRKIGSGSFGDIYLGTDIA..........AGEEVAIKLECV...........KTKHPQLHIESKIYKMMQGG
Src-1:SRC              ...SKHADGLCHRLTTVCPTSKPQTQGLAKDAWEIPRESLR.LEVKLGQGCFGEVWMGTWNG..........TTRVAIKTLKPG...........TMSPEAFLQEAQVMKKLR..
Src-2:HCK              ...KKGNDGLCQKLSVPCMSSKPQKPWEKDAWEIPRESLK.LEKKLGAGQFGEVWMATYNK..........HTKVAVKTMKPG...........SMSVEAFLAEANVMKTLQ.
Src-3:FRK              ..TKTSDGLCVKLGKPCLKIQVPAPFDLSYKTVDQWEIDRNSIQ.LLKRLGSGQFGEVWEGLWNN..........TTPVAVKTLKPG...........SMDPNDFLREAQIMKNLR.
Csk:CSK                ...TSDADGLCTRLIKPKVMEGTVAAQDEFYRSGWALNMKELK.LLQTIGKGEFGDVMLGDYR..........GNKVAVKCIKN...........DATAQAFLAEASVMTQLR
Eph:EPHB2              . ERADSEYTDKLQHYTSGHMTPGMKIYIDPFTYEDPNEAVREFAKEIDISCVK.IEQVIGAGEFGEVCSGHLKLPG..........KREIFVAIKTLKSGYT...........EKQRRDFLSEASIMGQFD..
VEGFR:KDR              IILRTVKRANGGELKTGYLSIVMDPDELPLDEHCERLPYDASKWEFPRDRLK.LGKPLGRGAFGQVIEADAFGIDK..........TATCRTVAVKMLKEGAT...........HSEHRALMSELKILIHIGH.
FGFR:FGFR1             ..TVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLV.LGKPLGEGCFGQVVLAEAIGLDKD..........KPNRVTKVAVKMLKSDAT...........EKDLSDLISEMEMMKMIGK.
CK1:CSNK1D             ........MELRVGNRYR.LGRKIGSGSFGDIYLGTDIA..........AGEEVAIKLECV...........KTKHPQLHIESKIYKMMQGG
JNK:MAPK10             ..LDVKIAFCQGFDKQVDVSYIAKHYNMSKSKVDNQFYSVEVGDSTFTVLKRYQNL.KPIGSGAQGIVCAAYDAV..........LDRNVAIKKLSRPFQN...........QTHAKRAYRELVLMKCVN..
PAK:PAK1               ..SPISPTENNTTPPDALTRNTEKQKKKPKMSDEEILEKLRSIVSVGDPKKKYTRF.EKIGQGASGTVYTAMDVA..........TGQEVAIKQMNLQQ...........QPKKELIINEILVMRENK..
TGFBR-1:TGFBR1         ..HHRVPNEEDPSLDRPFISEGTTLKDLIYDMTTSGSGSGLPLLVQRTIARTIV.LQESIGKGRFGEVWRGKWR..........GEEVAVKIFSS...........REERSWFREAEIYQTVMLR
InsR:INSR              ..GSIYLFLRKRQPDGPLGPLYASSNPEYLSASDVFPCSVYVPDEWEVSREKIT.LLRELGQGSFGMVYEGNARDIIK..........GEAETRVAVKTVNESAS...........LRERIEFLNEASVMKGFT..
CDK-1:CDK2             ........MENFQKV.EKIGEGTYGVVYKARNKL..........TGEVVALKKIRLDTET...........EGVPSTAIREISLLKELN.
CDK-2:CDK6             ........MEKDGLCRADQQYE.CVAEIGEGAYGKVFKARDLKN..........GGRFVALKRVRVQTGE...........EGMPLSTIREVAVLRHLETF
GSK3:GSK3B             ..RTTSFAESCKPVQQPSAFGSMKVSRDKDGSKVTTVVATPGQGPDRPQEVSYTDT.KVIGNGSFGVVYQAKLCD..........SGELVAIKKVLQ...........DKRFKNRELQIMRKLD..
PKA-1:PRKACA           ....MGNAAAAKKGSEQESVKEFLAKAKEDFLKKWESPAQNTAHLDQFERI.KTLGTGSFGRVMLVKHKE..........TGNHYAMKILDKQKVVK...........LKQIEHTLNEKRILQAVN..
CaMK-1:CAMK1           ........MLGAVEGPRWKQAEDIRDIYD.FRDVLGTGAFSEVILAEDKR..........TQKLVAIKCIAKEAL...........EGKEGSMENEIAVLHKIK..
ERK-1:MAPK1            ......MAAAAAAGAGPEMVRGQVFDVGPRYTNL SYIGEGAYGMVCSAYDNV..........NKVRVAIKKISPFEH...........QTYCQRTLREIKILLRFR..
Abl:ABL1               .....STVADGLITTLHYPAPKRNKPTVYGVSPNYDKWEMERTDIT.MKHKLGGGQYGEVYEGVWKK..........YSLTVAVKTLKED...........TMEVEEFLKEAAVMKEIK..
Tie:TEK                ..RANVQRRMAQAFQNVREEPAVQFNSGTLALNRKVKNNPDPTIYPVLDWNDIK.FQDVIGEGNFGQVLKARIKKD..........GLRMDAAIKRMKEYAS...........KDDHRDFAGELEVLCKLGH.
MLCK:TTN               .....EPSEPTITKEDKTRAMNYDEEVDETREVSMTKASHSSTKELYEKYM.IAEDLGRGEFGIVHRCVETS..........SKKTYMAKFVKVK...........GTDQVLVKKEISILNIAR..
p38:MAPK14             ........MSQERPTFYRQELNKTIWEVPERYQNL.SPVGSGAYGSVCAAFDTK..........TGLRVAVKKLSRPFQS...........IIHAKRTYRELRLLKHMK..
PHK:PHKG1              ........MTRDEALPDSHSAQDFYENYE.PKEILGRGVSSVVRRCIHKP..........TSQEYAVKVIDVTGGGSFSPEEV...........RELREATLKEVDILRKVSG.
CK2:CSNK2A1            .....MSGPVPSRARVYTDVNTHRPREYWDYESHVVEWGNQDDYQ.LVRKLGRGKYSEVFEAINIT..........NNEKVVVKILKP...........VKKKKIKREIKILENLRGG
PKA-2:PRKX             ....MEAPGLAQAAAAESDSRKVAEETPDGAPALCPSPEALSPEPPVYSLQDFD.TLATVGTGTFGRVHLVKEKT..........AKHFFALKVMSIPDVIR...........LKQEQHVHNEKSVLKEVS..
PDGFR:PDGFRA           ..IVLVVIWKQKPRYEIRWRVIESISPDGHEYIYVDPMQLPYDSRWEFPRDGLV LGRVLGSGAFGKVVEGTAYGLSR..........SQPVMKVAVKMLKPTAR...........SSEKQALMSELKIMTHLGP.
PKG:PRKG1              ........VSNKAYEDAEAKAKYEAEAAFFANLKLSDFN.IIDTLGVGGFGRVELVQLKSE..........ESKTFAMKILKKRHIVD...........TRQQEHIRSEKQIMQGAH .
Btk:BTK                ......QHNSAGLISRLKYPVSQQNKNAPSTAGLGYGSWEIDPKDLT.FLKELGTGQFGVVKYGKWRG..........QYDVAIKMIKEG...........SMSEDEFIEEAKVMMNLS..
Ret:RET                . MTFRRPAQAFPVSYSSSGARRPSLDSMENQVSVDAFKILEDPKWEFPRKNLV.LGKTLGEGEFGKVVKATAFHLKG..........RAGYTTVAVKMLKENAS...........PSELRDLLSEFNVLKQVN..
Ros:ROS1               .GVTVLINEDKELAELRGLAAGVGLANACYAIHTLPTQEEIENLPAFPREKLT.LRLLLGSGAFGEVYEGTAVDILGV..........GSGEIKVAVKTLKKGST...........DQEKIEFLKEAHLMSKFN..
Fes:FES                ......LSTQQPLTKKSGVVLHRAVPKDKWVLNHEDLV.LGEQIGRGNFGEVFSGRLRA..........DNTLVAVKSCRETLP...........PDLKAKFLQEARILKQYS..
ALK:ALK                ..LQAMQMELQSPEYKLSKLRTSTIMTDYNPNYCFAGKTSSISDLKEVPRKNIT.LIRGLGHGAFGEVYEGQVSGMPN..........DPSPLQVAVKTLPEVCS...........EQDELDFLMEALIISKFN..
CDK-4:CDK7             ........MALDVKSRAKRYEKL.DFLGEGQFATVYKARDKN..........TNQIVAIKKIKLGHRSEAK...........DGINRTALREIKLLQELS..
CDK-3:CDK10            .....MAEPDLECEQIRLKCIRKEGFFTVPPEHRLGRCRSVKEFEKL.NRIGEGTYGIVYRARDTQ..........TDEIVALKKVRMDKEK...........DGIPISSLREITLLLRLR .
Src-4:PTK6             .....RAQSLSHGLRLAAPCRKHEPEPLPHWDDWERPREEFT.LCRKLGSGYFGEVFEGLWKD..........RVQVAIKVISRDN...........LLHQQMLQSEIQAMKKLR..
CaMK-2:CAMK2A          ........MATITCTRFTEEYQ.LFEELGKGAFSVVRRCVKVL..........AGQEYAAKIINTKKLS...........ARDHQKLEREARICRLLK..
CDK9:CDK9              ........MAKQYDSVECPFCDEVSKYEKL.AKIGQGTFGEVFKARHRK..........TGQKVALKKVLMENEK...........EGFPITALREIKILQLLK..
STLK:STK24             ......MAHSPVQSGLPGMQNLKADPEELFTKL.EKIGKGSFGEVFKGIDNR..........TQKVVAIKIIDLEEA...........EDEIEDIQQEITVLSQCD..
MST:STK3               ......MEQPPAPKSKLKKLSEDSLTKQPEEVFD.VLEKLGEGSYGSVFKAIHKE..........SGQVVAIKQVPV...........ESDLQEIIKEISIMQQCD..
GCK:MAP4K2             ........MELRDVSLQDPRDRFE.LLQRVGAGTYGDVYKARDTV..........TSELAAVKIVKLDP...........GDDISSLQQEITILRECR..
NIK:MAP4K4             ......MANDSPAKSLVDIDLSSLRDPAGIFE.LVEVVGNGTYGQVYKGRHVK..........TGQLAAIKVMDVT...........EDEEEEIKLEINMLKKYSH.
LOK:STK10              ......MAFANFRRILRLSTFEKRKSREYEHVRRDLDPNEVWE.IVGELGDGAFGKVYKAKNKE..........TGALAAAKVIETKS...........EEELEDYIVEIEILATCD .
Trk:NTRK1              ..DGLAMSLHFMTLGGSSLSPTEGKGSGLQGHIIENPQYFSDACVHHIKRRDIV.LKWELGEGAFGKVFLAECHNLLP..........EQDKMLVAVKALKEAS...........ESARQDFQREAELLTMLQ .
MuSK:MUSK              ..KNKKRESAAVTLTTLPSELLLDRLHPNPMYQRMPLLLNPKLLSLEYPRNNIE.YVRDIGEGAFGRVFQARAPGLLP..........YEPFTMVAVKMLKEEAS...........ADMQADFQREAALMAEFD..
Ror:ROR1               ..FFICVCRNNQKSSSAPVQRQPKHVRGQNVEMSMLNAYKPKSKAKELPLSAVR FMEELGECAFGKIYKGHLYLPG..........MDHAQLVAIKTLKDYNN...........PQQWMEFQQEASLMAELH..
Akt:AKT1               ........GLKKQEEEEMDFRSGSPSDNSGAEEMEVSLAKPKHRVTMNEFE.YLKLLGKGTFGKVILVKEKA..........TGRYYAMKILKKEVIVA...........KDEVAHTLTENRVLQNSR..
SGK:SGK                ..ACKHPEVQSILKISQPQEPELMNANPSPPPSPSQQINLGPSSNPHAKPSDFH.FLKVIGKGSFGKVLLARHKA..........EEVFYAVKVLQKKAILK...........KKEEKHIMSERNVLLKNVK.
PKC-like:PRKCL1        ..KSSRDPPSSPSSLSSPIQESTAPELPSETQETPGPALCSPLRKSPLTLEDFK.FLAVLGRGHFGKVLLSEFRP..........SGELFAIKALKKGDIVA...........RDEVESLMCEKRILAAVTSA
PKC-classical:PRKCA    ..PIPEGDEEGNMELRQKFEKAKLGPAGNKVISPSEDRKQPSNNLDRVKLTDFN.FLMVLGKGSFGKVMLADRKG..........TEELYAIKILKKDVVIQ...........DDDVECTMVEKRVLALLDK.
PKC-novel:PRKCD        ..SRRSDSASSEPVGIYQGFEKKTGVAGEDMQDNSGTYGKIWEGSSKCNINNFI.FHKVLGKGSFGKVLLGELKG..........RGEYSAIKALKKDVVLI...........DDDVECTMVEKRVLTLAAE.
S6K-1:RPS6KA1-1        ..LMELVPLDPENGQTSGEEAGLQPSKDEGVLKEISITHHVKAGSEKADPSHFE LLKVLGQGSFGKVFLVRKVTRP..........DSGHLYAMKVLKKATLK...........VRDRVRTKMERDILADVN .
CCRK:CCRK              ........MDQYC.ILGRIGEGAHGIVFKAKHVE..........TGEIIALKKVALRRLE...........DGFPNQALREIKALQEMED.
TAO:TAO1               ......MPAGGRAGSLKDPDVAELFFKDDPEKLFSDL.REIGHGSFGAVYFARDVR..........NSEVVAIKKMSYSGKQS...........NEKWQDIIKEVRFLQKLR..
FAK:PTK2               ..SIPKLANSEKQGMRTHAVSVSETDDYAEIIDEEDTYTMPSTRDYEIQRERIE.LGRCIGEGQFGDVHQGIYMSPE..........NPALAVAIKTCKNCTS...........DSVREKFLQEACHYTSLHWN
DDR:DDR1               ..PPPQNSVPHYAEADIVTLQGVTGGNTYAVPALPPGAVGDGPPRVDFPRSRLR.FKEKLGEGQFGEVHLCEVDSPQDLVSLDFPLNVRKGHPLLVAVKILRPDAT...........KNARNDFLKEVKIMSRLK..
CCK4:PTK7              ..MECLNGGPLQNGQPSAEIQEEVALTSLGSGPAATNKRHSTSDKMHFPRSSLQ.PITTIGKSEFGEVFLAKAQGLEE..........GVAETLVLVKSLQSKD...........EQQQLDFRRELEMFGKLN..
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                                     β4                                      β5          αD
                                     90                                      100         110          120
PHKG1:2phk_          ........HPNIIQLKDTYETN..................TFFFLVFDLMKK.GELFDYLTEKVT..................
CAMK1:1a06_          ........HPNIVALDDIYESG..................GHLYLIMQLVSG.GELFDRIVEKGF...................
CDK2:1e1xA_          ........HPNIVKLLDVIHTE..................NKLYLVFEFLH..QDLKKFMDASALTG...............
CDK6:1blxA           E.......HPNVVRLFDVCTVSRTD..............RETKLTLVFEHVD..QDLTTYLDKVPEPG..............
MAPK12:1cm8A         ........HENVIGLLDVFTPDETL..............DDFTDFYLVMPFMG..TDLGXLMKHEK...................
MAPK14:1p38_         ........HENVIGLLDVFTPARSL..............EEFNDVYLVTHLMG..ADLNNIVKCQK..................
MAPK10:1jnk_         ........HKNIISLLNVFTPQKTL..............EEFQDVYLVMELMD..ANLCQVIQME...................
MAPK1:3erk_          ........HENIIGINDIIRAPTIE..............QMKDVYIVQDLME..TDLYKLLKTQH...................
HCK:1qcfA            ........HDKLVKLHAVVTKE..................PIYIITEFMAK.GSLLDFLKSDEGSK...............
LCK:1qpcA            ........HQRLVRLYAVVTQE..................PIYIITEYMEN.GSLVDFLKTPSGIK...............
SRC:2src_            ........HEKLVQLYAVVSEE..................PIYIVTEYMSK.GSLLDFLKGETGKY...............
ABL1:1lepA           ........HPNLVQLLGVCTRE..................PPFYIITEFMTY.GNLLDYLRECNRQE..............
EPHB2:1jpaA          ........HPNVIHLEGVVTKS..................TPVMIITEFMEN.GSLDSFLRQNDGQ...............
CSK:1bygA            ........HSNLVQLLGVIVEEK.................GGLYIVTEYMAK.GSLVDYLRSRGRSV...............
KDR:1vr2A            ........HLNVVNLLGACTKPG.................GPLMVIVEFCKF.GNLSTYLRSKRNEFVPYKV..........
FGFR1:1agwA          ........HKNIINLLGACTQD..................GPLYVIVEYASK.GNLREYLQARRPPGLEYSYNPSHNPEEQ..
TEK:1fvrA            ........HPNIINLLGACEHR..................GYLYLAIEYAPH.GNLLDFLRKSRVLETDPAFAIANSTAST..
IGF1R:1k3aA          ........CHHVVRLLGVVSQG..................QPTLVIMELMTR.GDLKSYLRSLRPEMENNPVLAP........
INSR:1ir3A           ........CHHVVRLLGVVSKG..................QPTLVVMELMAH.GDLKSYLRSLRPEAENNPGRPP........
GSK3B:1h8fA          ........HCNIVRLRYFFYSSGEK...............KDEVYLNLVLDYVP..ETVYRVARHYSRAKQT............
TTN:1tklA            ........HRNILHLHESFESM..................EELVMIFEFISG.LDIFERINTSAFE..................
CSNK2A1:1dawA        ........P.NIVKLLDIVRDQH.................SKTPSLIFEYVNN.TDFKVLYPT....................
PAK1:1f3mC           ........NPNIVNYLDSYLVG..................DELWVVMEYLAG.GSLTDVVTETC....................
SRPK2:1howA          DNT.....KEDSMGANHILKLLDHFNHKGP..........NGVHVVMVFEVLG..ENLLALIKKYEHRG..............
PRKACA:1cdkA         ........FPFLVKLEYSFKDN..................SNLYMVMEYVPG.GEMFSHLRRIGR..................
TGFBR1:1b6cB         ........HENILGFIAADNKDNG................TWTQLWLVSDYHEH.GSLFDYLNRYT..................
CSNK1P:1ckjA         ........V.GIPTIRWCGAEG..................DYNVMVMELLG..PSLEDLFNFCSRK..................
Src-1:SRC            ........HEKLVQLYAVVSEE..................PIYIVTEYMSK.GSLLDFLKGETGKY...............
Src-2:HCK            ........HDKLVKLHAVVTKEP.................IYIITEFMAK.GSLLDFLKSDEGSK................
Src-3:FRK            ........HPKLIQLYAVCTLE..................DPIYIITELMRH.GSLQEYLQNDTGSK...............
Csk:CSK              ........HSNLVQLLGVIVEEK.................GGLYIVTEYMAK.GSLVDYLRSRGRSV...............
Eph:EPHB2            ........HPNVIHLEGVVTKS..................TPVMIITEFMEN GSLDSFLRQNDGQ..................
VEGFR:KDR            ........HLNVVNLLGACTKPG.................GPLMVIVEFCKF.GNLSTYLRSKRNEFVPYKTKGARFRQGKDYV..............GAIPV
FGFR:FGFR1           ........HKNIINLLGACTQD..................GPLYVIVEYASK.GNLREYLQARRPPGLEYCYNPSHNPEEQ.
CK1:CSNK1D           ........V GIPTIRWCGAEG..................DYNVMVMELLG..PSLEDLFNFCSRK..................
JNK:MAPK10           ........HKNIISLLNVFTPQKTL...............EEFQDVYLVMELMD..ANLCQVIQME...................
PAK:PAK1             ........NPNIVNYLDSYLVG..................DELWVVMEYLAG.GSLTDVVTETC....................
TGFBR-1.TGFBR1       ........HENILGFIAADNKDNG................TWTQLWLVSDYHEH.GSLFDYLNRYT..................
InsR:INSR            ........CHHVVRLLGVVSKG..................QPTLVVMELMAH.GDLKSYLRSLRPEAENNPGRPP........
CDK-1:CDK2           ........HPNIVKLLDVIHTE..................NKLYLVFEFLH .QDLKKFMDASALTG...............
CDK-2:CDK6           E.......HPNVVRLFDVCTVSRTD...............RETKLTLVFEHVD..QDLTTYLDKVPEPG..............
GSK3:GSK3B           ........HCNIVRLRYFFYSSGEK...............KDEVYLNLVLDYVP..ETVYRVARHYSRAKQT............
PKA-1:PRKACA         ........FPFLVKLEFSFKDN..................SNLYMVMEYVPG.GEMFSHLRRIGR..................
CaMK-1:CAMK1         ........HPNIVALDDIYESG..................GHLYLIMQLVSG.GELFDRIVEKGF...................
ERK-1:MAPK1          ........HENIIGINDIIRAPTIE...............QMKDVYIVQDLME..TDLYKLLKTQH...................
Abl:ABL1             ........HPNLVQLLGVCTRE..................PPFYIITEFMTY.GNLLDYLRECNRQE..............
Tie:TEK              ........HPNIINLLGACEHR..................GYLYLAIEYAPH.GNLLDFLRKSRVLETDPAFAIANSTAST..
MLCK:TTN             ........HRNILHLHESFESM..................EELVMIFEFISG.LDIFERINTSAFE..................
p38:MAPK14           ........HENVIGLLDVFTPARSL...............EEFNDVYLVTHLMG..ADLNNIVKCQK..................
PHK:PHKG1            ........HPNIIQLKDTYETN..................TFFFLVFDLMKR.GELFDYLTEKVT..................
CK2:CSNK2A1          ........P.NIITLADIVKDPV.................SRTPALVFEHVNN.TDFKQLYQT....................
PKA-2:PRKX           ........HPFLIRLFWTWHDE..................RFLYMLMEYVPG GELFSYLRNRGR..................
PDGFR:PDGFRA         ........HLNIVNLLGACTKS..................GPIYIITEYCFY.GDLVNYLHKNRDSFLSHHPEKPKKELDIFGLNPADESTRSYVILSFENNGDYMDMKQADTTQYVPMLE
PKG:PRKG1            ........SDFIVRLYRTFKDS..................KYLYMLMEACLG.GELWTILRDRGS..................
Btk:BTK              ........HEKLVQLYGVCTKQ..................RPIFIITEYMAN.GCLLNYLREMRHR..................
Ret:RET              ........HPHVIKLYGACSQD..................GPLLLIVEYAKY.GSLRGFLRESRKVGPGYLGSGGSRNSSSLDHPDERA...
Ros:ROS1             ........HPNILKQLGVCLLN..................EPQYIILELMEG.GDLLTYLRKARMATFYGPL..........
Fes:FES              ........HPNIVRLIGVCTQK..................QPIYIVMELVQG.GDFLTFLRTEGAR...................
ALK:ALK              ........HQNIVRCIGVSLQS..................LPRFILLELMAG.GDLKSFLRETRPRPSQPSS..........
CDK-4:CDK7           ........HPNIIGLLDAFGHK..................SNISLVFDFME..TDLEVIIKDNSLV..................
CDK-3:CDK10          ........HPNIVELKEVVVGNH.................LESIFLVMGYCE..QDLASLLENMPTP..................
Src-4:PTK6           ........HKHILALYAVVSVG..................DPVYIITELMAK.GSLLELLRDSDEKV..................
CaMK-2:CAMK2A        ........HPNIVRLHDSISEE..................GHHYLIFDLVTG.GELFEDIVAREY..................
CDK9:CDK9            ........HENVVNLIEICRTKASPY..............NRCKGSIYLVFDFCE..HDLAGLLSNVLVK...............
STLK:STK24           ........SPYVTKYYGSYLKD..................TKLWIIMEYLGG.GSALDLLEPGP...................
MST:STK3             ........SPYVVKYYGSYFKN..................TDLWIVMEYCGA GSVSDIIRLRNKT..................
GCK:MAP4K2           ........HPNVVAYIGSYLRN..................DRLWICMEFCGG.GSLQEIYHATGP...................
NIK:MAP4K4           ........HRNIATYYGAFIKKSPP...............GHDDQLWLVMEFCGA.GSITDLVKNTKGNT................
LOK:STK10            ........HPYIVKLLGAYYHD..................GKLWIMIEFCPG.GAVDAIMLELDRG..................
Trk:NTRK1            ........HQHIVRFFGVCTEG..................RPLLMVFEYMRH.GDLNRFLRSHGPDAKLLAGGEDVAPGP.........
MuSK:MUSK            ........NPNIVKLLGVCAVG..................KPMCLLFEYMAY.GDLNEFLRSMSPHTVCSLSHSDLSMRAQVSSPGPPP....
Ror:ROR1             ........HPNIVCLLGAVTQE..................QPVCMLFEYINQ.GDLHEFLIMRSPHSDVGCSSDEDGTVKSS.........
Akt:AKT1             ........HPFLTALKYSFQTH..................DRLCFVMEYANG GELFFHLSRERV..................
SGK:SGK              ........HPFLVGLHFSFQTA..................DKLYFVLDYING GELFYHLQRERC..................
PKC-like:PRKCL1      G.......HPFLVNLFGCFQTP..................EHVCFVMEYSAG.GDLMLHIHSDV..................
PKC-classical:PRKCA  ........PPFLTQLHSCFQTV..................DRLYFVMEYVNG.GDLMYHIQQVGK..................
PKC-novel:PRKCD      ........NPFLTHLICTFQTK..................DHLFFVMEFLNG.GDLMYHIQDKGR..................
S6K-1:RPS6KA1-1      ........HPFVVKLHYAFQTE..................GKLYLILDFLRG.GDLFTRLSKEVM..................
CCRK:CCRK            ........NQYVVQLKAVFPHG..................GGFVLAFEFML..SDLAEVVRHAQRP..................
TAO:TAO1             ........HPNTIQYRGCYLRE..................HTAWLVMEYCL..GSASDLLEVHKKP..................
FAK.PTK2             WCRYISDPNVDACPDPRNAELTMRQFDHPHIVKLIGVITEN...PVWIIMELCTL.GELRSFLQVRKYS..................
DDR:DDR1             ........DPNIIRLLGVCVQD..................DPLCMITDYMEN.GDLNQFLSAHQLEDKAAEGAPGDGQAAQGPT.........
CCK4:PTK7            ........HANVVRLLGLCREA..................EPHYMVLEYVDL.GDLKQFLRISKSKDEKLKSQP..................
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	αE (130–140)	β7 (150–160)	β8 (170)
PHKG1:2phk_	LSEKETRKIMRALLEVICALHK	LNIVHRDLKPENILLDDD	MNIKLTDFGFSCQLDPGEK
CAMK1:1a06_	YTERDASRLIFQVLDAVKYLHD	LGIVHRDLKPENLLYYSLDE	DSKIMISDFGLSKMEDPGSV
CDK2:1e1xA	IPLPLIKSYLFQLLQGLAFCHS	HRVLHRDLKPQNLLINTE	GAIKLADFGLARAFGVPVRT
CDK6:1blxA	VPTETIKDMMFQLLRGLDFLHS	HRVVHRDLKPQNILVTSS	GQIKLADFGLARIYSFQMA
MAPK12:1cm8A	LGEDRIQFLVYQMLKGLRYIHA	AGIIHRDLKPGNLAVNED	CELKILDFGLARQADSE
MAPK14:1p38_	LTDDHVQFLIYQILRGLKYIHS	ADIIHRDLKPSNLAVNED	CELKILDFGLARHTDDE
MAPK10:1jnk_	LDHERMSYLLYQMLCGIKHLHS	AGIIHRDLKPSNIVVKSD	CTLKILDFGLARTAGTSFM
MAPK1:3erk_	LSNDHICYFLYQILRGLKYIHS	ANVLHRDLKPSNLLLNTT	CDLKICDFGLARVADPDHDHTGF
HCK:1qcfA	QPLPKLIDFSAQIAEGMAFIEQ	RNYIHRDLRAANILVSAS	LVCKIADFGLARVIEDNEYTA
LCK:1qpcA	LTINKLLDMAAQIAEGMAFIEE	RNYIHRDLRAANILVSDT	LSCKIADFGLARLIEDNEXTA
SRC:2src_	LRLPQLVDMAAQIASGMAYVER	MNYVHRDLRAANILVGEN	LVCKVADFGLARLIEDNEYTA
ABL1:1iepA	VSAVVLLYMATQISSAMEYLEK	KNFIHRDLAARNCLVGEN	HLVKVADFGLSRLMTGDTYTA
EPHB2:1jpaA	FTVIQLVGMLRGIAAGMKYLAD	MNYVHRDLAARNILVNSN	LVCKVSDFGLSRFLEDDTSDPTYTS
CSK:1bygA	LGGDCLLKFSLDVCEAMEYLEG	NNFVHRDLAARNVLVSED	NVAKVSDFGLTKEASST
KDR:1vr2A	APEDLYKDFLTLEHLICYSFQVAKGMEFLAS	RKCIHRDLAARNILLSEK	NVVKICDFGLARDIYKDPDXVR
FGFR1:1agwA	LSSKDLVSCAYQVARGMEYLAS	KKCIHRDLAARNVLVTED	NVMKIADFGLARDIHHIDYYKK
TEK:1fvrA	LSSQQLLHFAADVARGMDYLSQ	KQFIHRDLAARNILVGEN	YVAKIADFGL.SRGQEVYVK
IGF1R:1k3aA	PSLSKMIQMAGEIADGMAYLNA	NKFVHRDLAARNCMVAED	FTVKIGDFGMTRDIXETDXXRK
INSR:1ir3A	PTLQEMIQMAAEIADGMAYLNA	KKFVHRDLAARNCMVAHD	FTVKIGDFGMTRDIXETDXXRK
GSK3B:1h8fA	LPVIYVKLYMYQLFRSLAYIHS	FGICHRDIKPQNLLLDPD	TAVLKLCDFGSAKQLVRGEP
TTN:1tklA	LNEREIVSYVHQVCEALQFLHS	HNIGHFDIRPENIIYQTRR	SSTIKIIEFGQARQLKPGD
CSNK2A1:1dawA	LTDYDIRYYIYELLKALDYCHS	QGIMHRDVKPHNVMIDHE	LRKLRLIDWGLAEFYHPGKE
PAK1:1f3mC	MDEGQIAAVCRECLQALEFLHS	NQVIHRDIKSDNILLGMD	GSVKLTDFGFCAQITPEQSK
SRPK2:1howA	IPLIYVKQISKQLLLGLDYMHRR	CGIIHTDIKPENVLMEIVDSP	ENLIQIKIADLGNACWYDEH
PRKACA:1cdkA	FSEPHARFYAAQIVLTFEYLHS	LDLIYRDLKPENLLIDQQ	GYIQVTDFGFAKRVKGR
TGFBR1:1b6cB	VTVEGMIKLALSTASGLAHLHMEIVGTQG	KPAIAHRDLKSKNILVKKN	GTCCIADLGLAVRHDSATDTIDIA
CSNK1P:1ckjA	FSLKTVLLLADQMISRIEYIHS	KNFIHRDVKPDNFLMGLGKK	GNLVYIIDFGLAKKYRDARTHQHIPYRE
Src-1:SRC	LRLPQLVDMAAQIASGMAYVER	MNYVHRDLRAANILVGEN	LVCKVADFGLARLIEDNEYTA
Src-2:HCK	QPLPKLIDFSAQIAEGMAFIEQ	RNYIHRDLRAANILVSAS	LVCKIADFGLARVIEDNEYTA
Src-3:FRK	IHLTQQVDMAAQVASGMAYLES	RNYIHRDLAARNVLVGEHN	IYKVADFGLARVFKVDNEDIYES
Csk:CSK	LGGDCLLKFSLDVCEAMEYLEG	NNFVHRDLAARNVLVSED	NVAKVSDFGLTKEASST
Eph:EPHB2	FTVIQLVGMLRGIAAGMKYLAD	MNYVHRDLAARNILVNSN	LVCKVSDFGLSRFLEDDTSDPTYTS
VEGFR:KDR	DLKRRLDSITSSQSSASSGFVEEKSLSDVEEEEAPEDLYKDFLTLEHLICYSFQVAKGMEFLAS	RKCIHRDLAARNILLSEK	NVVKICDFGLARDIYKDPDYVR
FGFR:FGFR1	LSSKDLVSCAYQVARGMEYLAS	KKCIHRDLAARNVLVTED	NVMKIADFGLARDIHHIDYYKK
CK1:CSNK1D	FSLKTVLLLADQMISRIEYIHS	KNFIHRDVKPDNFLMGLGKK	GNLVYIIDFGLAKKYRDARTHQHIPYRE
JNK:MAPK10	LDHERMSYLLYQMLCGIKHLHS	AGIIHRDLKPSNIVVKSD	CTLKILDFGLARTAGTSFM
PAK:PAK1	MDEGQIAAVCRECLQALEFLHS	NQVIHRDIKSDNILLGMD	GSVKLTDFGFCAQITPEQSK
TGFBR-1:TGFBR1	VTVEGMIKLALSTASGLAHLHMEIVGTQG	KPAIAHRDLKSKNILVKKN	GTCCIADLGLAVRHDSATDTIDIA
InsR:INSR	PTLQEMIQMAAEIADGMAYLNA	KKFVHRDLAARNCMVAHD	FTVKIGDFGMTRDIYETDYYRK
CDK-1:CDK2	IPLPLIKSYLFQLLQGLAFCHS	HRVLHRDLKPQNLLINTEG	AIKLADFGLARAFGVPVRT
CDK-2:CDK6	VPTETIKDMMFQLLRGLDFLHS	HRVVHRDLKPQNILVTSS	GQIKLADFGLARIYSFQMA
GSK3:GSK3B	LPVIYVKLYMYQLFRSLAYIHS	FGICHRDIKPQNLLLDPDT	AVLKLCDFGSAKQLVRGEP
PKA-1:PRKACA	FSEPHARFYAAQIVLTFEYLHS	LDLIYRDLKPENLLIDQQ	GYIQVTDFGFAKRVKGR
CaMK-1:CAMK1	YTERDASRLIFQVLDAVKYLHD	LGIVHRDLKPENLLYYSLDE	DSKIMISDFGLSKMEDPGSV
ERK-1:MAPK1	LSNDHICYFLYQILRGLKYIHS	ANVLHRDLKPSNLLLNTT	CDLKICDFGLARVADPDHDHTGF
Abl:ABL1	VNAVVLLYMATQISSAMEYLEK	KNFIHRDLAARNCLVGEN	HLVKVADFGLSRLMTGDTYTA
Tie:TEK	LSSQQLLHFAADVARGMDYLSQ	KQFIHRDLAARNILVGEN	YVAKIADFGLSRGQEVYVK
MLCK:TTN	LNEREIVSYVHQVCEALQFLHS	HNIGHFDIRPENIIYQTRR	SSTIKIIEFGQARQLKPGD
p38:MAPK14	LTDDHVQFLIYQILRGLKYIHS	ADIIHRDLKPSNLAVNED	CELKILDFGLARHTDDE
PHK:PHKG1	LSEKETRKIMRALLEVICTLHK	LNIVHRDLKPENILLDDN	MNIKLTDFGFSCQLEPGER
CK2:CSNK2A1	LTDYDIRFYMYEILKALDYCHS	MGIMHRDVKPHNVMIDHEH	RKLRLIDWGLAEFYHPGQE
PKA-2:PRKX	FSSTTGLFYSAEIICALEYLHS	KEIVYRDLKPENILLDRD	GHIKITDFGFAXXLVDR
PDGFR:PDGFRA	RKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSFTYQVARGMEFLAS	KNCVHRDLAARNVLLAQG	KIVKICDFGLARDIMHDSNYV
PK[illegible]RKG1	FEDSTTRFYTACVVEAFAYLHS	KGIIYRDLKPENLILDHR	GYAKLVDFGFAKKIGFGKK
Bt[illegible]K	FQTQQLLEMCKDVCEAMEYLES	KQFLHRDLAARNCLVNDQ	GVVKVSDFGLSRYVLDDEYTS
Re[illegible]	LTMGDLISFAWQISQGMQYLAE	MKLVHRDLAARNILVAEG	RKMKISDFGLSRDVYEEDSYVK
Ro[illegible]ROS1	LTLVDLVDLCVDISKGCVYLER	MHFIHRDLAARNCLVSVKDY	TSPRIVKIGDFGLARDIYKNDYYRK
Fe[illegible]ES	LRVKTLLQMVGDAAAGMEYLES	KCCIHRDLAARNCLVTEKN	VLKISDFGMSREEADGVYAAS
AL[illegible]ALK	LAMLDLLHVARDIACGCQYLEE	NHFIHRDIAARNCLLTCPGP	GRVAKIGDFGMARDIYRASYYRK
CD[illegible]-4:CDK7	LTPSHIKAYMLMTLQGLEYLHQ	HWILHRDLKPNNLLLDEN	GVLKLADFGLAKSFGSPNRA
CDK-3:CDK10	FSEAQVKCIVLQVLRGLQYLHR	NFIIHRDLKVSNLLMTDK	GCVKTADFGLARAYGVPVKP
Src-4:PTK6	LPVSELLDIAWQVAEGMCYLES	QNYIHRDLAARNILVGEN	TLCKVGDFGLARLIKEDVYL
CaMK-2:CAMK2A	YSEADASHCIQQILEAVLHCHQ	MGVVHRDLKPENLLLASKLK	GAAVKLADFGLAIEVEGEQQA
CDK9:CDK9	FTLSEIKRVMQMLLNGLYYIHR	NKILHRDMKAANVLITRD	GVLKLADFGLARAFSLAKNSQPNR
STLK:STK24	LDETQIATILREILKGLDYLHS	EKKIHRDIKAANVLLSEH	GEVKLADFGVAGQLTDTQIK
MST:STK3	LIEDEIATILKSTLKGLEYLHF	MRKIHRDIKAGNILLNTE	GHAKLADFGVAGQLTDTMAK
GCK:MAP4K2	LEERQIAYVCRERLKGLHHLHS	QGKIHRDIKGANLLLTLQ	GDVKLADFGVSGELTASVAK
NIK:MAP4K4	LKEDWIAYISREILRGLAHLHI	HHVIHRDIKGQNVLLTEN	AEVKLVDFGVSAQLDRTVGR
LOK:STK10	LTEPQIQVVCRQMLEALNFLHS	KRIIHRDLKAGNVLMTLE	GDIRLADFGVSAKNLKTLQK
Trk:NTRK1	LGLGQLLAVASQVAAGMVYLAG	LHFVHRDLATRNCLVGQG	LVVKIGDFGMSRDIYSTDYYRV
MuSK:MUSK	LSCAEQLCIARQVAAGMAYLSE	RKFVHRDLATRNCLVGEN	MVVKIADFGLSRNIYSADYYKA
Ror:ROR1	LDHGDFLHIAIQIAAGMEYLSS	HFFVHKDLAARNILIGEQ	LHVKISDLGLSREIYSADYYRV
Akt:AKT1	FSEDRARFYGAEIVSALDYLHSE	KNVVYRDLKLENLMLDKD	GHIKITDFGLCKEGIKDGAT
SGK:SGK	FLEPRARFYAAEIASALGYLHS	LNIVYRDLKPENILLDSQ	GHIVLTDFGLCKENIEHNST
PKC-like:PRKCL1	FSEPRAIFYSACVVLGLQFLHE	HKIVYRDLKLDNLLLDTE	GYVKIADFGLCKEGMGYGDR
PKC-classical:PRKCA	FKEPQAVFYAAEISIGLFFLHK	RGIIYRDLKLDNVMLDSE	GHIKIADFGMCKEHMMDGVT
PKC-novel:PRKCD	FELYRATFYAAEIMCGLQFLHS	KGIIYRDLKLDNVLLDRD	GHIKIADFGMCKENIFGESR
S6K-1:RPS6KA1-1	FTEEDVKFYLAELALGLDHLHS	LGIIYRDLKPENILLDEE	GHIKLTDFGLSKEAIDHEKK
CCRK:CCRK	LAQAQVKSYLQMLLKGVAFCHA	NNIVHRDLKPANLLISAS	GQLKIADFGLARVFSPDGSRLYT
TAO:TAO1	LQEVEIAAVTHGALQGLAYLHS	HNMIHRDVKAGNILLSEP	GLVKLGDFGSASIMAP
FAK:PTK2	LDLASLILYAYQLSTALAYLES	KRFVHRDIAARNVLVSSN	DCVKLGDFGLSRYMEDSTYYK
DDR:DDR1	ISYPMLLHVAAQIASGMRYLAT	LNFVHRDLATRNCLVGEN	FTIKIADFGMSRNLYAGDYYRV
CCK4:PTK7	LSTKQKVALCTQVALGMEHLSN	NRFVHKDLAARNCLVSAQ	RQVKVSALGLSKDVYNSEYYH

SUBSTITUTE SHEET (RULE 26)

	αEF (180–200)	αF (210–220)	230	αG (240)	250
PHKG1:2phk_	LREVCGT.PSYLAPEIIECSMNDNHPG	YGKEVDMWSTGVIMYTLLA G	SPPFWH	RKQMLMLRMIMS	GNYQFGS
CAMK1:1a06_	LSTACGT.PGYVAPEVLAQKP	YSKAVDCWSIGVIAYILLC.G	YPPFYD	ENDAKLFEQILK	AEYEFDS
CDK2:1e1xA	YTHEVVT.LWYRAPEILLGCKY	YSTAVDIWSLGCIFAEMVTR	RALFPG	DSEIDQLFRIFRTLGTPDEVVWPGVTS	MPDYKPSFPKWARQ
CDK6:1blxA	LTSVVVT.LWYRAPEVLLQSS	YATPVDLWSVGCIFAEMFRR	KPLFRG	SSDVDQLGKILDVIGLPGEEDWPRDVA.	LPRQAFHSKSAQ
MAPK12:1cm8A	MXGXVVT.RWYRAPEVILNWMR	YTQTVDIWSVGCIMAEMIT.G	KTLFKG.	SDHLDQLKEIMKVTGTPPAEFVQRLQSDEAKNY	MKGL. ..PELEKK
MAPK14:1p38_	MTGYVAT.RWYRAPEIMLNWMH	YNQTVDIWSVGCIMAELLT.G	RTLFPG	TDHIDQLKLILRLVGTPGAELLKKISSESARNY	IQSL ...AQMPKM
MAPK10:1jnk_	MTPYVVT.RYYRAPEVILG.MG.	YKENVDIWSVGCIMGEMVRH	KILFPG	RDYIDQWNKVIEQLGTPCPEFMKKLQ.PTVRNY	VENR ...PKYAGL
MAPK1:3erk_	LTEYVAT.RWYRAPEIMLNSKG.	YTKSIDIWSVGCILAEMLSN	RPIFPG	KHYLDQLNHILGILGSPSQEDLNCIINLKARNY	LLSL....PHKNKV
HCK:1qcfA	REGAKFP.IKWTAPEAINFGS	FTIKSDVWSFGILLMEIVTYG	RIPYPG	MSNPEVIRALER	GYRMPR
LCK:1qpcA	REGAKFP.IKWTAPEAINYGT	FTIKSDVWSFGILLTEIVTHG	RIPYPG	MTNPEVIQNLER	GYRMVR
SRC:2src_	RQGAKFP.IKWTAPEAALYGR	FTIKSDVWSFGILLTELTTKG	RVPYPG	MVNREVLDQVER	GYRMPC
ABL1:1iepA	HAGAKFP.IKWTAPESLAYNK	FSIKSDVWAFGVLLWEIATYG	MSPYPG	IDLSQVYELLEK	DYRMER
EPHB2:1jpaA	ALGGKIP.IRWTAPEAIQYRK	FTSASDVWSYGIVMWEVMSYG	ERPYWD	MTNQDVINAIEQ	DYRLPP
CSK:1bygA	QDTGKLP.VKWTAPEALREKK	FSTKSDVWSFGILLWEIYSFG	RVPYPR	IPLKDVVPRVEK	GYKMDA
KDR:1vr2A	KGDARLP.LKWMAPETIFDRV	YTIQSDVWSFGVLLWEIFSLG	ASPYPGV	KIDEEFCRRLKE	GTRMRA
FGFR1:1agwA	TTNGRLP.VKWMAPEALFDRI	YTHQSDVWSFGVLLWEIFTLG	GSPYPG	VPVEELFKLLKE	GHRMDK
TEK:1fvrA	KTMGRLP.VRWMAIESLNYSV	YTTNSDVWSYGVLLWEIVSLG	GTPYCG	MTCAELYEKLPQ	GYRLEK
IGF1R:1k3aA	GGKGLLP.VRWMSPESLKDGV	FTTYSDVWSFGVVLWEIATLA	EQPYQG.	LSNEQVLRFVME	GGLLDK
INSR:1ir3A	GGKGLLP.VRWMAPESLKDGV	FTTSSDMWSFGVVLWEITSLA	EQPYQG	LSNEQVLKFVMD	GGYLDQ
GSK3B:1h8fA	NVSYICS.RYYRAPELIFGATD	YTSSIDVWSAGCVLAELLL.G	QPIFPG	DSGVDQLVEIIKVLGTPTREQIREMNP	NYTEFAFPQIKAH
TTN:1tklA	NFRLLFTAPEYYAPEVHQHDV	VSTATDMWSLGTLVYVLLS.G	INPFLA	ETNQQIIENIMN.	AEYTF
CSNK2A1:1dawA	YNVRVAS.RYFKGPELLVDLQD	YDYSLDMWSLGCMFAGMIFRK	EPFFYG	HDNHDQLVKIAKVLGTDGLNVYLNKYRIELDPQ	LEALV ..GRHSRK
PAK1:1f3mC	RSTMVGT PYWMAPEVVTRKA	YGPKVDIWSLGIMAIEMIE.G	EPPYLN	ENPLRALYLIAT	NGTPELQN
SRPK2:1howA	YTNSIQT.REYRSPEVLLGAP	WGCGADIWSTACLIFELIT G	DFLFEPDEGHSYT	KDDDHIAQIIELLGELPSYLLRNGKYTRTFFN	SRGLLRNISKLKFW
PRKACA:1cdkA	TWTLCGT.PEYLAPEIILSKG	YNKAVDWWALGVLIYEMAA.G	YPPFFA	DQPIQIYEKIVS	GKVRF
TGFBR1:1b6cB	PNHRVGT.KRYMAPEVLDDSINMKHFE.	SFKRADIYAMGLVFWEIARRCSIGGIHEDYQLPYYDLVPSD		PSVEEMRKVVCE	QKLRPNI
CSNK1P:1ckjA	NKNLTGT.ARYASINTHLGIE	QSRRDDLESLGYVLMYFNL.G	SLPWQGLKAATKR	QKYERISEKKMS.	T
Src-1:SRC	RQGAKFP IKWTAPEAALYGR	FTIKSDVWSFGILLTELTTKG	RVPYPG	MVNREVLDQVER	GYRMPC
Src-2:HCK	REGAKFP IKWTAPEAINFGS	FTIKSDVWSFGILLMEIVTYG	RIPYPG	MSNPEVIRALER	GYRMPR
Src-3:FRK	RHEIKLP.VKWTAPEAIRSNK	FSIKSDVWSFGILLYEIITYG	KMPYSG	MTGAQVIQMLAQN	YRLPQ
Csk:CSK	QDTGKLP.VKWTAPEALREKK	FSTKSDVWSFGILLWEIYSFG	RVPYPR	IPLKDVVPRVEK	GYKMDA
Eph:EPHB2	ALGGKIP.IRWTAPEAIQYRK	FTSASDVWSYGIVMWEVMSYG	ERPYWD	MTNQDVINAIEQ	DYRLPP
VEGFR:KDR	KGDARLP.LKWMAPETIFDRV	YTIQSDVWSFGVLLWEIFSLG	ASPYPGV	KIDEEFCRRLKE	GTRMRA
FGFR:FGFR1	TTNGRLP.VKWMAPEALFDRI	YTHQSDVWSFGVLLWEIFTLG	GSPYPG	VPVEELFKLLKEG	HRMDK
CK1:CSNK1D	NKNLTGT ARYASINTHLGIE	QSRRDDLESLGYVLMYFNLGS	LPWQGLKA	ATKRQKYERISE	KKMST
JNK:MAPK10	MTPYVVT.RYYRAPEVILGMG	YKENVDIWSVGCIMGEMVRHK	ILFPGR	DYIDQWNKVIEQLGTPCPEFMKKLQP ....T	VRNYVENRPKYAGL
PAK:PAK1	RSTMVGT.PYWMAPEVVTRKA	YGPKVDIWSLGIMAIEMIEGE	PPYLN	ENPLRALYLIATN	GTPELQN
TGFBR-1:TGFBR1	PNHRVGT.KRYMAPEVLDDSINMKHFE	SFKRADIYAMGLVFWEIARRCSIGGIHEDYQLPYYDLVPSD		PSVEEMRKVVCEQ	KLRPNI
InsR:INSR	GGKGLLP.VRWMAPESLKDGV	FTTSSDMWSFGVVLWEITSLA	EQPYQG	LSNEQVLKFVMD	GGYLDQ
CDK-1:CDK2	YTHEVVT.LWYRAPEILLGCKY	YSTAVDIWSLGCIFAEMVTRR	ALFPGD	SEIDQLFRIFRTLGTPDEVVWPGVTS	MPDYKPSFPKWARQ
CDK-2:CDK6	LTSVVVT LWYRAPEVLLQSS	YATPVDLWSVGCIFAEMFRRK	PLFRGS	SDVDQLGKILDVIGLPGEEDWPRDVALP	RQAFHSKSAQ
GSK3:GSK3B	NVSYICS.RYYRAPELIFGATD	YTSSIDVWSAGCVLAELLLGQ	PIFPGD	SGVDQLVEIIKVLGTPTREQIREMNPN.	YTEFKFPQIKAH
PKA-1:PRKACA	TWTLCGT.PEYLAPEIILSKG	YNKAVDWWALGVLIYEMAAGY	PPFFA	DQPIQIYEKIVS	GKVRF
CaMK-1:CAMK1	LSTACGT.PGYVAPEVLAQKP	YSKAVDCWSIGVIAYILLCGY	PPFYD	ENDAKLFEQILK	AEYEFDS
ERK-1:MAPK1	LTEYVAT.RWYRAPEIMLNSKG	YTKSIDIWSVGCILAEMLSNR.	PIFPGK	HYLDQLNHILGILGSPSQEDLNCIIN...LK	ARNYLLSLPHKNKV
Abl:ABL1	HAGAKFP.IKWTAPESLAYNK	FSIKSDVWAFGVLLWEIATYG	MSPYPG	IDRSQVYELLEK	DYRMKR
Tie:TEK	KTMGRLP VRWMAIESLNYSV	YTTNSDVWSYGVLLWEIVSLG	[illegible]	MTCAELYEKLPQG.	YRLEK
MLCK:TTN	NFRLLFTAPEYYAPEVHQHDV	VSTATDMWSLGTLVYVLLSGIN	PFLA	ETNQQIIENIMN	AEYTF
p38:MAPK14	MTGYVAT.RWYRAPEIMLNWMH.	YNQTVDIWSVGCIMAELLTGR	LFPGT	DHINQLQQIMRLTGTPPAYLINRMPSHEARN	YIQSLTQMPKM
PHK:PHKG1	LREVCGT.PSYLAPEIIECSMNEDHPG	YGKEVDMWSTGVIMYTLLAGS	PPFWH	RKQMLMLRMIMSG	NYQFGS
CK2.CSNK2A1	YNVRVAS.RYFKGPELLVDYQM	YDYSLDMWSLGCMLASMIFRK	PFFHGH	DNYDQLVRIAKVLGTEDLYDYIDKYN. .IEL	DPRFNDILGRHSRK
PKA-2:PRKX	TWTLCGT.PEYLAPEVIQSKG	HGRAVDWWALGILIFEMLSGF	PPFFD	DNPFGIYQKILAG	KIDF
PDGFR:PDGFRA	SKGSTFLPVKWMAPESIFDNL	YTTLSDVWSYGILLWEIFSLG	GTPYPGM	MVDSTFYNKIKS	GYRMAK
PKG:PRKG1	TWTFCGT.PEYVAPEIILNKG	HDISADYWSLGILMYELLTGS	PPFSG	PDPMKTYNIILRG	IDMIEF
Btk:BTK	SVGSKFP.VRWSPPEVLMYSK	FSSKSDIWAFGVLMWEIYS	KMPYER	FTNSETAEHIAQG	LRLYR
Ret:RET	RSQGRIP.VKWMAIESLFDHI	TTQSDVWSFGV	GNPYPG	IPPERLFNLLKTG	HRMER
Ros:ROS1	RGEGLLP.VRWMAPESLMDGI	FTTQSDVWSFGILIWEILTLG	HQPYPA	HSNLDVLNYVQTG	GRLEP
Fes:FES	GGLRQVP.VKWTAPEALNYGR	YSSESDVWSFGILLWETFSLG	ASPYPN	LSNQQTREFVEKG	GRLPC
ALK:ALK	GGCAMLP VKWMPPEAFMEGI	FTSKTDTWSFGVLLWEIFSLG	YMPYPS	KSNQEVLEFVTSG	GRMDP
CDK-4:CDK7	YTHQVVT.RWYRAPELLFGARM	YGVGVDMWAVGCILAELLLRV	PFLPGD	SDLDQLTRIFETLGTPTEEQWPDMCSLP	DYVTFKSFPGI
CDK-3:CDK10	MTPKVVT.LWYRAPELLLGTTT.	QTTSIDMWAVGCILAELLAHR	PLLPGT.	SEIHQIDLIVQLLGTPSENIWPGFSKLPLVG.	QYSLRKQ
Src-4:PTK6	SHDHNIP.YKWTAPEALSRGH	YSTKSDVWSFGILLHEMFSRG	QVPYPG.	MSNHEAFLRVDAG	YRMPC
CaMK-2:CAMK2A	WFGFAGT.PGYLSPEVLRKDP	YGKPVDLWACGVILYILLVGY.	PPFWD	EDQHRLYQQIKAG	AYDFPS
CDK9:CDK9	YTNRVVT.LWYRPPELLLGERD	YGPPIDLWGAGCIMAEMWTRS	PIMQG	NTEQHQLALISQLCGSITPEVWPN	VDNYELYE
STLK:STK24	RNTFVGT.PFWMAPEVIKQSA	YDSKADIWSLGITAIELARGE	PPHSE	LHPMKVLFLIPKN	NPPTL
MST:STK3	RNTVIGT PFWMAPEVIQEIG	YNCVADIWSLGITSIEMAEGK	PPYAD	IHPMRAIFMIPTN	PPPTFRK
GCK:MAP4K2	RRSFIGT.PYWMAPEVAAVERKGG	YNELCDVWALGITAIELGELQ	PPLFH	LHPMRALMLMSKS	SFQP
NIK:MAP4K4	RNTFIGT.PYWMAPEVIACDENPDAT	YDYRSDLWSCGITAIEMAEGA	PPLCD	MHPMRALFLIPRN	PPPRLKS
LOK:STK10	RDSFIGT.PYWMAPEVVMCETMKDTP.	YDYKADIWSLGITLIEMAQIE	PPHHE.	LNPMRVLLKIAKS	DPPTLLT
Trk:NTRK1	GGRTMLP.IRWMPPESILYRK	FTTESDVWSFGVVLWEIFTYG	KQPWYQ	LSNTEAIDCITQG	RELER
MuSK:MUSK	NENDAIP.IRWMPPESIFYNR	YTTESDVWAYGVVLWEIFSYG	LQPYYG	MAHEEVIYYVRDG	NILSC
Ror:ROR1	QSKSLLP.IRWMPPEAIMYGK	FSSDSDIWSFGVVLWEIFSFG	LQPYYG	FSNQEVIEMVRKR	QLLPC
Akt:AKT1	MKTFCGT.PEYLAPEVLEDND	YGRAVDWWGLGVVMYEMMCGR	LPFYN	QDHEKLFELILME	EIRF
SGK:SGK	TSTFCGT.PEYLAPEVLHKQP	YDRTVDWWCLGAVLYEMLYGL	PPFYS	RNTAEMYDNILN	KPLQL
PKC-like:PRKCL1	TSTFCGT.PEFLAPEVLTDTS	YTRAVDWWGLGVLLYEMLVGE	SPFPG	DDEEEVFDSIVN	DEVRY
PKC-classical:PRKCA	TRTFCGT.PDYIAPEIIAYQP	YGKSVDWWAYGVLLYEMLAGQ	PPFDG	EDEDELFQSIMEH	NVSY
PKC-novel:PRKCD	ASTFCGT.PDYIAPEILQGLK	YTFSVDWWSFGVLLYEMLIGQ	SPFHG	DDEDELFESIRVD	TPHY
S6K-1:RPS6KA1-1	AYSFCGT.VEYMAPEVVNRQG	HSHSADWWSYGVLMFEMLTGS	LPFQG	KDRKETMTLILKA	KLGM
CCRK:CCRK	HQVATRS.VGCIMGELLNGSPL	FPGKNDIEQLCYVLRILGTPN	PQVWPE	LTELPDYNKISFK	EQVPM
TAO:TAO1	ANSFVGT.PYWMAPEVILAMDEGQ	YDGKVDVWSLGITCIELAERK	PPLFN	MNAMSALYHIAQN	ESPVLQ
FAK:PTK2	ASKGKLP.IKWMAPESINFRR	FTSASDVWMFGVCMWEILMHG	VKPFQG	VKNNDVIGRIENG	ERLPM
DDR:DDR1	QGRAVLP.IRWMAWECILMGK.	FTTASDVWAFGVTLWEVLMLCR	AQPFGSAHR	RAGHRERGGVLPGPG	PAVYLSR
CCK4:PTK7	FRQAWVP.LRWMSPEAILEGD	FSTKSDVWAFGVLMWEVFTHG	EMPHGG	QADDEVLADLQAG	KARLPQ

		αH 260 270	αI 280 290
PHKG1:2phk_	PEWDDYS	DTVKDLVSRFLVVQPQKRYT	AEEALAHPFFQQYVVEEVRHF
CAMK1:1a06_	PYWDDIS	DSAKDFIRHLMEKDPEKRFT	CEQALQHPWIAGDTALDKNIHQSVSEQIKKNFAKSKWKQAFNATAVVRHMRKLQLGHQPGGTGTDS
CDK2:1e1xA_	DFSKVVPPLD	EDGRSLLSQMLHYDPNKRIS	AKAALAHPFFQDVTKPVPHLRL
CDK6:1blxA	PIEKFVTDID	ELGKDLLLKCLTFNPAKRIS	AYSALSHPYFQDLERCKENLDSHLPPSQNTSELNTA
MAPK12:1cm8A	DFASILTNAS	PLAVNLLEKMLVLDAEQRVT	AGEALAHPYFESLHDTEDEPQVQKYDDSFDDVDRTLDEWKRVTYKEVLSFKPPRQLGARVSKETPL
MAPK14:1p38_	NFANVFIGAN	PLAVDLLEKMLVLDSDKRIT	AAQALAHAYFAQYHDPDDEPVADPYDQSFESRDLLIDEWKSLTYDEVISFVPP.PLDQEEMES
MAPK10:1jnk_	TFPKLFPDSLFPADSEHNKLKA	SQARDLLSKMLVIDPAKRIS	VDDALQHPYINVWYDPAEVEAPPPQIYDKQLDEREHTIEEWKELIYKEVMNSEEKTKNGVVKGQPSPSAQVQQ
MAPK1:3erk_	PWNRLFPNAD	SKALDLLDKMLTFNPHKRIE	VEQALAHPYLEQYYDPSDEPIAEAPFKFDMELDDLPKEKLKELIFEETARFQPGYRS
HCK:1qcfA	PENCP	EELYNIMMRCWKNRPEERPT	FEYIQSVLDDFYTATESQXEEIP
LCK:1qpcA	PDNCP	EELYQLMRLCWKERPEDRPT	FDYLRSVLEDFFTATEGQYQPQP
SRC:2src_	PPECP	ESLHDLMCQCWRKEPEERPT	FEYLQAFLEDYFTSTEPQXQPGENL
ABL1:1iepA	PEGCP	EKVYELMRACWQWNPSDRPS	FAEIHQAFETMFQESSISDEVEKELGKRGT
EPHB2:1jpaA	PMDCP	SALHQLMLDCWQKDRNHRPK	FGQIVNTLDKMIRNPNSLKAMAPLSS
CSK:1bygA	PDGCP	PAVYEVMKNCWHLDAAMRPS	FLQLREQLEHIKTHELHL
KDR:1vr2A	PDYTT	PEMYQTMLDCWHGEPSQRPT	FSELVEHLGNLLQANAQQD
FGFR1:1agwA	PSNCT	NELYMMMRDCWHAVPSQRPT	FKQLVEDLDRIVALTSNQE
TEK:1fvrA	PLNCD	DEVYDLMRQCWREKPYERPS	FAQILVSLNRMLEERKTYVNTTLYEKFTYAGIDCSAEEAA
IGF1R:1k3aA	PDNCP	DMLLELMRMCWQYNPKMRPS	FLEIISSIKEEMEPGFREVSFYYSEENK
INSR:1ir3A	PDNCP	ERVTDLMRMCWQFNPKMRPT	FLEIVNLLKDDLHPSFPEVSFFHSEENK
GSK3B:1h8fA	PWTKVFRPRTP	PEAIALCSRLLEYTPTARLT	PLEACAHSFFDELRDPNVKLPNGRDTPALFNFTTQELSSNPPLATILIPPHARIQA
TTN:1tklA	DEEAFKEIS	IEAMDFVDRLLVKERKSRMT	ASEALQHPWLKQKIERVSTKVIRTLKHRRYYHTLIKKDLNMVVSAARISCGGAIRSQKGVSVAKVKVASI
CSNK2A1:1dawA	PWLKFMNADNQHLVS	PEAIDFLDKLLRYDHQERLT	ALEAMTHPYFQQVRAAENS
PAK1:1f3mC	PEKLS	AIFRDFLNRCLDMDVEKRGS	AKELLQHQFLKIAKPLSSLTPLIAAAKEATKNNH
SRPK2:1howA	PLEDVLTEKYKFSKDEA	KEISDFLSPMLQLDPRKRAD	AGGLVNHPWLKDTLGMEEIRVPDRELYGSGSDIPGWFEEVRDHKRH
PRKACA:1cdkA	PSHFS	SDLKDLLRNLLQVDLTKRFG	NLKDGVNDIKNHKWFATTDWIAIYQRKVEAPFIPKFKGPGDTSNFDDYEEEEIRVSINEKCGKEFSEF
TGFBR1:1b6cB	PNRWQSCEAL	RVMAKIMRECWYANGAARLT	ALRIKKTLSQLSQQEGIKM
CSNK1P:1ckjA	PIEVLCKGYP	SEFATYLNFCRSLRFDDKPD	YSYLRQLFRNLFHRQGFSYDYVFDWNMLKFGASRAADDAERERRDREERLRH
Src-1:SRC	PPECP	ESLHDLMCQCWRKEPEERPT	FEYLQAFLEDYFTSTEPQYQPGENL
Src-2:HCK	PENCP	EELYNIMMRCWKNRPEERPT	FEYIQSVLDDFYTATESQYQQQP
Src-3:FRK	PSNCP	QQFYNIMLECWNAEPKERPT	FETLRWKLEDYFETDSSYSDANNFIR
Csk.CSK	PDGCP	PAVYEVMKNCWHLDAAMRPS	FLQLREQLEHIKTHELHL
Eph:EPHB2	PMDCP	SALHQLMLDCWQKDRNHRPK	FGQIVNTLDKMIRNPNSLKAMAPLSSGINLPLLDRTIP
VEGFR:KDR	PDYTT	PEMYQTMLDCWHGEPSQRPT	FSELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLPTSPVSCMEEEEVCDPKF
FGFR:FGFR1	PSNCT	NELYMMMRDCWHAVPSQRPT	FKQLVEDLDRIVALTSNQEYLDLSMPLDQYSPSFPDTRSSTCSSGEDSVFSHEPLPEEPC
CK1:CSNK1D	PIEVLCKGYP	SEFATYLNFCRSLRFDDKPD	YSYLRQLFRNLFHRQGFSYDYVFDWNMLKFGASRAADDAERERRDREERLRHSRNPATRGLP
JNK:MAPK10	TFPKLFPDSLFPADSEHNKLKA	SQARDLLSKMLVIDPAKRIS	VDDALQHPYINVWYDPAEVEAPPPQIYDKQLDEREHTIEEWKELIYKEVMNSEEKTKNGV
PAK:PAK1	PEKLS	AIFRDFLNRCLDMDVEKRGS	AKELLQHQFLKIAKPLSSLTPLIAAAKEATKNNH
TGFBR-1:TGFBR1	PNRWQSCEAL	RVMAKIMRECWYANGAARLT	ALRIKKTLSQLSQQEGIKM
InsR:INSR	PDNCP	ERVTDLMRMCWQFNPKMRPT	FLEIVNLLKDDLHPSFPEVSFFHSEENKAPESEELEMEFEDMENVPLDRSSHCQREEAGG
CDK-1:CDK2	DFSKVVPPLD	EDGRSLLSQMLHYDPNKRIS	AKAALAHPFFQDVTKPVPHLRL
CDK-2:CDK6	PIEKFVTDID	ELGKDLLLKCLTFNPAKRIS	AYSALSHPYFQDLERCKENLDSHLPPSQNTSELNTA
GSK3:GSK3B	PWTKVFRPRTP	PEAIALCSRLLEYTPTARLT	PLEACAHSFFDELRDPNVKHPNGRDTPALFNFTTQELSSNPPLATILIPPHARIQAAAST
PKA-1:PRKACA	PSHFS	SDLKDLLRNLLQVDLTKRFGNLKNG	VNDIKNHKWF
CaMK-1:CAMK1	PYWDDIS	DSAKDFIRHLMEKDPEKRFT	CEQALQHPWIAGDTALDKNIHQSVSEQIKKNFAKSKWKQAFNATAVVRHMRKLQLGTSQE
ERK-1:MAPK1	PWNRLFPNAD	SKALDLLDKMLTFNPHKRIE	VEQALAHPYLEQYYDPSDEPIAEAPFKFDMELDDLPKEKLKELIFEETARFQPGYRS
Abl:ABL1	PEGCP	EKVYELMRACWQWNPSDRPS	FAEIHQAFETMFQESSISDEVEKELGKQGVRGAVTTLLQAPELPTKTRTSRRAAEHRDTT
Tie:TEK	PLNCD	DEVYDLMRQCWREKPYERPS	FAQILVSLNRMLEERKTYVNTTLYEKFTYAGIDCSAEEAA
MLCK:TTN	DEEAFKEIS	IEAMDFVDRLLVKERKSRMT	ASEALQHPWLKQKIERVSTKVIRTLKHRRYYHTLIKKDLNMVVSAARISCGGAIRSQKGV
p38:MAPK14	NFANVFIGAN	PLAVDLLEKMLVLDSDKRIT	AAQALAHAYFAQYHDPDDEPVADPYDQSFESRDLLIDEWKSLTYDEVISFVPPPLDQEEM
PHK:PHKG1	PEWDDYS	DTVKDLVSRFLVVQPQNRYT	AEEALAHPFFQQYLVEEVRHFSPRGKFKVIALTVLASVRIYYQYRRVKPVTREIVIRDPY
CK2:CSNK2A1	RWERFVHSENQHLVS	PEALDFLDKLLRYDHQSRLT	AREAMEHPYFYTVVKDQARMGSSSMPGGSTPVSSANMMSGISSVPTPSPLGPLAGSPVIA
PKA-2:PRKX	PRHLD	PHVKDLIKKLLVVDRTRRLGNMKNG	ANDVKHHRWF
PDGFR:PDGFRA	PDHAT	SEVYEIMVKCWNSEPEKRPS	FYHLSEIVENLLPGQYKKSYEKIHLDFLKSDHPAVARMRVDSDNAYIGVTYKNEEDKLKD
PKG:PRKG1	PKKIA	KNAANLIKKLCRDNPSERLGNLKNG	VKDIQKHKWF
Btk:BTK	PHLAS	EKVYTIMYSCWHEKADERPT	FKILLSNILDVMDEES
Ret:RET	PDNCS	EEMYRLMLQCWKQEPDKRPV	FADISKDLEKMMVKRRDYLDLAASTPSDSLIYDDGLSEEETPLVDCNNAPLPRALPSTWI
Ros:ROS1	PRNCP	DDLWNLMTQCWAQEPDQRPT	FHRIQNQLQLFRNFFLNSIYQCRDEANNSGVINESFEGEDGDVICLNSDDIMPVVLMETK
Fes:FES	PELCP	DAVFRLMEQCWAYEPGQRPS	FSTIYQELQSIRKRHR
ALK:ALK	PKNCP	GPVYRIMTQCWQHQPEDRPN	FAIILERIEYCTQDPDVINTALPIEYGPLVEEEEKVPVRPKDPEGVPPLLVSQQAKREEE
CDK-4:CDK7	PLHHIFSAAG	DDLLDLIQGLFLFNPCARIT	ATQALKMKYFSNRPGPTPGCQLPRPNCPVETLKEQSNPALAIKRKRTEALEQGGLPKKLI
CDK-3:CDK10	PYNNLKHKFPWLS	EAGLRLLHFLFMYDPKKRAT	AGDCLESSYFKEKPLPCEPELMPTFPHHRNKRAAPATSEGQSKRCKP
Src-4:PTK6	PLECP	PSVHKLMLTCWCRDPEQRPC	FKALRERLSSFTSYENPT
CaMK-2:CAMK2A	PEWDTVT	PEAKDLINKMLTINPSKRIT	AAEALKHPWISHRSTVASCMHRQETVDCLKKFNARRKLKGAILTTMLATRNFSGGKSGGN
CDK9:CDK9	KLELVKGQKRKVKDRLKAYVRD	PYALDLIDKLLVLDPAQRID	SDDALNHDFFWSDPMPSDLKGMLSTHLTSMFEYLAPPRRKGSQITQQSTNQSRNPATTNQ
STLK:STK24	EGNYS	KPLKEFVEACLNKEPSFRPT	AKELLKHKFILRNAKKTSYLTELIDRYKRWKAEQSHDDSSSEDSDAETDGQASGGSDSGD
MST:STK3	PELWS	DDFTDFVKKCLVKNPEQRAT	ATQLLQHPFIKNAKPVSILRDLITEAMEIKAKRHDEQQRELEEEEENSDEDELDSHTMVK
GCK.MAP4K2	PKLRDKTRWT	QNFHHFLKLALTKNPKKRPT	AEKLLQHPFTTQQLPRALLTQLLDKASDPHLGTPSPEDCELETYDMFPDTIHSRGQHGPA
NIK:MAP4K4	KKWS	KKFFSFIEGCLVKNYMQRPS	TEQLLKHPFIRDQPNERQVRIQLKDHIDRTRKKRGEKDETEYEYSGSEEEEEEVPEQEGE
LOK:STK10	PSKWS	VEFRDFLKIALDKNPETRPS	AAQLLEHPFVSSITSNKALRELVAEAKAEVMEEIEDGRDEGEEEDAVDAASTLENHTQNS
Trk:NTRK1	PRACP	PEVYAIMRGCWQREPQQRHS	IKDVHARLQALAQAPPVYLDVLG
MuSK:MUSK	PENCP	VELYNLMRLCWSKLPADRPS	FTSIHRILERMCERAEGTVSV
Ror:ROR1	SEDCP	PRMYSLMTECWNEIPSRRPR	FKDIHVRLRSWEGLSSHTSSTTPSGGNATTQTTSLSASPVSNLSNPRYPNYMFPSQGITP
Akt:AKT1	PRTLG	PEAKSLLSGLLKKDPKQRLGGGSED	AKEIMQHRFF
SGK:SGK	KPNIT	NSARHLLEGLLQKDRTKRLGAKDD	FMEIKSHVFF
PKC-like:PRKCL1	PRFLS	AEAIGIMRRLLRRNPERRLGSSERD	AEDVKKQPFF
PKC-classical:PRKCA	PKSLS	KEAVSICKGLMTKHPAKRLGCGPEG	ERDVREHAFF
PKC-novel:PRKCD	PRWIT	KESKDILEKLFEREPTKRLGM	TGNIKIHPFF
S6K-1:RPS6KA1-1	PQFLS	TEAQSLLRALFKRNPANRLGSGPDG	AEEIKRHVFY
CCRK:CCRK	PLEEVLPDVS	PQALDLLGQFLLYPPHQRIA	ASKALLHQYFFTAPLPAHPSELPIPQRLGGPAPKAHPGPPHIHDFHVDRPLEGVAVEPRA
TAO:TAO1	SGHWS	EYFRNFVDSCLQKIPQDRPT	SEVLLKHRFVLRERPPTVIMDLIQRTKDAVRELDNLQYRKMKKILFQEAPNGPGAEAPEE
FAK:PTK2	PPNCP	PTLYSLMTKCWAYDPSRRPR	FTELKAQLSTILEEEKAQQEERMRMESRRQATVSWDSGGSDEAPPKPSRPGYPSPRSSEG
DDR:DDR1	PPACP	QGLYELMLRCWSRESEQRPP	FSQLHRFLAEDALNTV
CCK4:PTK7	PEGCP	SKLYRLMQRCWALSPKDRPS	FSEIASALGDSTVDSKP

MAST:KIAA0303	..SQLGLNKDPLEEMAHLGNYDSGTAETPETDESVSSSNASLKLRRKPRESDFE.TIKLTSNGAYGAVYFVRHKE	.........SRQRFAMKKINKQNLIL..........	.........RNQIQQAFVERDILTFAE..
MAST205:MAST205	..IVSQLGLTRDPLEEMAQLSSCDSPDTPETDDSIEGHGASLPSKKTPSEEDFE.TIKLISNGAYGAVFLVRHKS....	.........TRQRFAMKKINKQNLIL..........	.........RNQIQQAFVERDILTFAE..
CDKL:CDKL1	....MMEKYEKI.GKIGEGSYGVVFKCRNRD..............	.TGQIVAIKKFLESEDD.....	..........PVIKKIALREIRMLKQLK..
NLK:NLK	..GQQQPYFPSPAPGQAPGPAAAAPAQVQAAAAATVKAHHHQHSHHPQQQLDIE PDRPIGYGAFGVVWSVTDPR...	..........DGKRVALKKMPNVFQN.......	...........LVSCKRVFRELKMLCFFK..
ACK:ACK1	.MSKVFSGKRLEAEFPPHHSQSTFRKTSPAPGGPAGEGPLQSLTCLIGEKDLR.LLEKLGDGSFGVVRRGEWDAPS..........	.GKTVSVAVKCLKPDVLSQ..	..........PEAMDDFIREVNAMHSLD..
EGFR:EGFR	..LGIGLFMRRRHIVRKRTLRRLLQERELVEPLTPSGEAPNQALLRILKETEFKKI.KVLGSGAFGTVYKGLWIPEG..........	EKVKIPVAIKELREATS....	..........PKANKEILDEAYVMASVD .
Axl:AXL	..EPTVERGELVVRYRVRKSYSRRTTEATLNSLGISEELKEKLRDVMVDRHKVA.LGKTLGEGEFGAVMEGQLNQD..........	...DSILKVAVKTMKIAICT......	..........RSELEDFLSEAVCMKEFD..
Met:MET	..LTDMSPILTSGDSDISSPLLQNTVHIDLSALNPELVQAVQHVVIGPSSLIVH.FNEVIGRGHFGCVYHGTLLDND..........	...GKKIHCAVKSLNRITD..........	..........IGEVSQFLTEGIIMKDFS..
TGFBR-2:TGFBR2	..QQKLSSTWETGKTRKLMEFSEHCAIILEDDRSDISSTCANNINHNTELLPIE.LDTLVGKGRFAEVYKAKLKQNT....	.....SEQFETVAVKIFP......	..........YEEYASWKTEKDIFSDINLK
SYK:SYK	. NPYEPELAPWAADKGPQREALPMDTEVYESPYADPEEIRPKEVYLDRKLLTL.EDKELGSGNFGTVKKGYYQMK..........	.KVVKTVAVKILKNEAND.......	..........PALKDELLAEANVMQQLD..
JAK:JAK1-2	. ...NKLEEQNPDIVSRKKNQPTEVDPTHFEKRFLKRI.RDLGEGHFGKVELCRYDPED..........	..NTGEQVAVKSLKPESG....	..........GNHIADLKKEIEILRNLY..
Ryk:RYK	.TTQYLRADTPNNATPITSYPTLRIEKNDLRSVTLLEAKGKVKDIAISRERIT.LKDVLQEGTFGRIFHGILIDEKD..........	.PNKEKQAFVKTVKDQAS......	..........EIQVTMMLTESCKLRGLH.
PDPK1:PDPK1	..QTESSTPPGIPGGSRQGPAMDGTAAEPRPGAGSLQHAQPPPQPRKKRPEDFK.FGKILGEGSFSTVVLARELA..........	...TSREYAIKILEKRHIIK.....	..........ENKVPYVTRERDVMSRLD .
GRK:RHOK	..........................QWKWLEAQPMGEDWFLDF.RVLGKGGFGEVSACQMKA..........	...TGKLYACKKLNKKRLKK......	..........RKGYQGAMVEKKILMKVH..
DMPK:DMPK	..GLEPLLDLLLGVHQELGASELAQDKYVADFLQWAEPIVVRLKEVRLQRDDFEIL.KVIGRGAFSEVAVVKMKQ..........	...TGQVYAMKIMNKWDMLK.....	..........RGEVSCFREERDVLVNGD..
NDR:STK38	..EEREMRQKKLEKVMEEEGLKDEEKRLRRSAHARKETEFLRLKRTRLGLEDFESL.KVIGRGAFGEVRLVQKKD..........	...TGHVYAMKILRKADMLE.....	..........KEQVGHIRAERDILVEAD..
MAK.MAK	................................MNRYTTM.RQLGDGTYGSVLMGKSNE..........	...SGELVAIKRMKRKFY......	..........SWDECMNLREVKSLKKLN..
RAGE:RAGE	................................MKNYKAI.GKIGEGTFSEVMKMQSLR..........	...DGNYYACKQMKQRFE......	..........SIEQVNNLREIQALRRLNP.
SPAK:STK39	..QQAAPVTAAAAAAPAAATAAPAPAAPAAPAPAPAPAPAAQAVGWPICRDAYE.LQEVIGSGATAVVQAALCKP..........	...RQERVAIKRINLEKC.....	..........QTSMDELLKEIQAMSQCS..
S6K-1:RPS6KA1-2	...........MEDDGKPRAPQAPLHSVVQQLHGKNLVFSDGYV.VKETIGVGSYSECKRCVHKA..........	...TNMEYAVKVID........	..........KSKRDPSEEIEILLRYGQ.
MAPKAPK:MAPKAPK2	..FPAPAPPQPPTPALPHPPAQPPPPPQQFPQFHVKSGLQIKKNAIIDDYKV TSQVLGLGINGKVLQIFNKR..........	...TQEKFALKMLQ........	..........DCPKARREVELHWRASQ.
ERK-2:MAPK6	......................MAEKFESLMNIHGFDLGSRYMDL.KPLGCGGNGLVFSAVDND..........	...CDKRVAIKKIVLTD......	..........PQSVKHALREIKIIRRLD..
MKNK:MKNK1	....MVSSQKLEKPIEMGSSEPLPIADGDRRRKKKRRGRATDSLPGKFEDMYKL.TSELLGEGAYAKVQGAVSLQ..........	...NGKEYAVKIIEKQA......	..........GHSRSRVFREVETLYQCQG
DAPK:DAPK1	..........................MTVFRQENVDDYYD.TGEELGSGQFAVVKKCREKS..........	.TGLQYAAKFIKKRRTKSSRR......	..........GVSREDIEREVSILKEIQ..
TRIO:TRIO	...............VNDMGSASSSASLRVLGPGMDGIMVTWKDNFDSFYSEV.AELGRGRFSVVKKCDQKG..........	...TKRAVATKFVNKK.......	..........LMKRDQVTHELGILQSLQ..
STE11:MAP3K2	..HSLSTSSGSSIFTPEYDDSRIRRRGSDIDNPTLTVMDISPPSRSPRAPTNWR LGKLLGQGAFGRVYLCYDVD..........	...TGRELAVKQVQFDPDSPET.	..........SKEVNALECEIQLLKNFL..
EMK:MARK1	..VNERDTVNHTTVDGYTEPHIQPTKSSSRQNIPRCRNSITSATDEQPHIGNYR.LQKTIGKGNFAKVKLARHVL..........	...TGREVAVKIIDKTQLN.....	..........PTSLQKLFREVRIMKILN..
AMPK:PRKAA1	......................MATAEKQKHDGRVKIGHYI.LGDTLGVGTFGKVKVGKHEL..........	...TGHKVAVKILNRQKIRS. ..	..........LDVVGKIRREIQNLKLFR..
CHK2:CHEK1	..........................MAVPFVEDWD.LVQTLGEGAYGEVQLAVNRV..........	...TEEAVAVKIVDMKRA.....	..........VDCPENIKKEICINKMLN.
CAMKK:CAMKK2	. LDMNGRCICPSLPYSPVSSPQSSPRLPRRPTVESHHVSITGMQDCVQLNQYT.LKDEIGKGSYGVVKLAYNEN..........	DNTYYAMKVLSKKKLIRQAGFPRRPPPRGTRPAPGGCIQPRGPIEQVYQEIAILKKLD .	
LKB1:STK11	....MEVVDPQQLGMFTEGELMSVGMDTFIHRIDSTEVIYQPRRKRAKLIGKYL.MGDLLGEGSYGKVKEVLDSE..........	.TLCRRAVKILKKKKLRRI.....	..........PNGEANVKKEIQLLRRLR .
PLK:PLK	..AAVTAGKLARAPADPGKAGVPGVAAPGAPAAAPPAKEIPEVLVDPRSRRRYV RGRFLGKGGFAKCFEISDAD..........	...TKEVFAGKIVPKSLLLK.....	..........PHQREKMSMEISIHRSLA..
AUR:STK6	..TSVPHPVSRPLNNTQKSKQPLPSHLKIILRRNWHQNRKMKNQKEAVALEDFE.IGRPLGKGKFGNVYLAREKQ..........	...SKFILALKVLFKAQLEK.....	..........AGVEHQLRREVEIQSHLR..
VRK:VRK1	..............QSSAKRHLAEQFAVGEIITDMAKKEWK.VGLPIGQGGFGCIYLADMNSSES	.VGSDAPCVVKVEPSDNGPLFTEL....	..........KFYQRAAKPEQIQKWIRTRK
ULK:ULK1	.........................MEPGRGGTETVGKFEFS.RKDLIGHGAFAVVFKGRHREK..........	...HDLEVAVKCINKKNL......	..........AKSQTLLGKEIKILKELK..
STE7:MAP2K1	..SAVNGTSSAETNLEALQKKLEELELDEQQRKRLEAFLTQKQKVGELKDDDFEKI.SELGAGNGGVVFKVSHKP..........	...SGLVMARKLIHLEIK......	..........PAIRNQIIRELQVLHECN..
UTK1:DKFZp761P1010	...........WEAGHGGNVALPLKETSVENFLGATTPALAKLQVPREQLSEVL.EQLCSGSCGPIFRANMNTGD..........	.PSKPKSVILKALKEPAG..	..........LHEVQDFLGRIQFHQYLGK.
PKC-atypical:PRKCM	...........PVIPKGSSVGTGTNLHRDISVSISVSNCQIQENVDISTVYQIF.PDEVLGSGQFGIVYGGKHRK..........	...TGRDVAIKIIDKLRFP......	..........TKQESQLRNEVAILQNLH..
CLK:CLK1	..SSYKSKHRIHHSTSHRRSHGKSHRRKRTRSVEDDEEGHLICQSGDVLSARYE.IVDTLGEGAFGKVVECIDHKA..........	...GGRHVAVKIVKNV......	..........DRYCEAARSEIQVLEHLNTT
DYRK:DYRK1A	..EVYYAKKKRRHQQGRGDDSSHKKERKVYNDGYDDDNYDYIVKNGEKWMDRYE.IDSLIGKGSFGQVVKAYDRV..........	...EQEWVAIKIIKNK......	..........KAFLNQAQIEVRLLELMNK.
HIPK:HIPK2	..EHPPMIQNNASGATVATATTSTATSKNSGSNSEGDYQLVQHEVLCSMTNTYE.VLEFLGRGTFGQVVKCWKRG..........	...TNEIVAIKILKNR......	..........PSYARQGQIEVSILARLSTE
PRP4:PRP4	..DDMFAAYFDSARLRAAGIGKDFKENPNLRDNWTDAEGYYRVNIGEVLDKRYN.VYGYTGQGVFSNVVRARDNAR..........	...ANQEVAVKIIRNN......	..........ELMQKTGLKELEFLKKLNDA
TAK1:MAP3K7	...............MSTASAASSSSSSSAGEMIEAPSQVLNFEEIDYKEIE.VEEVVGRGAFGVVCKAKWR..........	...AKDVAIKQIES.......	..........ESERKAFIVELRQLSRVN..
MLK:MAP3K10	........................APAAPAGLQLPQEIPFHELQ LEEIIGVGGFGKVYRALWR..........	...GEEVAVKAARLDPEKDP....	..........AVTAEQVCQEARLFGALQ..
ZAK:ZAK	..........................MSSLGASFVQIKFDDLQ.FFENCGGGSFGSVYRAKWIS..........	...QDKEVAVKKLL.......	..........KIEKEAEILSVLS..
ARCK:LOC51086	..CNEYSQPGGDGSYVSVPSPLGKIKSMTKEKADILLLRAGLPSHFHLQLSEIE.FHEIIGSGSFGKVYKGRCR..........	...NKIVAIKRYRANTYCS......	..........KSDVDMFCREVSILCQLN..
Raf:RAF1	..NLSPTGWSQPKTPVPAQRERAPVSGTQEKNKIRPRGQRDSSYYWEIEASEVM.LSTRIGSGSFGTVYKGKWH..........	...GDVAVKILKVVDPT......	..........PEQFQAFRNEVAVLRKTR..
RIPK:ANKRD3	........................MEGDGGTPWALALLRTFDAGEFTGW.EKVGSGGFGQVYKVRHVH..........	...WKTWLAIKCSPSLHVD......	..........DRERMELLEEAKKMEMAK..
LIM:LIMK1	..RQKPVLRSCSIDRSPGAGSLGSPASQRKDLGRSESLRVVCRPHRIFRPSDLI.HGEVLGKGCFGQAIKVTHRE..........	...TGEVMVMKELIRFD......	..........EETQRTFLKEVKVMRCLE..
TESK:TESK1	.PLRGPGPGPGEVPGEGPPGPGGTGGGPGRGRPSSYRVLRSAVSSLARVDDFH.CAEKIGAGFFSEVYKVRHRQ..........	...SGQVMVLKMNKL......	..........PSNRGNTLREVQLMNRLR..
APKA:LOC51135	..TPVQNLEQSYMPPDSSSPENKSLEVSDTRFHSFSFYELKNVTNNFDERPISV.GGNKMGEGGFGVVYKGYVN..........	...NTTVAVKKLAAMVDITT......	..........EELKQQFDQEIKVMAKCQ..
IRAK:IRAK1	..PSPASLWPPPPSPAPSSTKPGPESSVSLLQGARPSPFCWPLCEISRGTHNFS.EELKIGEGGFGCVYRAVMR..........	...NTVYAVKRLKENADLEW......	..........TAVKQSFLTEVEQLSRFR..
IKK:CHUK	..........................MERPPGLRPGAGGPWE.MRERLGTGGFGNVCLYQHRE..........	...LDLKIAIKSCRLELS......	..........TKNRERWCHEIQIMKKLN..
IKKE:IKKE	...........................MQSTANYLWH.TDDLLGQGATASVYKARNKK..........	...SGELVAVKVFNTTSY......	..........LRPREVQVREFEVLRKLN..
AATK:KIAA1079	..IDFTPPAEDTPSVQSPAEVFTLSVPNISLPAPSQFQPSVEGLKSQVARHSLN.YIQEIGNGWFGKVLLGEIYTG..........	.TSVARVIVKELKASAN......	..........PKEQDTFLKNGEPYYILQ..
NEK:NEK2	...........................MPSRAEDYE.VLYTIGTGSYGRCQKIRRKS..........	...DGKILVWKELDYGSMT......	..........EAEKQMLVSEVNLLRELK..
EIF2AK:PRKR	.SNSDSLNSSSLLMNGLRNNQRKAKRSLAPRFDLPDMKETKYTVDKRFGMDFKEI.ELIGSGGFGQVFKAKHRI..........	...DGKTYVIKRVK	..........YNNEKAEREVKALAKLD.
Pim:PIM1	...............MLLSKINSLAHLRAAPCNDLHATKLAPGKEKEPLESQYQ.VGPLLGSGGFGSVYSGIRVS..........	...DNLPVAIKHVEKDRISDWGE......	..........LPNGTRVPMEVVLLKKVSSG
TLK:TLK1	..RLGHLKKEEAGIQAELERLERVRNLHIRELKRIHNEDNSQFKDHPTLNERYL.LLHLLGRGGFSEVDKAFDLS..........	...EQRYAAVKIHQLNKSWRDEKK......	..........ENYHKHACREYRIHKELD..
WNK:PRKWNK1	..LVGSKEEPPPARSGSGGGSAKEPQEERSQQQDDIEELETKAVGMSNDGRFLK.FDIEIGRGSFKTVYKGLDTE..........	...TTVEVAWCELQDRKLT......	..........KSERQRFKEEAEMLKGLQ..
PKMYT:PKMYT1	..SIPISRLFPPRTPGWHQLQPRRVSFRGEASETLQSPGYDPSRPESFFQQSFQRL.SRLGHGSYGEVFKVRSKE..........	...DGRLYAVKRSMSPFRG......	..........PKDRARKLAEVGSHEKVG..
Wee1:WEE1	..GQCRRRKRTYWNDSCGEDMEASDYELEDETRPAKRITITESNMKSRYTTEFHEL.EKIGSGEFGSVFKCVKRL..........	...DGCIYAIKRSKKPLAG......	..........SVDEQNALREVYAHAVLG..
Cot:MAP3K8	..ANHISNTAKHFYGQRPQESGILLNMVITPQNGRYQIDSDVLLIPWKLTYRNIGS.DFIPRGAFGKVYLAQDIK..........	...TKKRMACKLIP........	..........VDQFKPSDVEIQACFR....
JAK:JAK1-1	. TDNISFMLKRCCQPKPREISNLLVATKKAQEWQPVYPMSQLSFDRILKKDLV.QGEHLGRGTRTHIYSGTLMDYKDDE..........	.GTSEEKKIKVILKVLDPS.....	..........HRDISLAFFEAASMMRQVS.
MPS1:TTK	..FPPACQLSTPYGQPACFQQQQHQILATPLQNLQVLASSSANECISVKGRIYS.ILKQIGSGGSSKVFQVLNEK..........	...KQIYAIKYVNLEEAD......	..........NQTLDSYRNEIAYLNKLQQH
Mos:MOS	..YLRSEFSPSVDARPCSSPSELPAKLLLGATLPRAPRLPRRLAWCSIDWEQVC.LLQRLGAGGFGSVYKATYR..........	...GVPVAIKQVNKCTKNR......	..........LASRRSFWAELNVARLRH..
IRE:ERN1	..SGTSSPSTSPRASNHSLCSGSSASKAGSSPSLEQDDGDEETSVVIVGKISFC.PKDVLGHGAEGTIVYRGMFD..........	...NRDVAVKRIL......	..........PECFSFADREVQLLRESDE.
MPSK:STK16	........................MGHALCVCSRGTVIIDNKRYL.FIQKLGEGGFSYVDLVEGLH..........	...DGHFYALKRILCHE......	..........QQDREEAQREADMHRLFN.
GAK:GAK	............MSLLQSALDFLAGPGSLGGASGRDQSDFVGQTVELGELRLR.VRRVLAEGGFAFVYEAQDVG..........	...SGREYALKRLLSNE......	..........EEKNRAIIQEVCFMKKLSG.
BIKE:BIKE	..MKKFSRMPKSEGGSGGGAAGGGAGGAGAGAGCGSGGSSVGVRVFAVGRHQVT.LEESLAEGGFSTVFLVRTHG..........	...GIRCALKRMYVNN......	..........MPDLNVCKREITIMKELSG.
TOPK:TOPK	...............MEGISNFKTPSKLSEKKKSVLCSTPTINIPASP.FMQKLGFGTGVNVYLMKRSPRG..........	.LSHSPWAVKKINPICNDHYR......	..........SVYQKRLMDEAKILKSLH..
ILK:ILK	..PLRELLRERAEKMGQNLNRIPYKDTFWKGTTRTRPRNGTLNKHSGIDFKQLN.FLTKLNENHSGELWKGRWQ..........	...GNDIVVKVLKVRDWS......	..........TRKSRDFNEECPRLRIFS .

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MAST:KIAA0303          ............NPFVVSMYCSFETR..........RHLCMVMEYVEG.GDCATLMKNMGP............
MAST205:MAST205        ............NPFVVSMFCSFDTK..........RHLCMVMEYVEG.GDCATLLKNIGA............
CDKL:CDKL1             ............HPNLVNLLEVFRRK..........RRLHLVFEYCDH.TVLHELDRYQRG............
NLK:NLK                ............HDNVLSALDILQPPHID.......YFEEIYVVTELMQ .SDLHKIIVSPQP.........
ACK:ACK1               ............HRNLIRLYGVVLTP............PMKMVTELAPL.GSLLDRLRKHQGH..........
EGFR:EGFR              ............NPHVCRLLGICLTS............TVQLITQLMPF.GCLLDYVREHKDN..........
Axl:AXL                ............HPNVMRLIGVCFQGSER.......ESFPAPVVILPFMKH GDLHSFLLYSRLGGQPVY....
Met:MET                ............HPNVLSLLGICLRSE.........GSPLVVLPYMKH.GDLRNFIRNETHN..........
TGFBR-2:TGFBR2         ............HENILQFLTAEERKTE........LGKQYWLITAFHAK.GNLQEYLTRHVIS.........
SYK:SYK                ............NPYIVRMIGICEAE...........SWMLVMEMAEL.GPLNKYLQQNRH...........
JAK:JAK1-2             ............HENIVKYKGICTEDG.........GNGIKLIMEFLPS.GSLKEYLPKNKNK.........
Ryk:RYK                ............HRNLLPITHVCIEEG.........EKPMVILPYMNW.GNLKLFLRQCKLVEANNPQA....
PDPK1:PDPK1            ............HPFFVKLYFTFQDD..........EKLYFGLSYAKN.GELLKYIRKIGS............
GRK:RHOK               ............SRFIVSLAYAFETK..........ADLCLVMTIMNG.GDIRYHIYNVNEENPG........
DMPK:DMPK              ............RRWITQLHFAFQDE..........NYLYLVMEYYVG.GDLLTLLSKFGER...........
NDR:STK38              ............SLWVVKMFYSFQDK..........LNLYLIMEFLPG.GDMMTLLMKKDT............
MAK:MAK                ............HANVIKLKEVIREN..........DHLYFIFEYMK. ENLYQLMKDRNKL..........
RAGE:RAGE              ............HPNILMLHEVVFDRK.........SGSLALICELMD. MNIYELIRGRRYP.........
SPAK:STK39             ............HPNVVTYYTSFVVK..........DELWLVMKLLSG GSMLDIIKYIVNRGEHKNGV...
S6K-1:RPS6KA1-2        ............HPNIITLKDVYDDG..........KHVYLVTELMRG.GELLDKILRQKF...........
MAPKAPK:MAPKAPK2       ............CPHIVRIVDVYENLYA........GRKCLLIVMECLDG.GELFSRIQDRGDQA........
ERK-2:MAPK6            ............HDNIVKVFEILGPSGSQLTDDV..GSLTELNSVYIVQEYME..TDLANVLEQGP.......
MKNK:MKNK1             ............NKNILELIEFFEDD..........TRFYLVFEKLQG.GSILAHIQKQKH...........
DAPK:DAPK1             ............HPNVITLHEVYENK..........TDVILILELVAG.GELFDFLAEKES............
TRIO:TRIO              ............HPLLVGLLDTFETP..........TSYILVLEMADQ.GRLLDCVVRWGS............
STE11:MAP3K2           ............HERIVQYYGCLRDPQ.........EKTLSIFMEYMPG.GSIKDQLKAYGA..........
EMK:MARK1              ............HPNIVKLFEVIETE..........KTLYLVMEYASG.GEVFDYLVAHGR...........
AMPK:PRKAA1            ............HPHIIKLYQVISTP..........SDIFMVMEYVSG.GELFDYICKNGR...........
CHK2:CHEK1             ............HENVVKFYGHRREG..........NIQYLFLEYCSG GELFDRIEPDIG............
CAMKK:CAMKK2           ............HPNVVKLVEVLDDPN.........EDHLYMVFELVNQ.GPVMEVPTLKP............
LKB1:STK11             ............HKNVIQLVDVLYNEE.........KQKMYMVMEYCV .CGMQEMLDSVPEKR.........
PLK:PLK                ............HQHVVGFHGFFEDN..........DFVFVVLELCRR.RSLLEPHKRRKA............
AUR:STK6               ............HPNILRLYGYFHDA..........TRVYLILEYAPL.GTVYRELQKLSK............
VRK:VRK1               LK..........YLGVPKYWGSGLHDKN........GKSYRFMIMDRFG..SDLQKIYEANAKR.........
ULK:ULK1               ............HENIVALYDFQEMA..........NSVYLVMEYCNG.GDLADYLHAMRT............
STE7:MAP2K1            ............SPYIVGFYGAFYSD..........GEISICMEHMDG.GSLDQVLKKAGR............
UTK1:DKFZp761P1010     ............HKNLVQLEGCCTEK..........LPLYMVLEDVAQ GDLLGFLWTCRRDVMTMDGLLYD..
PKC-atypical:PRKCM     ............HPGVVNLECMFETP..........ERVFVVMEKLH..GDMLEMILSSEKGR..........
CLK:CLK1               DPNS........TFRCVQMLEWFEHH..........GHICIVFELLG..LSTYDFIKENGFLP..........
DYRK:DYRK1A            ............HDTEMKYYIVHLKRHFM.......FRNHLCLVFEMLS. YNLYDLLRNTNFRG........
HIPK:HIPK2             S...........ADDYNFVRAYECFQHK........NHTCLVFEMLE..QNLYDFLKQNKFSP..........
PRP4:PRP4              DP..........DDKFHCLRLFRHFYHK........QHLCLVFEPLS..MNLREVLKKYGKDVG.........
TAK1:MAP3K7            ............HPNIVKLYGACLN...........PVCLVMEYAEG.GSLYNVLHGAEPLPY..........
MLK:MAP3K10            ............HPNIIALRGACLNP..........PHLCLVMEYARG.GALSRVLAGRR.............
ZAK:ZAK                ............HRNIIQFYGVILEP..........PNYGIVTEYASL.GSLYDYINSNRSEE..........
ARCK:LOC51086          ............HPCVIQFVGACLNDP.........SQFAIVTQYISG.GSLFSLLHEQKRI...........
Raf:RAF1               ............HVNILLFMGYMTKD..........NLAIVTQWCEG.SSLYKHLHVQETK............
RIPK:ANKRD3            ............PRYILPVYGICRE...........PVGLVMEYMET.GSLEKLLASEP..............
LIM:LIMK1              ............HPNVLKFIGVLYKD..........KRLNFITEYIKG.GTLRGIIKSMDSQ...........
TESK:TESK1             ............HPNILRFMGVCVHQ..........GQLHALTEYMNG.GTLEQLLSSPEP............
APKA:LOC51135          ............HENLVELLGFSSDG..........DDLCLVYVYMPN.GSLLDRLSCLDGTPP.........
IRAK:IRAK1             ............HPNIVDFAGYCAQN..........GFYCLVYGFLPN GSLEDRLHCQTQACPP........
IKK:CHUK               ............HANVVKACDVPEELNIL.......IHDVPLLAMEYCSG GDLRKLLNKPENCCG........
IKKE:IKKE              ............HQNIVKLFAVEETGG.........SRQKVLVMEYCSS.GSLLSVLESPENAFG........
AATK:KIAA1079          ............HPNILQCVGQCVEA..........IPYLLVFEFCDL.GDLKAYLRSEQEHMRGD.......
NEK:NEK2               ............HPNIVRYYDRIIDRT.........NTTLYIVMEYCEG.GDLASVITKGTKERQY........
EIF2AK:PRKR            ............HVNIVHYNGCWDGFDYDPETSDDSLESSDYDPENSKNSSRSKTKCLFIQMEFCDKGTLEQWIEKRRGEK....
Pim:PIM1               ............FSGVIRLLDWFERP..........DSFVLILERPEPVQDLFDFITERGA.............
TLK:TLK1               ............HPRIVKLYDYFSLDT.........DTFCTVLEYCEG.NDLDFYLKQHKL............
WNK:PRKWNK1            ............HPNIVRFYDSWESTVK........GKKCIVLVTELMTS.GTLKTYLKRFKV..........
PKMYT:PKMYT1           ............QHPCCVRLEQAWEEG.........GILYLQTELCG..PSLQQHCEAWGAS...........
Wee1:WEE1              ............QHSHVVRYFSAWAED.........DHMLIQNEYCNG.GSLADAISENYRIMSY.......
Cot:MAP3K8             ............HENIAELYGAVLWG..........ETVHLFMEAGEG.GSVLEKLESCGP............
JAK:JAK1-1             ............HKHIVYLYGVCVR...........DVENIMVEEFVEGGPLDLFMHRKSDV...........
MPS1:TTK               ............SDKIIRLYDYEITD..........QYIYMVMECGN.IDLNSWLKKKKS.............
Mos:MOS                ............DNIVRVVAASTRTPAG........SNSLGTIIMEFGGN VTLHQVIYGAAGHPEGDAGEPHCRTGGQ.
IRE:ERN1               ............HPNVIRYFCTEKDR..........QFQYIAIELCA.ATLQEYVEQKDFA.............
MPSK:STK16             ............HPNILRLVAYCLRERG........AKHEAWLLLPFFKR.GTLWNEIERLKDKGNF.......
GAK:GAK                ............HPNIVQFCSAASIGKEES......DTGQAEFLLLTELCK.GQLVEFLKKMESRGP......
BIKE:BIKE              ............HKNIVGYLDCAVNSISD.......NVWEVLILMEYCRA.GQVVNQMNKKLQTG........
TOPK:TOPK              ............HPNIVGYRAFTEASD.........GSLCLAMEYGGE.KSLNDLIEERYKASQDP......
ILK:ILK                ............HPNVLPVLGACQSPP.........APHPTLITHWMPY.GSLYNVLHEGTNFV.........
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MAST:KIAA0303	LPVDMARMYFAETVLALEYLHN	YGIVHRDLKPDNLLVTSM	GHIKLTDFGLSKVGLMSMTTNLYEGHIEKDAREFL
MAST205:MAST205	LPVDMVRLYFAETVLALEYLHN	YGIVHRDLKPDNLLITSM	GHIKLTDFGLSKMGLMSLTTNLYEGHIEKDAREFL
CDKL:CDKL1	VPEHLVKSITWQTLQAVNFCHK	HNCIHRDVKPENILITKH	SVIKLCDFGFARLLTGPSDY
NLK:NLK	LSSDHVKVFLYQILRGLKYLHS	AGILHRDIKPGNLLVNSN	CVLKICDFGLARVEELDESRH
ACK:ACK1	FLLGTLSRYAVQVAEGMGYLES	KRFIHRDLAARNLLLATR	DLVKIGDFGLMRALPQNDDHYVM
EGFR:EGFR	IGSQYLLNWCVQIAKGMNYLED	RRLVHRDLAARNVLVKTP	QHVKITDFGLAKLLGAEEKEYH
Axl:AXL	LPTQMLVKFMADIASGMEYLST	KRFIHRDLAARNCMLNEN	MSVCVADFGLSKKIYNGDYYRQ
Met:MET	PTVKDLIGFGLQVAKAMKYLAS	KKFVHRDLAARNCMLDEK	FTVKVADFGLARDMYDKEYYSVHN
TGFBR-2:TGFBR2	WEDLRKLGSSLARGIAHLHSDHTPCGRPKMPIVHRDLKSSNILVKND		LTCCICDFGLSLRLDPTLSVDDLA
SYK:SYK	VKDKNIIELVHQVSMGMKYLEE	SNFVHRDLAARNVLLVTQ	HYAKISDFGLSKALRADENYYKA
JAK:JAK1-2	INLKQQLKYAVQICKGMDYLGS	RQYVHRDLAARNVLVESE	HQVKIGDFGLTKAIETDKEYYTV
Ryk:RYK	ISQQDLVHMAIQIACGMSYLAR	REVIHKDLAARNCVIDDT	LQVKITDNALSRDLFPMDYHCL
PDPK1:PDPK1	FDETCTRFYTAEIVSALEYLHG	KGIIHRDLKPENILLNED	MHIQITDFGTAKVLSPESKQAR
GRK:RHOK	FPEPRALFYTAQIICGLEHLHQ	RRIVYRDLKPENVLLDND	GNVRISDLGLAVELLDGQSK
DMPK:DMPK	IPAEMARFYLAEIVMAIDSVHR	LGYVHRDIKPDNILLDRC	GHIRLADFGSCLKLRADGTVR
NDR:STK38	LTEEETQFYIAETVLAIDSIHQ	LGFIHRDIKPDNLLLDSK	GHVKLSDFGLCTGLKKAHRTEFYRNLNHSLPSDFTFQNMNS
MAK:MAK	FPESVIRNIMYQILQGLAFIHK	HGFFHRDMKPENLLCMGP	ELVKIADFGLARELRSQPP
RAGE:RAGE	LSEKKIMHYMYQLCKSLDHIHR	NGIFHRDVKPENILIKQD	VLKLGDFGSCRSVYSKQP
SPAK:STK39	LEEAIIATILKEVLEGLDYLHR	NGQIHRDLKAGNILLGED	GSVQIADFGVSAFLATGGDVTRNKV
SGK-1:RPS6KA1-2	FSEREASFVLHTIGKTVEYLHS	QGVVHRDLKPSNILYVDESG	NPECLRICDFGFAKQLRAENGL
MAPKAPK:MAPKAPK2	FTEREASEIMKSIGEAIQYLHS	INIAHRDVKPENLLYTSKRP	NAILKLTDFGFAKETTSHNS
ERK-2:MAPK6	LLEEHARLFMYQLLRGLKYIHS	ANVLHRDLKPANLFINTED	LVLKIGDFGLARIMDPHYSHKGH
MKNK:MKNK1	FNEREASRVVRDVAAALDFLHT	KGIAHRDLKPENILCESPEK	VSPVKICDFDLGSGMKLNNSCTPITTPE
DAPK:DAPK1	LTEEEATEFLKQILNGVYYLHS	LQIAHFDLKPENIMLLDRNV	PKPRIKIIDFGLAHKIDFGNE
TRIO:TRIO	LTEGKIRAHLGEVLEAVRYLHN	CRIAHLDIKPENILVDESLA	KPTIKLADFGDAVQLNTTYY
STE11:MAP3K2	LTENGTRKYTRQILEGVHYLHS	NMILHRDIKGANILRDST	GNVKLGDFGASKRLQTICLSGTG
EMK:MARK1	MKEKEARAKFRQIVSAVQYCHQ	KYIVHRDLKAENLLLDGD	MNIKIADFGFSNEFTVGNK
AMPK:PRKAA1	LDEKESRRLFQQILSGVDYCHR	HMVVHRDLKPENVLLDAH	MNAKIADFGLSNMMSDGEF
CHK2:CHEK1	MPEPDAQRFFHQLMAGVVYLHG	IGITHRDIKPENLLLDER	DNLKISDFGLATVFRYNNRERL
CAMKK:CAMKK2	LSEDQARFYFQDLIKGIEYLHY	QKIIHRDIKPSNLLVGED	GHIKIADFGVSNEFKGSDAL
LKB1:STK11	FPVCQAHGYFCQLIDGLEYLHS	QGIVHKDIKPGNLLLTTG	GTLKISDLGVAEALHPFAADDT
PLK:PLK	LTEPEARYYLRQIVLGCQYLHR	NRVIHRDLKLGNLFLNED	LEVKIGDFGLATKVEYDGER
AUR:STK6	FDEQRTANLYNRIANALSYCHS	KRVIHRDIKPENLLLGSA	GELKIADFGWSVHAPSSR
VRK:VRK1	FSRKTVLQLSLRILDILEYIHE	HEYVHGDIKASNLLLNYKN	PDQVYLVDYGLAYRYCPEGVHKEYKEDP
ULK:ULK1	LSEDTIRLFLQQIAGAMRLLHS	KGIIHRDLKPQNILLSNPAGRR	ANPNSIRVKIADFGFARYLQSNMM
STE7:MAP2K1	IPEQILGKVSIAVIKGLTYLREK	HKIMHRDVKPSNILVNSR	GEIKLCDFGVSGQLIDSM
UTK1:DKFZp761P1010	LTEKQVYHIGKQVLLALEFLQE	KHLFHGDVAARNILMQSD	LTAKICGLGLAYEVYTRGAI
PKC-atypical:PRKCM	LPSHITKFLITQILVALRHLHF	KNIVHCDLKPENVLLASAD	PFPQVKLCDFGFARIIGEKSF
CLK:CLK1	FRLDHIRKMAYQICKSVNFLHS	NKLTHTDLKPENILFVQSDYTEAYNPKIKRDERTLINPDIKVVDFGSATYDDEH	
DYRK:DYRK1A	VSLNLTRKFAQQMCTALLFLATPE	LSIIHCDLKPENILLCNPK	RSAIKIVDFGSSCQLGQR
HIPK:HIPK2	LPLKYIRPVLQQVATALMKLKS	LGLIHADLKPENIMLVDPSR	QPYRVKVIDFGSASHVSKAV
PRP4:PRP4	LHIKAVRSYSQQLFLALKLLKR	CNILHADIKPDNILVNESK	TILKLCDFGSASHVADND
TAK1:MAP3K7	YTAAHAMSWCLQCSQGVAYLHSMQP	KALIHRDLKPPNLLLVAGG	TVLKICDFGTACDIQTH
MLK:MAP3K10	VPPHVLVNWAVQVARGMNYLHNDAP	VPIIHRDLKSINILILEAIENH	NLADTVLKITDFGLAREWHKTT
ZAK:ZAK	MDMDHIMTWATDVAKGMHYLHMEAP	VKVIHRDLKSRNVVIAAD	GVLKICDFGASRFHNHTT
ARCK:LOC51086	LDLQSKLIIAVDVAKGMEYLHNLT	QPIIHRDLNSHNILLYED	GHAVVADFGESRFLQSLDEDN
Raf:RAF1	FQMFQLIDIARQTAQGMDYLHA	KNIIHRDMKSNNIFLHEG	LTVKIGDFGLATVKSRWSGSQQ
RIPK:ANKRD3	LPWDLRFRIIHETAVGMNFLHCMA	PPLLHLDLKPANILLDAH	YHVKISDFGLAKCNGLSHSHDLS
LIM:LIMK1	YPWSQRVSFAKDIASGMAYLHS	MNIIHRDLNSHNCLVREN	KNVVVADFGLARLMVDEKTQPEGLRSLKKPDRKK
TESK:TESK1	LSWPVRLHLALDIARGLRYLHS	KGVFHRDLTSKNCLVRREDR	GFTAVVGDFGLAEKIPVYREGARKE
APKA:LOC51135	LSWHMRCKIAQGAANGINFLHE	NHHIHRDIKSANILLDEA	FTAKISDFGLARASEKFAQTVM
IRAK:IRAK1	LSWPQRLDILLGTARAIQFLHQDS	PSLIHGDIKSSNVLLDER	LTPKLGDFGLARFSRFAGSSPSQSSMVAR
IKK:CHUK	LKESQILSLLSDIGSGIRYLHE	NKIIHRDLKPENIVLQDVGG	KIIHKIIDLGYAKDVDQGSL
IKKE:IKKE	LPEDEFLVVLRCVVAGMNHLRE	NGIVHRDIKPGNIMRLVGEE	GQSIYKLTDFGAARELDDDEK
AATK:KIAA1079	SQTMLLQRMACEVAAGLAAMHK	LHFLHSDLALRNCFLTSD	LNVKVGDYGIGFSRYKEDYIET
NEK:NEK2	LDEEFVLRVMTQLTLALKECHRRSDGG	HTVLHRDLKPANVFLDGK	QNVKLGDFGLARILNHDTSF
EIF2AK:PRKR	LDKVLALELFEQITKGVDYIHS	KKLIHRDLKPSNIFLVDT	KQVKIGDFGLVTSLKNDGK
Pim:PIM1	LQEELARSFFWQVLEAVRHCHN	CGVLHRDIKDENILIDLNR	GELKLIDFGSGALLKDTV
TLK:TLK1	MSEKEARSIVMQIVNALRYLNEIK	PPIIHYDLKPGNILLVDGTA	CGEIKITDFGLSKIMDDDSYGVDGMVL
WNK:PRKWNK1	MKIKVLRSWCRQILKGLQFLHTRT	PPIIHRDLKCDNIFITGPT	GSVKIGDLGLATLKRASF
PKMYT:PKMYT1	LPEAQVWGYLRDTLLALAHLHS	QGLVHLDVKPANIFLGPR	GRCKLGDFGLLVELGTAGA
Wee1:WEE1	FKEAELKDLLLQVGRGLRYIHS	MSLVHMDIKPSNIFISRTSIPNAASEEGDEDDWASNKVMFKIGDLGHVTRISS	
Cot:MAP3K8	MREFEIIWVTKHVLKGLDFLHS	KKVIHHDIKPSNIVFMST	KAVLVDFGLSVQMTEDVYF
JAK:JAK1-1	LTTPWKFKVAKQLASALSYLED	KDLVHGNVCTKNLLLAREGID	SECGPFIKLSDPGIPITVLS
MPS1:TTK	IDPWERKSYWKNMLEAVHTIHQ	HGIVHSDLKPANFLIVDG	MLKLIDFGIANQMQPDTTSVV
Mos:MOS	LSLGKCLKYSLDVVNGLLFLHS	QSIVHLDLKPANILISEQ	DVCKISDFGCSEKLEDLLCFQTP
IRE:ERN1	HLGLEPITLLQQTTSGLAHLHS	LNIVHRDLKPHNILISMPNA	HGKIKAMISDFGLCKKLAVGRHSFSR
MPSK:STK16	LTEDQILWLLLGICRGLEAIHA	KGYAHRDLKPTNILLGDE	GQPVLMDLGSMNQACIHVEGSRQALTLQD
GAK:GAK	LSCDTVLKIFYQTCRAVQHMHRQK	PPIIHRDLKVENLLLSNQ	GTIKLCDFGSATTISHYPDYSWSAQRRALVEE
BIKE:BIKE	FTEPEVLQIFCDTCEAVARLHQCK	TPIIHRDLKVENILLNDG	GNYVLCDFGSATNKFLNPQKDGVNVVEE
TOPK:TOPK	FPAAIILKVALNMARGLKYLHQE	KKLLHGDIKSSNVVIKGDF	ETIKICDVGVSLPLDENMTVTDP
ILK:ILK	VDQSQAVKFALDMARGMAFLHTLE	PLIPRHALNSRSVMIDEDM	TARISMADVKFSFQCPG

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MAST:KIAA0303          .............DKQVCGT.PEYIAPEVILRQG..........YGKPVDWWAMGIILYEFLVGC.........VPFFG..............DTPEELFGQVISD.............................EINW
MAST205:MAST205        .............DKQVCGT.PEYIAPEVILRQG..........YGKPVDWWAMGIILYEFLVGC.........VPFFG..............DTPEELFGQVISD.............................EIVW
CDKL:CDKL1             .............YTDYVAT RWYRSPELLVGDTQ.........YGPPVDVWAIGCVFAELLSGV.........PLWPG..............KSDVDQLYLIRKTLGDLIPRHQQVFSTN..............QYFSGVKIPD
NLK:NLK                .............MTQEVVT.QYYRAPEILMGSRH.........YSNAIDIWSVGCIFAELLGRR.........ILFQA..............QSPIQQLDLITDLLGTPSLEAMRTACEG..............AKAHILRG
ACK:ACK1               .............QEHRKVP.FAWCAPESLKTRT..........FSHASDTWMFGVTLWEMFTYG.........QEPWIG.............LNGSQILHKIDKE.............................GERLPR
EGFR:EGFR              .............AEGGKVP.IKWMALESILHRI..........YTHQSDVWSYGVTVWELMTFG.........SKPYDG.............IPASEISSILEKG.............................ERLPQ
Axl:AXL                .............GRIAKMP.VKWIAIESLADRV..........YTSK[illegible]DVWSFGVTMWEIATRG.........QTPYPG.............VENSEIYDYLRQG.............................NRLKQ
Met:MET                .............KTGAKLP.VKWMALESLQTQK..........FTTKSDVWSFGVVLWELMTRG.........APPYPD.............VNTFDITVYLLQG.............................RRLLQ
TGFBR-2:TGFBR2         .............NSGQVGT.ARYMAPEVLESRMNLENAE....SFKQTDVYSMALVLWEMTSRCNAVGEVKDYEPPFGSKVREH........PCVESMKDNVLRDRGRPEIPSFWLNHQGI.............
SYK:SYK                .............QTHGKWP VKWYAPECINYYK..........FSSKSDVWSFGVLMWEAFSYG.........QKPYRG.............MKGSEVTAMLEKG.............................ERMGC
JAK:JAK1-2             .............KDDRDSP.VFWYAPECLMQSK..........FYIASDVWSFGVTLHELLTYCDSDSSPMALFLKMIGPTHGQ.........MTVTRLVNTLKEG.............................KRLPC
Ryk:RYK                .............GDNENRP.VRWMALESLVNNE..........FSSASDVWAFGVTLWELMTLG.........QTPYVD.............IDPFEMAAYLKDG.............................YRIAQ
PDPK1:PDPK1            .............ANSFVGT.AQYVSPELLTEKS..........ACKSSDLWALGCIIYQLVAGL.........PPFRA..............GNEYLIFQKIIKL.............................EYDF
GRK:RHOK               .............TKGYAGT.PGFMAPELLQGEE..........YDFSVDYFALGVTLYEMIAAR.........GPFRARGEK..........VENKELKHRIIS..............................EPVKY
DMPK:DMPK              .............SLVAVGT.PDYLSPEILQAVGGGPGTGS...YGPECDWWALGVFAYEMFYGQ.........TPFYA..............DSTAETYGKIVHY.............................KEHLSL
NDR:STK38              KRKAETWKRNRRQLAFSTVGT PDYIAPEVFMQTG.........YNKLCDWWSLGVIMYEMLIGY.........PPFCS..............ETPQETYKKVMNWK............................ETLTF
MAK:MAK                .............YTDYVST.RWYRAPEVLLRSSV.........YSSPIDVWAVGSIMAELYMLR.........PLFPG..............TSEVDEIFKICQVLGTPKKSDWPEG.................YQLASSMNFRF
RAGE:RAGE              .............YTEYIST.RWYRAPECLLTDGF.........YTYKMDLWSAGCVFYEIASLQ.........PLFPG..............VNELDQISKIHDVIGTPAQKILTKFKQS..............RAMNFDF
SPAK:STK39             .............RKTFVGT.PCWMAPEVMEQVRG.........YDFKADMWSFGITAIELATGA.........APYHKY.............PPMKVLMLTLQND.............................PPTLET
S6K-1:RPS6KA1-2        .............LMTPCYT.ANFVAPEVLKRQG..........YDEGCDIWSLGILLYTMLAGY.........TPFANGPS...........DTPEEILTRIGSG.............................KFTLSG
MAPKAPK:MAPKAPK2       .............LTTPCYT.PYYVAPEVLGPEK..........YDKSCDMWSLGVIMYILLCGY.........PPFYSNHGL..........AISPGMKTRIRMG.............................QYEFPN
ERK-2:MAPK6            .............LSEGLVT KWYRSPRLLLSPNN.........YTKAIDMWAAGCIFAEMLTGK.........TLFAGA.............HELEQMQLILESIPVVHEEDRQELLSVIP.............VYIRNDMTE
MKNK:MKNK1             .............LTTPCGS.AEYMAPEVVEVFTDQATF.....YDKRCDLWSLGVVLYIMLSGY.........PPFVGHCGADCGWDRGEVCRVCQNKLFESIQEG...........................KYEFPD
DAPK:DAPK1             .............FKNIFGT.PEFVAPEIVNYEP..........LGLEADMWSIGVITYILLSGA.........SPFLG..............DTKQETLANVSAVN............................YEFED
TRIO:TRIO              .............IHQLLGN.PEFAAPEIILGNP..........VSLTSDTWSVGVLTYVLLSGVS........PFLD...............DSVEETCLNICR..............................LDFSF
STE11:MAP3K2           .............MKSVTGT.PYWMSPEVISGQG..........YGRKADIWSVACTVVEMLTEK.........PPWAE..............FEAMAAIFKIATQP............................TNPKL
EMK:MARK1              .............LDTFCGS.PPYAAPELFQGKKY.........DGPEVDVWSLGVILYTLVSGS.........LPFDG..............QNLKELRERVLRG.............................KYRI
AMPK:PRKAA1            .............LRTSCGS PNYAAPEVISGRLY.........AGPEVDIWSSGVILYALLCGT.........LPFDD..............DHVPTLFKKICDG.............................IFYT
CHK2:CHEK1             .............LNKMCGT LPYVAPELLKRREF.........HAEPVDVWSCGIVLTAMLAGE.........LPWDQP.............SDSCQEYSDWKEK.............................KTYLN
CAMKK:CAMKK2           .............LSNTVGT.PAFMAPESLSETRKIF.......SGKALDVWAMGVTLYCFVFGQ.........CPFMD..............ERIMCLHSKIKS..............................QALEF
LKB1:STK11             .............CRTSQGS.PAFQPPEIANGLDTF........SGFKVDIWSAGVTLYNITTGL.........YPFEG..............DNIYKLFENIGKG.............................SYAI
PLK:PLK                .............KKTLCGT.PNYIAPEVLSKKE..........HSFEVDVWSIGCIMYTLLVGK.........[illegible]..............SCLKETYLRIKKN.............................EYSI
AUR:STK6               .............RTTLCGT.LDYLPPEMIEGRM..........HDEKVDLWSLGVLCYEFLVGK.........PPFEA..............NTYQETYKRISR..............................VEFTF
VRK:VRK1               .............KRCHDGT.IEFTSIDAHNGVA..........PSRRGDLEILGYCMIQWLTGH.........[illegible]..............KDPKYVRDSKIRYREN..........................IASLMDKCF
ULK:ULK1               .............AATLCGS PMYMAPEVIMSQH..........YDGKADLWSIGTIVYQCLTGK.........APFQA..............SSPQDLRLFYEKNKT...........................LVPTI
STE7:MAP2K1            .............ANSFVGT.RSYMSPERLQGTH..........YSVQSDIWSMGLSLVEMAVGR.........[illegible]..............AKELELMFGCQVEG............................DAAETPPR
UTK1:DKFZp761P1010     .............SSTQTIP.LKWLAPERLLLRP..........ASIRADVWSFGILLYEMVTLG.........APPYPE.............VPPTSILEHLQRR.............................KIMKR
PKC-atypical:PRKCM     .............RRSVVGT.PAYLAPEVLRNKG..........YNRSLDMWSVGVIIYVSLSGT.........[illegible]..............NEDEDIHDQIQN..............................AAFMY
CLK:CLK1               .............HSTLVST.RHYRAPEVILALG..........WSQPCDVWSIGCILIEYYLGFT........VSPTKDS............KEHLAMMERILG..............................PLPK
DYRK:DYRK1A            .............IYQYIQS.RFYRSPEVLLGMP..........YDLAIDMWSLGCILVEMHTGE.........PLFSG..............ANEVDQMNKIVEVLGIPPAHILDQAPKARKFFENLPDGTWNLKKTKDGKREYKP
HIPK:HIPK2             .............CSTYLQS.RYYRAPEIILGLP..........FCEAIDMWSLGC[illegible].........PLYPG..............ASEYDQIRYISQTQGLPAEYLLSAGTKTTRFFN.........RDTDSPYPLWRLKT
PRP4:PRP4              .............ITPYLVS.RFYRAPEIIIGKS..........YDYGIDMWSV[illegible]CTLYELYTGK.........ILPPG..............KTNNHMLKLAMDLKG.........................KMPNKMIRKGVFKDQHFDQN
TAK1:MAP3K7            .............MTNNKGS.AAWMAPEVFEGSN..........YSEKCDVFSWGIILWEVITRR.........KPFDEIG............GPAFRIMWAVHNG.............................TRPPL
MLK:MAP3K10            .............KMSAAGT.YAWMAPEVIRLSL..........FSKSSDVWSFGVLLWELLTGE.........VPYRE..............IDALAVAYGVAMN.............................KLTLPI
ZAK:ZAK                .............HMSLVGT.FPWMAPEVIQSLP..........VSETCDTYSYGVVLWEMLTRE.........VPFKG..............LEGLQVAWLVVEK.............................NERLTI
AR[illegible]:LOC51086 .............MTKQPGN.LRWMAPEVFTQCTR.........YTIKADVFSYALCLWEILTGE.........IPFAH..............LKPAAAAADMAYH.............................HIRP
Raf[illegible]         .............VEQPTGS.VLWMAPEVIRMQDNNP........FSFQSDVYSYGIVLYELMTGE.........LPYSHI.............NNRDQIIFMVGRG.............................YAS
RIP:ANKRD3             .............MDGLFGT.IAYLPPERIREKSRL.........FDTKHDVYSFAIVIWGVLTQK.........KPFADE.............KNILHIMVKVVKG.............................HRPEL
LIMK:LIMK1             .............RYTVVGN.PYWMAPEMINGRS..........YDEKVDVFSFGIVLCEIIGRVN........ADPDYL.............PRTMDFGLNVRG..............................FLDRYC
TESK:TESK1             .............PLAVVGS.PYWMAPEVLRGEL..........YDEKADVFAFGIVLCELIARVP........ADPDYL.............PRTEDFGLDVPA..............................FRTLV
APK:LOC51135           .............TSRIVGT.TAYMAPEALRGE...........ITPKSDIYSFGVVLLEIITGLP........AVDEHREP...........QLLLDIKEEIED..............................EEKT
IRAK:IRAK1             .............TQTVRGT.LAYLPEEYIKTGR..........LAVDTDTFSFGVVVLETLAGQR........AVKTHGART..........KYLKDLVEEEAEEAGVALRSTQSTLQAGLAADAWAAPIAMQIYKKHLDPRPGPC
IKK:CHUK               .............CTSFVGT.LQYLAPELFENKP..........YTATVDYWSFGTMVFECIAGY.........RPFLHH.............LQPFTWHEKIKKKD............................PKCIFAC
IKKE:IKKE              .............FVSVYGT.EEYLHPDMYERAVLRKPQQKA..PGVTVDLWSIGVTLYHAATGSLP.......FIPFGGP............RRNKEIMYRITTEKPAGAIAGAQRRENGP.............LEWSYTL
AATK:KIAA1079          .............DDKKVFP LRWTAPELVTSFQDRLLTAD....QTKYSNIWSLGVTLWELFDNA.........AQPYSN.............LSNLDVLNQVIRER............................DTKLPK
NEK:NEK2               .............AKTFVGT.PYYMSPEQMNRMS..........YNEKSDIWSLGCLLYELCALM.........PPFTA..............FSQKELAGKIREG.............................KFRRI
EIF2AK:PRKR            .............RTRSKGT.LRYMSPEQISSQD..........YGKEVDLYALGLILAELLHVCD........TA.................FETSKFFTDLRDG.............................II
Pim:PIM1               .............YTDFDGT.RVYSPPEWIRYHRY.........HGRSAAVWSLGILLYDMVCGD.........IPF................EHDEEIIRGQV...............................FF
TLK:TLK1               .............TSQGAGT.YWYLPPECFVVGKEPPK......ISNKVDVWSVGVIFYQCLYGR.........KPFGHN.............QSQQDILQENTILK............................ATEVQF
WNK:PRKWNK1            .............AKSVIGT.PEFMAPEMYEEK...........YDESVDVYAFGMCMLEMATSEY........PYSEC..............QNAAQIYRRVTSG.............................VKPAS
PKMYT:PKMYT1           .............GEVQEGD.PRYMAPELLQGS...........YGTAADVFSLGLTILEVACNM.........ELPHGG.............EGWQQLRQGYLPP.............................
Wee1:WEE1              .............PQVEEGD.SRFLANEVLQENYT.........HLPKADIFALALTVVCAAGAEP........LPRNG..............DQWHEIRQG.................................RLPRI
Col:MAP3K8             .............PKDLRGT.EIYMSPEVILCRG..........HSTKADIYSLGATLIHMQTGT.........PPWVKRYPR..........SAYPSYLYIIHKQAP...........................PLEDI
JAK:JAK1-1             .............RQECIER.IPWIAPECVEDSKN.........LSVAADKWSFGTTLWEICYNG.........EIPLKD.............KTLIEKERFYESR.............................CRPV
MPS1:TTK               .............KDSQVGT.VNYMPPEAIKDMSSSRENGKSKSKISPKSDVWSLGCILYYMTYGK.........TPFQQII............NQISKLHAIIDPN.............................HEIEF
Mos:MOS                .............SYPLGGT.YTHRAPELLKGEG..........VTPKADIYSFAITLWQMTTKQ.........APYSG..............ERQHILYAVVAYDLR...........................PSLSA
IRE:ERN1               .............RSGVPGT.EGWIAPEMLSEDCKEN.......PTYTVDIFSAGCVFYYVVSEGS........HPFGK..............SLQRQANILLGACS............................LDCLH
MPSK:STK16             .............WAAQRCT.ISYRAPELFSVQSHCV.......IGERTDVWSLGCVLYAMMFGE.........GPYDMVF............QKGDSVALAVQN..............................QLSI
GAK:GAK                .............EITRNTT.PMYRTPEIIDLYSNFP.......IGEKQDIWALGCILYLLCFRQ.........HPFEDG.............AKLRIVNGKYSIP.............................
BIKE:BIKE              .............EIKKYTT.LSYRAPEMINLYGGKP.......ITTKADIWALGCLLYKLCFFT.........LPF................GESQVAICDG................................NFTI
TOPK:TOPK              .............EACYIGT.EPWKPKEAVEENGV.........ITDKADIFAFGLTLWEMMTLS.........IPHINLSNDD.........DDEDKTFDESDFDDEA..........................YYAALGTR
ILK:ILK                ................RMYAPAWVAPEALQKKPEDT.......NRRSADMWSFAVLLWELVTRE.........VPFAD..............LSNMEIGMKVALEG............................LRPTI
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MAST:KIAA0303          PEKDEAPP.................PDAQDLITLLLRQNPLERLGTGG...AYEVKQHRFF...............
MAST205:MAST205        PEGDEALP.................PDAQDLTSKLLHQNPLERLGTGS...AYEVKQHPFFTGLDWTGLLRQKAEFIPQLESEDDTSYFDTRSERYHHMDSEDEEEVSEDG.......
CDKL:CDKL1             PEDMEPLELKFPNIS..........YPALGLLKGCLHMDPTERLT.....CEQLLHHPYFENIREIEDLAKEHDKPTRKTLRKSRKHHCFTETSKLQYLPQLTGSSILPA.......
NLK:NLK                PHKQPSLPVLYTLSSQAT.......HEAVHLLCRMLVFDPSKRIS.... AKDALAHPYLDEGRLRYHTCMCKCCFSTSTGRVYTSDFEPVTNPKFDDTFEKNLSSVRQV.......
ACK:ACK1               PEDCP....................QDIYNVMVQCWAHKPEDRPT.....FVALRDFLLEAQP...............
EGFR:EGFR              PPICT....................IDVYMIMVKCWMIDADSRPK.....FRELIIEFSKMARDPQRYLVIQGDERMHLPSPTDSNFYRALMDEEDMDDVVDADEYLIPQ.......
Axl:AXL                PADCL....................DGLYALMSRCWELNPQDRPS.....FTELREDLENTLKALPPAQEPDEILYVNMDEGGGYPEPPGAAGGADPPTQPDPKDSCSCL.......
Met:MET                PEYCP....................DPLYEVMLKCWHPKAEMRPS.....FSELVSRISAIFSTFIGEHYVHVNATYVNVKCVAPYPSLLSSEDNADDEVDTRPASFWET.......
TGFBR-2:TGFBR2         .........................QMVCETLTECWDHDPEARLT.....AQCVAERFSELEHLDRLSGRSCSEEKIPEDGSLNTTK...............
SYK:SYK                PAGCP....................REMYDLMNLCWTYDVENRPG.... FAAVELRLRNYYYDVVN...............
JAK:JAK1-2             PPNCP....................DEVYQLMRKCWEFQPSNRTS.... .FQNLIEGFEALLK...............
Ryk:RYK                PINCP....................DELFAVMACCWALDPEERPK.....FQQLVQCLTEFHAALGAYV...............
PDPK1:PDPK1            PEKFF....................PKARDLVEKLLVLDATKRLGCEEMEGYGPLKAHPFFESVTWENLHQQTPPKLTAYLPAMSEDDEDCYGNYDNLLSQFGCMQVSSSS.......
GRK:RHOK               PDKFS....................QASKDFCEALLEKDPEKRLGFRDET.CDKLRAHPLF...............
DMPK:DMPK              PLVDEGVP.................EEARDFIQRLLCP PETRLGRGG ..AGDFRTHPFFFGLDWDGLRDSVPPFTPDFEGATDTCNFDLVEDGLTAMTLSDIREGAPLG.......
NDR:STK38              PPEVPIS..................EKAKDLILRFCCE WEHRIGAPG...VEEIKSNSFFEGVDWEHIRERPAAISIEIKSIDDTSNFDEFPESDILKPTVATSNHPETDY.......
MAK:MAK                PQCVPINLKTLIPNAS.........NEAIQLMTEMLNWDPKKRPT.....ASQALKHPYFQVGQVLGPSSNHLESKQSLNKQLQPLESKPSLVEVEPKPLPDIIDQVVGQ.......
RAGE:RAGE              PFKKGSGIPLLTTNLS.........PQCLSLLHAMVAYDPDERIA.... .AHQALQHPYFQEQRKTEKRALGSHRKAGFPEHPVAPEPLSNSCQISKEGRKQKQSLKQEE.......
SPAK:STK39             GVEDKEMMKKYG.............KSFRKLLSLCLQKDPSKRPT.... .AAELLKCKFFQKAKNREYLIEKLLTRTPDIAQRAKKVRRVPGSSGHLHKTEDGDWEWSDD .......
S6K-1:RPS6KA1-2        GNWNTVS .................ETAKDLVSKMLHVDPHQRLT.. ...AKQVLQHPWVTQKDKLPQSQLSHQDLQLVKGAMAATYSALNSSKPTPQLKPIESSILAQR.......
MAPKAPK:MAPKAPK2       PEWSEVS..................EEVKMLIRNLLKTEPTQRMT.. ...ITEFMNHPWIMQSTKVPQTPLHTSRVLKEDKERWEDVKGCLHDKNSDQATWLTRL.......
ERK-2:MAPK6            PHKPLTQLLPGIS............REALDFLEQILTFSPMDRLT.....AEEALSHPYMSIYSFPMDEPISSHPFHIEDEVDDILLMDETHSHIYNWERYHDCQFSEHD.......
MKNK:MKNK1             KDWAHIS..................SEAKDLISKLLVRDAKQRLS.....AAQVLQHPWVQGQAPEKGLPTPQVLQRNSSTMDLTLFAAEAIALNRQLSQHEENELAEEP.......
DAPK:DAPK1             EYFSNTS..................ALAKDFIRRLLVKDPKKRMT.....IQDSLQHPWIKPKDTQQALSRKASAVNMEKFKKFAARKKWKQSVRLISLCQRLSRSFLSR.......
TRIO:TRIO              PDDYFKGVS................QKAKEFVCFLLQEDPAKRPS.....AALALQEQWLQAGNGRSTGVLDTSRLTSFIERRKHQNDVRPIRSIKNFLQSRLLPRV.......
STE11:MAP3K2           PPHVS....................DYTRDFLKRIFVE.AKLRPS.... .ADELLRHMFVHYH...............
EMK:MARK1              PFYMS....................TDCENLLKKLLVLNPIKRGS... ..LEQIMKDRWMNVGHEEEELKPYTEPDPDF...............
AMPK:PRKAA1            PQYLN....................PSVISLLKHMLQVDPMKRAS.. ...IKDIREHEWFKQDLPKYLFPEDPSYSSTMIDDEALKEVCEKFECSEEEVLSCLYNRNHQD.......
CHK2:CHEK1             PWKKID...................SAPLALLHKILVENPSARIT. ....IPDIKKDRWYNKPLKKGAKRPRVTSGGVSESPSGFSKHIQSNLDFSPVNSASSEENVKYS.......
CAMKK:CAMKK2           PDQPDIA.................. EDLKDLITRMLDKNPESRIV .....VPEIKLHPWVTRHGAEPLPSEDENCTLVEVTEEEVENSVKHIPSLATVILVKTMIRKRSF .......
LKB1:STK11             PGDCG....................PPLSDLLKGMLEYEPAKRFS.....IRQIRQHSWFRKKHPPAEAPVPIPPSPDTKDRWRSMTVVPYLEDLHGADEDEDLFDIEDD.......
PLK:PLK                PKHIN....................PVAASLIQKMLQTDPTARPT.....INELLNDEFFTSGYIPARLPITCLTIPPRFSIAPSSLDPSNRKPLTVLNKGLENPLPERP.......
AUR:STK6               PDFVT....................EGARDLISRLLKHNPSQRPM.....LREVLEHPWITANSSKPSNCQNKESASKQS...............
VRK:VRK1               PEKNKP ..........GEIAKYMETVKLLDYTEKPLY....ENLRDILLQGLKA.IGSKDDGKLD. LSVVENGGLKAKTITKKRKKEIEESKEPGVEDTEWSNTQTEEAIQTRSRTR.......
ULK:ULK1               PRETS....................APLRQLLLALLQRNHKDRMD.. ...FDEFFHHPFLDASPSVRKSPPVPVPSYPSSGSGSSSSSSSTSHLASPPSLGEMQQLQKTL.......
STE7:MAP2K1            PRTPGRPLSSYGMDSRPP...MAIFELLDYIVNEPPPKLPSGVFS..LEFQDFVNKCLIKNPAERAD.....LKQLMVHAFIKRSDAEEVDFAGWLCSTIGLNQPSTPTHAAGV.......
UTK1:DKFZp761P1010     PSSCT.................... HTMYSIMKSCWRWREADRPS. ....PRELRLRLEAAIKTADDEAVLQVPELVVPELYAAVAGIRVESLFYNYSML.......
PKC-atypical:PRKCM     PPNPWKEIS................HEAIDLINNLLQVKMRKRYS.....VDKTLSHPWLQDYQTWLDLRELECKIGERYITHESDDLRWEKYAGEQRLQYPTHLINPSA.......
CLK:CLK1               HMIQKTRKRKYFHHDRLDWDEHSSAGRYVSRACKPLKEFMLSQDVEHERLFDLIQKMLEYDPAKRIT.....LREALKHPFFDLLKKSI...............
DYRK:DYRK1A            PGTRKLHNILGVETGGPGGR.............RAGESGHTVADYLKFKDLILRMLDYDPKTRIQ.... PYYALQHSFFKKTADEGTNTSNSVSTSPAMEQSQSSGTTSSTSSSSGGSSGTSNSGRARS.......
HIPK:HIPK2             PDDHEAETGIKSKEARKYIFNCLDDMAQVNMTTDLEGSDMLVEKADRREFIDLLKKMLTIDADKRIT.... .PIETLNHPFVTMTHLLDFPHSTHVKSCFQNMEICKRRVNMYDTVNQSKTPFITHVAPSTS .......
PRP4:PRP4              LNFMYIEVDKVTEREKVTVMSTINPTKDLLADLIGCQRLPEDQRKKVHQLKDLLDQILMLDPAKRIS.....INQALQHAFIQEKI...............
TAK1:MAP3K7            IKNLP....................KPIESLMTRCWSKDPSQRPS.....MEEIVKIMTHLMRYFPGADEPLQYPCQYSDEGQSNSATSTGSFMDIASTNTSNKSDTNME.......
MLK:MAP3K10            PSTCP....................EPFARLLEECWDPDPHGRPD.....FGSILKRLEVIEQSALFQMPLESFHSLQEDWKLEIQHMFDDLRTKEKELRSREEELLRAA.......
ZAK:ZAK                PSSCP....................RSFAELLHQCWEADAKKRPS.....FKQIISILESMSNDTSLPDKCNSFLHNKAEWRCEIEATLERLKKLERDLSFKEQELKERE.......
ARCK:LOC51086          PIGYSIP..................KPISSLLIRGWNACPEGRPE.....FSEVVMKLEECLCNIELMSPASSNSSGSLSPSSSSDCLVNRGGPGRSHVAALRSRFELEY.......
Raf:RAF1               PDLSKLYKNCP..............KAMKRLVADCVKKVKEERPL.....FPQILSSIELLQHSLPKINRSASEPSLHRAAHTEDINACTLTTSPRLPVF.......
RIPK:ANKRD3            PPVCRARPRAC..............SHLIRLMQRCWQGDPRVRPT.... .FQEITSETEDLCEKPDDEVKETAHDLDVKSPPEPRSEVVPARLKRASAPTFDNDYSLSEL.......
LIM:LIMK1              PPNCP....................PSFFPITVRCCDLDPEKRPS... ..FVKLEHWLETLRMHLAGHLPLGPQLEQLDRGFWETYRRGESGLPAHPEVPD.......
TESK:TESK1             GDDCP....................LPFLLLAIHCCNLEPSTRAP.....FTEITQHLEWILEQLPEPAPLTRTALTHNQGSVARGGPSATLPRPDPRLSRSRSDLFLPPS.......
APKA:LOC51135          IEDYIDKKMNDAD............STSVEAMYSGASQCRHEKKNKSPD..IKKVHQLLQEMTAS...............
IRAK:IRAK1             PPELG.................... LGLGQLACCCLHRRAKRRPP.....MTQVYERLEKLQAVVAGVPGHLEAASCIPPSPQENSYVSSTGRAHSGAAPWQP .......
IKK:CHUK               EEMSGEVRFSSHLPQPNSLCSLIV.EPMENWLQLMLNWDPQQRGG.....PVDLTLKQPRCFVLMDHILNLKIVHILNMTSAKIISFLLP...............
IKKE:IKKE              PITCQLSLGLQ..............SQLVPILANILEV.EQAKCWG.....FDQFFAETSDILQRVVVHVFSLSQAVLHHIYIHAHNTIAIFQEAVHKQTSVAP.......
AATK:KIAA1079          PQLEQPYS.................DRWYEVLQFCWLS.PEKRPA.....AEDVHRLLTYLRLQSQRDSEVDFEQQWNALKPNTNSRDSSNNAAFPILDHFARDRLGREM.......
NEK:NEK2               PYRYS....................DELNEIITRMLNLKDYHRPS.....VEEILENPLIADLVADEQRRNLERRGRQLGEPEKSQDSSPVLSELKLKEIQLQERERALK.......
EIF2AK:PRKR            SDIFD....................KKEKTLLQKLLSKKPEDRPN... . TSEILRTLTVWKKSPEKNERHTC...............
Pim:PIM1               RQRVS....................SECQHLIRWCLALRPSDRPT.....FEEIQNHPWMQDVLLPQETAEIHLHSLSPGPSK...............
TLK:TLK1               PVKPVVS .................SEAKAFIRRCLAYRKEDRFD.....VHQLACDPYLLPHMRRSNSSGNLHMAGLTASPTPPSSSIITY.......
WNK:PRKWNK1            FDKVAI...................PEVKEIIEGCIRQNKDERYS.....IKDLLNHAFFQEETGVRVELAEEDDGEKIAIKLWLRIEDIKKLKGKYKDNEAIEFSFDLE.......
PKMYT:PKMYT1           .EFTAGLS.................SELRSVLVMMLEPDPKLRAT.....AEALLALPVLRQPRAWGVLWCMAAEALSRGWALWQALLALLCWLWHGLAHPASWLQPLGP.......
Wee1:WEE1              PQVLS....................QEFTELLKVMIHPDPERRPS.....AMALVKHSVLLSASRKSAEQLRIELNAEKFKNSLLQKELKKAQMAKAAAEERALFTDRMA .......
Cot:MAP3K8             ADDCS....................PGMREIIEASLERNPNHRPR.....AADLLKHEALNPPREDQPRCTSLDSALLERKRLLSRKELELPENIADSSCTGSTEESEML.......
JAK:JAK1-1             TPSC.....................KELADLMTRCMNYDPNQRPF.....FRAIMRDINKLEEQNPDIVSRKKNQPTEVDPTHFEKRF...............
MPS1:TTK               PDIPE....................KDLQDVLKCCLKRDPKQRIS... . IPELLAHPYVQIQTHPVNQMAKGTTEEMKYVLGQLVGLNSPNSILKAAKTLYEHYSGGES.......
Mos:MOS                AVFEDSLPG................QRLGDVIQRCWRPSAAQRPS. ....ARLLLVDLTSLKAELG...............
IRE:ERN1               PEKHED ...................VIARELIEKMIAMDPQKRPS.....ANDVLKHPFFWSLEKQLQFFQDVSDRIEKESLDGPIVKQLERGGRAVVKMDWRENITDPL.......
MPSK:STK16             PQSPRHS..................SALRQLLNSMMTVDPHQRPH.....IPLLLSQLEALQPPAPGQHTTQIEKAAC...............
GAK:GAK                .PHDTQY..................TVFHSLIRAMLQVNPEERLS.... .IAEVVHQLQEIAAARNVNPKSPITELLEQNGGYGSATLSRGPPPPVGPAGSGYSGGLALA.......
BIKE:BIKE              PDNSRYS..................RNIHCLIRFMLEPDPEHRPD.....IFQVSYFAFKFAKKDCPVSNINKCCKQLLRHGALLTEILLFLQLFLNR.......
TOPK:TOPK              PPINMEELDESY.............QKVIELFSVCTNEDPKDRPS.....AAHIVEALETDV...............
ILK:ILK                PPGIS....................PHVCKLMKICMNEDPAKRPK.....FDMIVPILEKMQDK ...............
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Table 4

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HEADER    ----                                        XX-XXX-XX    xxxx
COMPND    ---
REMARK   3
REMARK   3 REFINEMENT.
REMARK   3   PROGRAM     : REFMAC 5.1.21
REMARK   3   AUTHORS     : MURSHUDOV,VAGIN,DODSON
REMARK   3
REMARK   3    REFINEMENT TARGET : MAXIMUM LIKELIHOOD
REMARK   3
REMARK   3  DATA USED IN REFINEMENT.
REMARK   3   RESOLUTION RANGE HIGH (ANGSTROMS) :   2.03
REMARK   3   RESOLUTION RANGE LOW  (ANGSTROMS) :  81.65
REMARK   3   DATA CUTOFF            (SIGMA(F)) : NONE
REMARK   3   COMPLETENESS FOR RANGE        (%) :  99.81
REMARK   3   NUMBER OF REFLECTIONS             :   25766
REMARK   3
REMARK   3  FIT TO DATA USED IN REFINEMENT.
REMARK   3   CROSS-VALIDATION METHOD           : THROUGHOUT
REMARK   3   FREE R VALUE TEST SET SELECTION   : RANDOM
REMARK   3   R VALUE     (WORKING + TEST SET) : 0.19077
REMARK   3   R VALUE           (WORKING SET) :  0.18920
REMARK   3   FREE R VALUE                     :  0.22121
REMARK   3   FREE R VALUE TEST SET SIZE   (%) :  5.0
REMARK   3   FREE R VALUE TEST SET COUNT      :  1368
REMARK   3
REMARK   3  FIT IN THE HIGHEST RESOLUTION BIN.
REMARK   3   TOTAL NUMBER OF BINS USED           :      20
REMARK   3   BIN RESOLUTION RANGE HIGH           :   2.030
REMARK   3   BIN RESOLUTION RANGE LOW            :   2.083
REMARK   3   REFLECTION IN BIN     (WORKING SET) :    1894
REMARK   3   BIN R VALUE           (WORKING SET) :   0.289
REMARK   3   BIN FREE R VALUE SET COUNT          :     113
REMARK   3   BIN FREE R VALUE                    :   0.297
REMARK   3
REMARK   3  NUMBER OF NON-HYDROGEN ATOMS USED IN REFINEMENT.
REMARK   3   ALL ATOMS                 :     2400
REMARK   3
REMARK   3  B VALUES.
REMARK   3   FROM WILSON PLOT           (A**2) : NULL
REMARK   3   MEAN B VALUE      (OVERALL, A**2) :  27.297
REMARK   3   OVERALL ANISOTROPIC B VALUE.
REMARK   3    B11 (A**2) :     0.50
REMARK   3    B22 (A**2) :     0.50
REMARK   3    B33 (A**2) :    -0.74
REMARK   3    B12 (A**2) :     0.25
REMARK   3    B13 (A**2) :     0.00
REMARK   3    B23 (A**2) :     0.00
REMARK   3
REMARK   3  ESTIMATED OVERALL COORDINATE ERROR.
REMARK   3   ESU BASED ON R VALUE                                (A):   0.151
REMARK   3   ESU BASED ON FREE R VALUE                           (A):   0.140
REMARK   3   ESU BASED ON MAXIMUM LIKELIHOOD                     (A):   0.105
REMARK   3   ESU FOR B VALUES BASED ON MAXIMUM LIKELIHOOD (A**2):   3.960
REMARK   3
REMARK   3 CORRELATION COEFFICIENTS.
REMARK   3   CORRELATION COEFFICIENT FO-FC      :   0.959
REMARK   3   CORRELATION COEFFICIENT FO-FC FREE :   0.946
REMARK   3
REMARK   3  RMS DEVIATIONS FROM IDEAL VALUES         COUNT    RMS    WEIGHT
REMARK   3   BOND LENGTHS REFINED ATOMS        (A):  2334 ; 0.011 ; 0.021
REMARK   3   BOND ANGLES REFINED ATOMS   (DEGREES):  3174 ; 1.105 ; 1.959
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REMARK   3   TORSION ANGLES, PERIOD 1     (DEGREES):   273 ; 5.228 ; 5.000
REMARK   3   CHIRAL-CENTER RESTRAINTS         (A**3):   336 ; 0.080 ; 0.200
REMARK   3   GENERAL PLANES REFINED ATOMS        (A):  1800 ; 0.004 ; 0.020
REMARK   3   NON-BONDED CONTACTS REFINED ATOMS (A):  1070 ; 0.202 ; 0.200
REMARK   3   H-BOND (X...Y) REFINED ATOMS        (A):   150 ; 0.145 ; 0.200
REMARK   3   SYMMETRY VDW REFINED ATOMS          (A):    46 ; 0.199 ; 0.200
REMARK   3   SYMMETRY H-BOND REFINED ATOMS       (A):    10 ; 0.267 ; 0.200
REMARK   3
REMARK   3  ISOTROPIC THERMAL FACTOR RESTRAINTS.      COUNT   RMS    WEIGHT
REMARK   3   MAIN-CHAIN BOND REFINED ATOMS  (A**2):  1365 ; 0.799 ; 1.500
REMARK   3   MAIN-CHAIN ANGLE REFINED ATOMS (A**2):  2214 ; 1.519 ; 2.000
REMARK   3   SIDE-CHAIN BOND REFINED ATOMS  (A**2):   969 ; 2.024 ; 3.000
REMARK   3   SIDE-CHAIN ANGLE REFINED ATOMS (A**2):   960 ; 3.247 ; 4.500
REMARK   3
REMARK   3  NCS RESTRAINTS STATISTICS
REMARK   3   NUMBER OF NCS GROUPS : NULL
REMARK   3
REMARK   3
REMARK   3  TLS DETAILS
REMARK   3   NUMBER OF TLS GROUPS  :    2
REMARK   3
REMARK   3   TLS GROUP :     1
REMARK   3    NUMBER OF COMPONENTS GROUP :    1
REMARK   3    COMPONENTS        C SSSEQI   TO  C SSSEQI
REMARK   3    RESIDUE RANGE :   A    33        A   306
REMARK   3    ORIGIN FOR THE GROUP (A):  65.5800  27.1270  -0.6960
REMARK   3    T TENSOR
REMARK   3      T11:   0.1410 T22:   0.1266
REMARK   3      T33:   0.0824 T12:  -0.0364
REMARK   3      T13:  -0.0112 T23:  -0.0301
REMARK   3    L TENSOR
REMARK   3      L11:   1.3945 L22:   0.7253
REMARK   3      L33:   0.8680 L12:   0.1248
REMARK   3      L13:  -0.3386 L23:   0.0070
REMARK   3    S TENSOR
REMARK   3      S11:  -0.0668 S12:   0.0858 S13:   0.0787
REMARK   3      S21:  -0.0201 S22:   0.1089 S23:   0.0287
REMARK   3      S31:   0.0298 S32:   0.0689 S33:  -0.0421
REMARK   3
REMARK   3   TLS GROUP :     2
REMARK   3    NUMBER OF COMPONENTS GROUP :    1
REMARK   3    COMPONENTS        C SSSEQI   TO  C SSSEQI
REMARK   3    RESIDUE RANGE :   L     1        L     1
REMARK   3    ORIGIN FOR THE GROUP (A):  73.8810  32.6080   1.3720
REMARK   3    T TENSOR
REMARK   3      T11:   0.1174 T22:   0.1943
REMARK   3      T33:   0.1391 T12:  -0.1003
REMARK   3      T13:  -0.0486 T23:  -0.0722
REMARK   3    L TENSOR
REMARK   3      L11:  14.6629 L22:  15.7148
REMARK   3      L33:   8.9109 L12: -11.1563
REMARK   3      L13:  -1.8290 L23: -15.1157
REMARK   3    S TENSOR
REMARK   3      S11:   0.2483 S12:   0.1966 S13:   0.0403
REMARK   3      S21:   0.0302 S22:   0.1725 S23:   0.8712
REMARK   3      S31:  -0.4688 S32:   0.8689 S33:  -0.4208
REMARK   3
REMARK   3
REMARK   3  BULK SOLVENT MODELLING.
REMARK   3   METHOD USED : BABINET MODEL WITH MASK
REMARK   3   PARAMETERS FOR MASK CALCULATION
REMARK   3   VDW PROBE RADIUS   :  1.40
REMARK   3   ION PROBE RADIUS   :  0.80
REMARK   3   SHRINKAGE RADIUS   :  0.80
REMARK   3
REMARK   3  OTHER REFINEMENT REMARKS: NULL
REMARK   3
CISPEP   1 GLU A  124    PRO A  125                     0.00
CRYST1   95.566   95.566   80.862  90.00  90.00 120.00 P 65
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SCALE1      0.010464  0.006041  0.000000        0.00000
SCALE2      0.000000  0.012083  0.000000        0.00000
SCALE3      0.000000  0.000000  0.012367        0.00000
ATOM      1  N   PRO A  33      89.149  40.408 -18.445  1.00 67.30           N
ATOM      2  CA  PRO A  33      88.476  41.476 -17.647  1.00 67.14           C
ATOM      3  CB  PRO A  33      86.997  41.088 -17.742  1.00 67.23           C
ATOM      4  CG  PRO A  33      86.877  40.393 -19.088  1.00 67.40           C
ATOM      5  CD  PRO A  33      88.243  39.825 -19.451  1.00 67.35           C
ATOM      6  C   PRO A  33      88.938  41.544 -16.180  1.00 66.89           C
ATOM      7  O   PRO A  33      89.154  42.657 -15.690  1.00 67.00           O
ATOM      8  N   LEU A  34      89.091  40.388 -15.519  1.00 66.32           N
ATOM      9  CA  LEU A  34      89.499  40.274 -14.100  1.00 65.68           C
ATOM     10  CB  LEU A  34      90.888  40.895 -13.835  1.00 65.85           C
ATOM     11  CG  LEU A  34      91.302  41.230 -12.390  1.00 66.30           C
ATOM     12  CD1 LEU A  34      91.714  39.982 -11.600  1.00 66.80           C
ATOM     13  CD2 LEU A  34      92.418  42.268 -12.376  1.00 67.23           C
ATOM     14  C   LEU A  34      88.454  40.795 -13.100  1.00 64.94           C
ATOM     15  O   LEU A  34      87.873  41.869 -13.284  1.00 64.93           O
ATOM     16  N   GLU A  35      88.242  40.036 -12.027  1.00 63.77           N
ATOM     17  CA  GLU A  35      87.186  40.343 -11.061  1.00 62.65           C
ATOM     18  CB  GLU A  35      86.798  39.087 -10.270  1.00 63.13           C
ATOM     19  CG  GLU A  35      87.856  38.599  -9.297  1.00 65.02           C
ATOM     20  CD  GLU A  35      87.245  37.871  -8.122  1.00 67.48           C
ATOM     21  OE1 GLU A  35      87.017  38.518  -7.069  1.00 68.53           O
ATOM     22  OE2 GLU A  35      86.987  36.654  -8.260  1.00 68.44           O
ATOM     23  C   GLU A  35      87.444  41.549 -10.130  1.00 61.12           C
ATOM     24  O   GLU A  35      86.859  41.645  -9.049  1.00 61.05           O
ATOM     25  N   SER A  36      88.299  42.477 -10.561  1.00 59.16           N
ATOM     26  CA  SER A  36      88.360  43.797  -9.923  1.00 56.76           C
ATOM     27  CB  SER A  36      89.767  44.375  -9.977  1.00 57.09           C
ATOM     28  OG  SER A  36      90.185  44.711  -8.665  1.00 57.93           O
ATOM     29  C   SER A  36      87.321  44.757 -10.537  1.00 54.68           C
ATOM     30  O   SER A  36      87.465  45.987 -10.482  1.00 54.42           O
ATOM     31  N   GLN A  37      86.278  44.159 -11.121  1.00 51.69           N
ATOM     32  CA  GLN A  37      85.055  44.844 -11.531  1.00 48.71           C
ATOM     33  CB  GLN A  37      84.288  44.000 -12.556  1.00 48.70           C
ATOM     34  CG  GLN A  37      85.032  43.705 -13.853  1.00 48.89           C
ATOM     35  CD  GLN A  37      84.357  42.614 -14.681  1.00 48.93           C
ATOM     36  OE1 GLN A  37      83.235  42.790 -15.159  1.00 48.57           O
ATOM     37  NE2 GLN A  37      85.041  41.490 -14.849  1.00 49.23           N
ATOM     38  C   GLN A  37      84.159  45.068 -10.309  1.00 46.45           C
ATOM     39  O   GLN A  37      83.061  45.621 -10.425  1.00 45.80           O
ATOM     40  N   TYR A  38      84.634  44.634  -9.142  1.00 43.79           N
ATOM     41  CA  TYR A  38      83.815  44.599  -7.935  1.00 41.47           C
ATOM     42  CB  TYR A  38      83.277  43.178  -7.683  1.00 40.80           C
ATOM     43  CG  TYR A  38      82.415  42.680  -8.813  1.00 37.71           C
ATOM     44  CD1 TYR A  38      81.078  43.060  -8.913  1.00 36.03           C
ATOM     45  CE1 TYR A  38      80.283  42.622  -9.970  1.00 34.69           C
ATOM     46  CZ  TYR A  38      80.834  41.799 -10.940  1.00 33.35           C
ATOM     47  OH  TYR A  38      80.058  41.362 -11.982  1.00 33.33           O
ATOM     48  CE2 TYR A  38      82.156  41.409 -10.861  1.00 33.59           C
ATOM     49  CD2 TYR A  38      82.941  41.853  -9.801  1.00 35.25           C
ATOM     50  C   TYR A  38      84.546  45.110  -6.711  1.00 40.70           C
ATOM     51  O   TYR A  38      85.729  44.835  -6.522  1.00 40.55           O
ATOM     52  N   GLN A  39      83.820  45.882  -5.907  1.00 39.47           N
ATOM     53  CA  GLN A  39      84.267  46.331  -4.602  1.00 38.56           C
ATOM     54  CB  GLN A  39      83.781  47.755  -4.350  1.00 39.00           C
ATOM     55  CG  GLN A  39      84.391  48.448  -3.148  1.00 41.12           C
ATOM     56  CD  GLN A  39      83.988  49.920  -3.066  1.00 44.96           C
ATOM     57  OE1 GLN A  39      84.489  50.753  -3.833  1.00 45.76           O
ATOM     58  NE2 GLN A  39      83.081  50.241  -2.139  1.00 46.18           N
ATOM     59  C   GLN A  39      83.673  45.376  -3.567  1.00 37.29           C
ATOM     60  O   GLN A  39      82.451  45.224  -3.473  1.00 36.66           O
ATOM     61  N   VAL A  40      84.546  44.738  -2.797  1.00 35.79           N
ATOM     62  CA  VAL A  40      84.124  43.757  -1.808  1.00 34.34           C
ATOM     63  CB  VAL A  40      85.190  42.667  -1.580  1.00 34.42           C
ATOM     64  CG1 VAL A  40      84.573  41.470  -0.871  1.00 34.56           C
ATOM     65  CG2 VAL A  40      85.822  42.238  -2.908  1.00 34.84           C
ATOM     66  C   VAL A  40      83.794  44.435  -0.487  1.00 33.17           C
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ATOM	67	O	VAL A	40	84.544	45.296	-0.021	1.00	32.88	O
ATOM	68	N	GLY A	41	82.659	44.047	0.094	1.00	31.35	N
ATOM	69	CA	GLY A	41	82.253	44.508	1.407	1.00	29.70	C
ATOM	70	C	GLY A	41	82.304	43.395	2.438	1.00	28.50	C
ATOM	71	O	GLY A	41	83.121	42.480	2.315	1.00	28.62	O
ATOM	72	N	PRO A	42	81.435	43.470	3.446	1.00	27.60	N
ATOM	73	CA	PRO A	42	81.406	42.494	4.543	1.00	27.00	C
ATOM	74	CB	PRO A	42	80.355	43.073	5.501	1.00	27.10	C
ATOM	75	CG	PRO A	42	80.182	44.506	5.089	1.00	27.33	C
ATOM	76	CD	PRO A	42	80.416	44.521	3.618	1.00	27.63	C
ATOM	77	C	PRO A	42	80.958	41.091	4.127	1.00	26.95	C
ATOM	78	O	PRO A	42	80.212	40.921	3.149	1.00	26.22	O
ATOM	79	N	LEU A	43	81.421	40.114	4.905	1.00	26.40	N
ATOM	80	CA	LEU A	43	81.016	38.726	4.827	1.00	26.26	C
ATOM	81	CB	LEU A	43	81.928	37.888	5.737	1.00	26.16	C
ATOM	82	CG	LEU A	43	81.741	36.367	5.836	1.00	26.71	C
ATOM	83	CD1	LEU A	43	81.971	35.666	4.486	1.00	25.17	C
ATOM	84	CD2	LEU A	43	82.656	35.790	6.911	1.00	25.63	C
ATOM	85	C	LEU A	43	79.573	38.592	5.292	1.00	26.23	C
ATOM	86	O	LEU A	43	79.234	39.010	6.409	1.00	25.53	O
ATOM	87	N	LEU A	44	78.737	37.998	4.439	1.00	25.89	N
ATOM	88	CA	LEU A	44	77.321	37.786	4.746	1.00	26.23	C
ATOM	89	CB	LEU A	44	76.460	37.994	3.500	1.00	25.73	C
ATOM	90	CG	LEU A	44	76.500	39.383	2.881	1.00	25.94	C
ATOM	91	CD1	LEU A	44	75.804	39.381	1.516	1.00	24.87	C
ATOM	92	CD2	LEU A	44	75.881	40.399	3.846	1.00	26.24	C
ATOM	93	C	LEU A	44	77.027	36.416	5.345	1.00	26.74	C
ATOM	94	O	LEU A	44	76.107	36.274	6.148	1.00	26.63	O
ATOM	95	N	GLY A	45	77.796	35.409	4.946	1.00	27.42	N
ATOM	96	CA	GLY A	45	77.585	34.056	5.434	1.00	28.81	C
ATOM	97	C	GLY A	45	78.642	33.077	4.932	1.00	29.90	C
ATOM	98	O	GLY A	45	79.203	33.254	3.854	1.00	29.36	O
ATOM	99	N	SER A	46	78.908	32.061	5.745	1.00	31.14	N
ATOM	100	CA	SER A	46	79.794	30.964	5.385	1.00	33.14	C
ATOM	101	CB	SER A	46	81.242	31.182	5.786	1.00	33.24	C
ATOM	102	OG	SER A	46	81.336	31.107	7.161	1.00	31.40	O
ATOM	103	C	SER A	46	79.263	29.523	6.104	1.00	34.64	C
ATOM	104	O	SER A	46	78.131	29.727	6.594	1.00	35.16	O
ATOM	105	N	GLY A	47	80.033	28.675	6.168	1.00	36.14	N
ATOM	106	CA	GLY A	47	79.552	27.513	6.960	1.00	37.77	C
ATOM	107	C	GLY A	47	78.827	26.410	6.202	1.00	38.06	C
ATOM	108	O	GLY A	47	78.803	25.261	6.665	1.00	38.85	O
ATOM	109	N	GLY A	48	78.228	26.756	5.058	1.00	38.13	N
ATOM	110	CA	GLY A	48	77.816	25.765	4.072	1.00	37.47	C
ATOM	111	C	GLY A	48	79.007	25.489	3.163	1.00	37.20	C
ATOM	112	O	GLY A	48	80.154	25.459	3.631	1.00	37.27	O
ATOM	113	N	PHE A	49	78.757	25.324	1.865	1.00	36.60	N
ATOM	114	CA	PHE A	49	79.845	25.099	0.905	1.00	36.12	C
ATOM	115	CB	PHE A	49	79.322	24.532	-0.421	1.00	36.73	C
ATOM	116	CG	PHE A	49	78.733	23.153	-0.310	1.00	39.10	C
ATOM	117	CD1	PHE A	49	77.363	22.960	-0.454	1.00	40.06	C
ATOM	118	CE1	PHE A	49	76.806	21.681	-0.357	1.00	42.14	C
ATOM	119	CZ	PHE A	49	77.624	20.575	-0.105	1.00	43.04	C
ATOM	120	CE2	PHE A	49	79.003	20.755	0.045	1.00	43.48	C
ATOM	121	CD2	PHE A	49	79.550	22.043	-0.061	1.00	42.11	C
ATOM	122	C	PHE A	49	80.702	26.339	0.614	1.00	34.83	C
ATOM	123	O	PHE A	49	81.884	26.195	0.286	1.00	35.14	O
ATOM	124	N	GLY A	50	80.109	27.536	0.717	1.00	32.72	N
ATOM	125	CA	GLY A	50	80.770	28.772	0.303	1.00	30.18	C
ATOM	126	C	GLY A	50	80.831	29.895	1.335	1.00	28.53	C
ATOM	127	O	GLY A	50	80.161	29.832	2.367	1.00	28.21	O
ATOM	128	N	SER A	51	81.676	30.895	1.061	1.00	26.40	N
ATOM	129	CA	SER A	51	81.722	32.156	1.803	1.00	23.83	C
ATOM	130	CB	SER A	51	83.157	32.509	2.190	1.00	24.19	C
ATOM	131	OG	SER A	51	83.773	31.474	2.937	1.00	23.82	O
ATOM	132	C	SER A	51	81.167	33.245	0.888	1.00	22.65	C
ATOM	133	O	SER A	51	81.640	33.423	-0.242	1.00	21.83	O
ATOM	134	N	VAL A	52	80.150	33.948	1.369	1.00	20.93	N
ATOM	135	CA	VAL A	52	79.427	34.917	0.568	1.00	20.09	C

ATOM	136	CB	VAL	A	52	77.917	34.574	0.518	1.00	19.63	C
ATOM	137	CG1	VAL	A	52	77.182	35.536	-0.391	1.00	19.68	C
ATOM	138	CG2	VAL	A	52	77.705	33.133	0.035	1.00	19.27	C
ATOM	139	C	VAL	A	52	79.629	36.330	1.119	1.00	20.59	C
ATOM	140	O	VAL	A	52	79.406	36.576	2.309	1.00	19.74	O
ATOM	141	N	TYR	A	53	80.053	37.241	0.250	1.00	20.61	N
ATOM	142	CA	TYR	A	53	80.316	38.624	0.640	1.00	21.62	C
ATOM	143	CB	TYR	A	53	81.737	39.034	0.247	1.00	21.19	C
ATOM	144	CG	TYR	A	53	82.842	38.256	0.922	1.00	22.16	C
ATOM	145	CD1	TYR	A	53	83.201	36.980	0.470	1.00	21.94	C
ATOM	146	CE1	TYR	A	53	84.225	36.265	1.078	1.00	22.80	C
ATOM	147	CZ	TYR	A	53	84.921	36.830	2.146	1.00	23.82	C
ATOM	148	OH	TYR	A	53	85.937	36.114	2.736	1.00	23.97	O
ATOM	149	CE2	TYR	A	53	84.597	38.099	2.614	1.00	23.07	C
ATOM	150	CD2	TYR	A	53	83.559	38.810	1.994	1.00	23.01	C
ATOM	151	C	TYR	A	53	79.354	39.597	-0.024	1.00	22.34	C
ATOM	152	O	TYR	A	53	78.888	39.373	-1.153	1.00	22.35	O
ATOM	153	N	SER	A	54	79.066	40.681	0.680	1.00	23.48	N
ATOM	154	CA	SER	A	54	78.404	41.822	0.074	1.00	24.82	C
ATOM	155	CB	SER	A	54	77.980	42.840	1.140	1.00	25.09	C
ATOM	156	OG	SER	A	54	77.307	43.939	0.545	1.00	25.39	O
ATOM	157	C	SER	A	54	79.384	42.461	-0.889	1.00	25.68	C
ATOM	158	O	SER	A	54	80.586	42.513	-0.616	1.00	25.83	O
ATOM	159	N	GLY	A	55	78.878	42.932	-2.023	1.00	26.75	N
ATOM	160	CA	GLY	A	55	79.720	43.609	-2.991	1.00	27.76	C
ATOM	161	C	GLY	A	55	78.986	44.633	-3.827	1.00	28.87	C
ATOM	162	O	GLY	A	55	77.762	44.772	-3.737	1.00	28.62	O
ATOM	163	N	ILE	A	56	79.750	45.358	-4.641	1.00	30.03	N
ATOM	164	CA	ILE	A	56	79.200	46.346	-5.557	1.00	31.52	C
ATOM	165	CB	ILE	A	56	79.291	47.773	-4.953	1.00	31.73	C
ATOM	166	CG1	ILE	A	56	78.306	47.955	-3.790	1.00	32.00	C
ATOM	167	CD1	ILE	A	56	78.762	48.992	-2.750	1.00	34.29	C
ATOM	168	CG2	ILE	A	56	79.038	48.830	-6.014	1.00	32.25	C
ATOM	169	C	ILE	A	56	79.927	46.274	-6.901	1.00	32.27	C
ATOM	170	O	ILE	A	56	81.153	46.245	-6.956	1.00	32.20	O
ATOM	171	N	ARG	A	57	79.147	46.225	-7.976	1.00	33.45	N
ATOM	172	CA	ARG	A	57	79.664	46.308	-9.332	1.00	34.77	C
ATOM	173	CB	ARG	A	57	78.574	45.902	-10.319	1.00	34.53	C
ATOM	174	CG	ARG	A	57	79.075	45.541	-11.692	1.00	35.85	C
ATOM	175	CD	ARG	A	57	78.037	45.746	-12.766	1.00	37.31	C
ATOM	176	NE	ARG	A	57	77.459	44.488	-13.210	1.00	38.72	N
ATOM	177	CZ	ARG	A	57	76.191	44.334	-13.580	1.00	39.18	C
ATOM	178	NH1	ARG	A	57	75.347	45.360	-13.561	1.00	38.58	N
ATOM	179	NH2	ARG	A	57	75.764	43.143	-13.967	1.00	40.00	N
ATOM	180	C	ARG	A	57	80.134	47.740	-9.604	1.00	35.42	C
ATOM	181	O	ARG	A	57	79.329	48.667	-9.609	1.00	35.07	O
ATOM	182	N	VAL	A	58	81.438	47.901	-9.822	1.00	36.96	N
ATOM	183	CA	VAL	A	58	82.069	49.221	-9.962	1.00	38.44	C
ATOM	184	CB	VAL	A	58	83.626	49.118	-10.083	1.00	38.53	C
ATOM	185	CG1	VAL	A	58	84.270	50.494	-10.251	1.00	38.65	C
ATOM	186	CG2	VAL	A	58	84.226	48.422	-8.863	1.00	38.97	C
ATOM	187	C	VAL	A	58	81.472	50.033	-11.125	1.00	39.26	C
ATOM	188	O	VAL	A	58	81.243	51.238	-10.989	1.00	39.41	O
ATOM	189	N	SER	A	59	81.194	49.357	-12.239	1.00	40.32	N
ATOM	190	CA	SER	A	59	80.704	50.007	-13.459	1.00	41.50	C
ATOM	191	CB	SER	A	59	80.627	49.012	-14.625	1.00	41.60	C
ATOM	192	OG	SER	A	59	80.059	47.777	-14.225	1.00	42.83	O
ATOM	193	C	SER	A	59	79.380	50.778	-13.310	1.00	41.87	C
ATOM	194	O	SER	A	59	79.205	51.830	-13.933	1.00	42.28	O
ATOM	195	N	ASP	A	60	78.463	50.269	-12.488	1.00	42.04	N
ATOM	196	CA	ASP	A	60	77.147	50.897	-12.330	1.00	41.97	C
ATOM	197	CB	ASP	A	60	76.118	50.187	-13.223	1.00	42.37	C
ATOM	198	CG	ASP	A	60	75.881	48.739	-12.810	1.00	43.55	C
ATOM	199	OD1	ASP	A	60	76.449	48.309	-11.781	1.00	44.32	O
ATOM	200	OD2	ASP	A	60	75.142	47.959	-13.451	1.00	43.86	O
ATOM	201	C	ASP	A	60	76.631	50.996	-10.878	1.00	41.41	C
ATOM	202	O	ASP	A	60	75.479	51.372	-10.657	1.00	41.59	O
ATOM	203	N	ASN	A	61	77.484	50.667	-9.905	1.00	40.49	N
ATOM	204	CA	ASN	A	61	77.122	50.639	-8.475	1.00	39.60	C

ATOM	205	CB	ASN	A	61	76.722	52.026	-7.961	1.00	39.96	C
ATOM	206	CG	ASN	A	61	77.888	52.981	-7.902	1.00	41.52	C
ATOM	207	OD1	ASN	A	61	78.785	52.837	-7.065	1.00	42.83	O
ATOM	208	ND2	ASN	A	61	77.883	53.971	-8.792	1.00	42.64	N
ATOM	209	C	ASN	A	61	76.058	49.615	-8.056	1.00	38.30	C
ATOM	210	O	ASN	A	61	75.557	49.667	-6.930	1.00	38.56	O
ATOM	211	N	LEU	A	62	75.724	48.685	-8.947	1.00	36.52	N
ATOM	212	CA	LEU	A	62	74.768	47.623	-8.623	1.00	34.93	C
ATOM	213	CB	LEU	A	62	74.519	46.720	-9.832	1.00	35.10	C
ATOM	214	CG	LEU	A	62	73.421	45.662	-9.712	1.00	35.38	C
ATOM	215	CD1	LEU	A	62	72.047	46.269	-9.961	1.00	36.89	C
ATOM	216	CD2	LEU	A	62	73.679	44.527	-10.677	1.00	35.30	C
ATOM	217	C	LEU	A	62	75.222	46.778	-7.425	1.00	33.33	C
ATOM	218	O	LEU	A	62	76.351	46.288	-7.404	1.00	32.86	O
ATOM	219	N	PRO	A	63	74.340	46.624	-6.436	1.00	32.03	N
ATOM	220	CA	PRO	A	63	74.576	45.708	-5.312	1.00	30.66	C
ATOM	221	CB	PRO	A	63	73.328	45.893	-4.440	1.00	30.79	C
ATOM	222	CG	PRO	A	63	72.770	47.219	-4.848	1.00	32.09	C
ATOM	223	CD	PRO	A	63	73.039	47.311	-6.319	1.00	32.13	C
ATOM	224	C	PRO	A	63	74.657	44.263	-5.804	1.00	28.94	C
ATOM	225	O	PRO	A	63	73.788	43.821	-6.570	1.00	28.84	O
ATOM	226	N	VAL	A	64	75.705	43.554	-5.393	1.00	26.63	N
ATOM	227	CA	VAL	A	64	75.862	42.135	-5.723	1.00	24.40	C
ATOM	228	CB	VAL	A	64	76.903	41.905	-6.870	1.00	24.56	C
ATOM	229	CG1	VAL	A	64	76.430	42.528	-8.195	1.00	23.44	C
ATOM	230	CG2	VAL	A	64	78.292	42.436	-6.471	1.00	23.53	C
ATOM	231	C	VAL	A	64	76.295	41.339	-4.488	1.00	23.30	C
ATOM	232	O	VAL	A	64	76.650	41.922	-3.451	1.00	22.79	O
ATOM	233	N	ALA	A	65	76.259	40.014	-4.609	1.00	21.63	N
ATOM	234	CA	ALA	A	65	76.828	39.124	-3.608	1.00	20.83	C
ATOM	235	CB	ALA	A	65	75.761	38.231	-2.984	1.00	20.55	C
ATOM	236	C	ALA	A	65	77.892	38.290	-4.281	1.00	20.04	C
ATOM	237	O	ALA	A	65	77.704	37.828	-5.408	1.00	21.14	O
ATOM	238	N	ILE	A	66	79.015	38.111	-3.600	1.00	18.86	N
ATOM	239	CA	ILE	A	66	80.165	37.439	-4.186	1.00	17.57	C
ATOM	240	CB	ILE	A	66	81.422	38.346	-4.117	1.00	17.68	C
ATOM	241	CG1	ILE	A	66	81.148	39.723	-4.747	1.00	18.56	C
ATOM	242	CD1	ILE	A	66	82.220	40.772	-4.424	1.00	19.55	C
ATOM	243	CG2	ILE	A	66	82.602	37.668	-4.775	1.00	16.32	C
ATOM	244	C	ILE	A	66	80.402	36.161	-3.408	1.00	16.96	C
ATOM	245	O	ILE	A	66	80.775	36.206	-2.227	1.00	16.17	O
ATOM	246	N	LYS	A	67	80.179	35.031	-4.077	1.00	16.24	N
ATOM	247	CA	LYS	A	67	80.255	33.718	-3.444	1.00	15.79	C
ATOM	248	CB	LYS	A	67	78.975	32.905	-3.707	1.00	15.38	C
ATOM	249	CG	LYS	A	67	79.010	31.493	-3.119	1.00	14.88	C
ATOM	250	CD	LYS	A	67	77.664	30.772	-3.303	1.00	17.48	C
ATOM	251	CE	LYS	A	67	77.585	29.486	-2.479	1.00	18.05	C
ATOM	252	NZ	LYS	A	67	76.184	28.951	-2.470	1.00	18.14	N
ATOM	253	C	LYS	A	67	81.478	32.943	-3.915	1.00	16.15	C
ATOM	254	O	LYS	A	67	81.667	32.705	-5.122	1.00	15.33	O
ATOM	255	N	HIS	A	68	82.293	32.534	-2.951	1.00	16.82	N
ATOM	256	CA	HIS	A	68	83.519	31.792	-3.235	1.00	17.55	C
ATOM	257	CB	HIS	A	68	84.683	32.368	-2.435	1.00	17.11	C
ATOM	258	CG	HIS	A	68	85.043	33.764	-2.818	1.00	17.46	C
ATOM	259	ND1	HIS	A	68	84.358	34.860	-2.348	1.00	18.28	N
ATOM	260	CE1	HIS	A	68	84.897	35.958	-2.844	1.00	17.55	C
ATOM	261	NE2	HIS	A	68	85.909	35.614	-3.617	1.00	17.90	N
ATOM	262	CD2	HIS	A	68	86.019	34.245	-3.622	1.00	17.05	C
ATOM	263	C	HIS	A	68	83.319	30.353	-2.829	1.00	18.47	C
ATOM	264	O	HIS	A	68	82.899	30.085	-1.707	1.00	17.74	O
ATOM	265	N	VAL	A	69	83.628	29.434	-3.735	1.00	19.87	N
ATOM	266	CA	VAL	A	69	83.538	28.016	-3.441	1.00	21.97	C
ATOM	267	CB	VAL	A	69	82.386	27.316	-4.229	1.00	22.09	C
ATOM	268	CG1	VAL	A	69	82.270	25.863	-3.809	1.00	22.01	C
ATOM	269	CG2	VAL	A	69	81.049	28.011	-3.992	1.00	22.34	C
ATOM	270	C	VAL	A	69	84.870	27.345	-3.768	1.00	23.59	C
ATOM	271	O	VAL	A	69	85.331	27.388	-4.903	1.00	23.28	O
ATOM	272	N	GLU	A	70	85.474	26.719	-2.766	1.00	26.14	N
ATOM	273	CA	GLU	A	70	86.719	25.981	-2.948	1.00	29.32	C

ATOM	274	CB	GLU	A	70	87.280	25.543	-1.599	1.00	29.52	C
ATOM	275	CG	GLU	A	70	88.286	26.512	-1.001	1.00	32.13	C
ATOM	276	CD	GLU	A	70	88.827	26.043	0.342	1.00	34.86	C
ATOM	277	OE1	GLU	A	70	89.185	24.847	0.448	1.00	34.79	O
ATOM	278	OE2	GLU	A	70	88.899	26.871	1.288	1.00	35.33	O
ATOM	279	C	GLU	A	70	86.486	24.760	-3.834	1.00	31.18	C
ATOM	280	O	GLU	A	70	85.485	24.044	-3.674	1.00	30.70	O
ATOM	281	N	LYS	A	71	87.402	24.540	-4.774	1.00	33.73	N
ATOM	282	CA	LYS	A	71	87.292	23.422	-5.718	1.00	36.85	C
ATOM	283	CB	LYS	A	71	88.426	23.459	-6.734	1.00	36.40	C
ATOM	284	CG	LYS	A	71	88.228	24.487	-7.822	1.00	35.73	C
ATOM	285	CD	LYS	A	71	89.373	24.457	-8.814	1.00	35.72	C
ATOM	286	CE	LYS	A	71	89.168	25.490	-9.898	1.00	35.77	C
ATOM	287	NZ	LYS	A	71	90.289	25.535	-10.874	1.00	35.56	N
ATOM	288	C	LYS	A	71	87.206	22.046	-5.047	1.00	39.35	C
ATOM	289	O	LYS	A	71	86.492	21.169	-5.536	1.00	39.62	O
ATOM	290	N	ASP	A	72	87.904	21.872	-3.922	1.00	42.63	N
ATOM	291	CA	ASP	A	72	87.873	20.615	-3.161	1.00	46.03	C
ATOM	292	CB	ASP	A	72	89.021	20.560	-2.145	1.00	46.33	C
ATOM	293	CG	ASP	A	72	90.396	20.511	-2.811	1.00	48.21	C
ATOM	294	OD1	ASP	A	72	90.519	19.935	-3.918	1.00	49.79	O
ATOM	295	OD2	ASP	A	72	91.418	21.025	-2.300	1.00	50.39	O
ATOM	296	C	ASP	A	72	86.539	20.371	-2.452	1.00	47.89	C
ATOM	297	O	ASP	A	72	86.138	19.221	-2.253	1.00	48.61	O
ATOM	298	N	ARG	A	73	85.861	21.457	-2.085	1.00	50.08	N
ATOM	299	CA	ARG	A	73	84.592	21.405	-1.352	1.00	52.11	C
ATOM	300	CB	ARG	A	73	84.430	22.662	-0.486	1.00	52.39	C
ATOM	301	CG	ARG	A	73	85.333	22.711	0.739	1.00	54.59	C
ATOM	302	CD	ARG	A	73	84.894	23.708	1.827	1.00	58.87	C
ATOM	303	NE	ARG	A	73	83.451	23.686	2.113	1.00	62.15	N
ATOM	304	CZ	ARG	A	73	82.792	22.682	2.708	1.00	63.76	C
ATOM	305	NH1	ARG	A	73	83.427	21.579	3.094	1.00	64.18	N
ATOM	306	NH2	ARG	A	73	81.484	22.779	2.917	1.00	63.67	N
ATOM	307	C	ARG	A	73	83.376	21.251	-2.272	1.00	52.88	C
ATOM	308	O	ARG	A	73	82.246	21.100	-1.793	1.00	52.85	O
ATOM	309	N	ILE	A	74	83.613	21.307	-3.585	1.00	54.14	N
ATOM	310	CA	ILE	A	74	82.553	21.153	-4.583	1.00	55.27	C
ATOM	311	CB	ILE	A	74	83.013	21.668	-5.983	1.00	55.13	C
ATOM	312	CG1	ILE	A	74	83.104	23.193	-5.985	1.00	54.96	C
ATOM	313	CD1	ILE	A	74	83.829	23.776	-7.180	1.00	55.18	C
ATOM	314	CG2	ILE	A	74	82.053	21.205	-7.084	1.00	55.44	C
ATOM	315	C	ILE	A	74	82.107	19.691	-4.638	1.00	56.17	C
ATOM	316	O	ILE	A	74	82.902	18.798	-4.973	1.00	56.10	O
ATOM	317	N	SER	A	75	80.836	19.459	-4.298	1.00	57.17	N
ATOM	318	CA	SER	A	75	80.287	18.101	-4.234	1.00	58.19	C
ATOM	319	CB	SER	A	75	78.943	18.064	-3.485	1.00	58.21	C
ATOM	320	OG	SER	A	75	78.112	19.161	-3.831	1.00	58.80	O
ATOM	321	C	SER	A	75	80.178	17.482	-5.629	1.00	58.59	C
ATOM	322	O	SER	A	75	80.890	16.520	-5.939	1.00	58.89	O
ATOM	323	N	ASP	A	76	79.313	18.055	-6.469	1.00	58.93	N
ATOM	324	CA	ASP	A	76	79.125	17.581	-7.840	1.00	59.19	C
ATOM	325	CB	ASP	A	76	77.646	17.265	-8.101	1.00	59.25	C
ATOM	326	CG	ASP	A	76	77.174	16.004	-7.377	1.00	60.21	C
ATOM	327	OD1	ASP	A	76	75.950	15.733	-7.378	1.00	60.76	O
ATOM	328	OD2	ASP	A	76	77.946	15.218	-6.783	1.00	61.47	O
ATOM	329	C	ASP	A	76	79.655	18.576	-8.875	1.00	59.17	C
ATOM	330	O	ASP	A	76	79.536	19.794	-8.702	1.00	59.08	O
ATOM	331	N	TRP	A	77	80.245	18.043	-9.943	1.00	59.21	N
ATOM	332	CA	TRP	A	77	80.737	18.850	-11.059	1.00	59.31	C
ATOM	333	CB	TRP	A	77	82.186	18.497	-11.399	1.00	58.89	C
ATOM	334	CG	TRP	A	77	83.207	18.816	-10.338	1.00	57.61	C
ATOM	335	CD1	TRP	A	77	83.449	18.112	-9.191	1.00	56.71	C
ATOM	336	NE1	TRP	A	77	84.469	18.695	-8.480	1.00	56.23	N
ATOM	337	CE2	TRP	A	77	84.921	19.793	-9.166	1.00	55.87	C
ATOM	338	CD2	TRP	A	77	84.149	19.899	-10.345	1.00	55.83	C
ATOM	339	CE3	TRP	A	77	84.416	20.957	-11.226	1.00	54.75	C
ATOM	340	CZ3	TRP	A	77	85.429	21.857	-10.909	1.00	54.49	C
ATOM	341	CH2	TRP	A	77	86.179	21.722	-9.728	1.00	54.62	C
ATOM	342	CZ2	TRP	A	77	85.942	20.700	-8.846	1.00	54.88	C

ATOM	343	C	TRP	A	77	79.880	18.620	-12.297	1.00	59.97	C
ATOM	344	O	TRP	A	77	79.309	17.539	-12.479	1.00	59.95	O
ATOM	345	N	GLY	A	78	79.814	19.636	-13.152	1.00	60.60	N
ATOM	346	CA	GLY	A	78	79.019	19.573	-14.362	1.00	61.69	C
ATOM	347	C	GLY	A	78	79.663	20.261	-15.546	1.00	62.62	C
ATOM	348	O	GLY	A	78	80.722	20.887	-15.425	1.00	62.53	O
ATOM	349	N	GLU	A	79	79.016	20.127	-16.700	1.00	63.55	N
ATOM	350	CA	GLU	A	79	79.470	20.764	-17.932	1.00	64.55	C
ATOM	351	CB	GLU	A	79	79.841	19.724	-19.007	1.00	64.74	C
ATOM	352	CG	GLU	A	79	78.740	18.730	-19.386	1.00	65.56	C
ATOM	353	CD	GLU	A	79	78.780	18.319	-20.857	1.00	67.08	C
ATOM	354	OE1	GLU	A	79	79.892	18.197	-21.428	1.00	67.41	O
ATOM	355	OE2	GLU	A	79	77.693	18.111	-21.446	1.00	66.84	O
ATOM	356	C	GLU	A	79	78.425	21.745	-18.456	1.00	64.93	C
ATOM	357	O	GLU	A	79	77.218	21.485	-18.388	1.00	64.82	O
ATOM	358	N	LEU	A	80	78.902	22.878	-18.963	1.00	65.56	N
ATOM	359	CA	LEU	A	80	78.039	23.875	-19.589	1.00	66.20	C
ATOM	360	CB	LEU	A	80	78.763	25.227	-19.663	1.00	66.19	C
ATOM	361	CG	LEU	A	80	79.128	25.944	-18.359	1.00	66.08	C
ATOM	362	CD1	LEU	A	80	79.914	27.225	-18.646	1.00	65.61	C
ATOM	363	CD2	LEU	A	80	77.881	26.238	-17.525	1.00	65.99	C
ATOM	364	C	LEU	A	80	77.662	23.402	-20.996	1.00	66.59	C
ATOM	365	O	LEU	A	80	78.387	22.585	-21.575	1.00	66.81	O
ATOM	366	N	PRO	A	81	76.539	23.885	-21.547	1.00	66.88	N
ATOM	367	CA	PRO	A	81	76.220	23.634	-22.963	1.00	66.94	C
ATOM	368	CB	PRO	A	81	75.035	24.573	-23.226	1.00	67.02	C
ATOM	369	CG	PRO	A	81	74.363	24.703	-21.892	1.00	67.04	C
ATOM	370	CD	PRO	A	81	75.477	24.665	-20.877	1.00	66.98	C
ATOM	371	C	PRO	A	81	77.408	23.972	-23.884	1.00	66.80	C
ATOM	372	O	PRO	A	81	77.505	23.438	-24.990	1.00	66.90	O
ATOM	373	N	ASN	A	82	78.296	24.842	-23.405	1.00	66.49	N
ATOM	374	CA	ASN	A	82	79.543	25.182	-24.087	1.00	66.14	C
ATOM	375	CB	ASN	A	82	80.114	26.482	-23.492	1.00	66.36	C
ATOM	376	CG	ASN	A	82	81.498	26.816	-24.015	1.00	67.00	C
ATOM	377	OD1	ASN	A	82	81.734	26.837	-25.225	1.00	67.52	O
ATOM	378	ND2	ASN	A	82	82.424	27.089	-23.100	1.00	67.69	N
ATOM	379	C	ASN	A	82	80.576	24.044	-24.035	1.00	65.50	C
ATOM	380	O	ASN	A	82	81.273	23.787	-25.019	1.00	65.53	O
ATOM	381	N	GLY	A	83	80.664	23.369	-22.888	1.00	64.74	N
ATOM	382	CA	GLY	A	83	81.614	22.284	-22.683	1.00	63.59	C
ATOM	383	C	GLY	A	83	82.826	22.690	-21.857	1.00	62.70	C
ATOM	384	O	GLY	A	83	83.967	22.600	-22.326	1.00	62.98	O
ATOM	385	N	THR	A	84	82.571	23.149	-20.632	1.00	61.37	N
ATOM	386	CA	THR	A	84	83.621	23.529	-19.682	1.00	59.87	C
ATOM	387	CB	THR	A	84	83.742	25.067	-19.576	1.00	60.05	C
ATOM	388	OG1	THR	A	84	83.799	25.643	-20.888	1.00	60.81	O
ATOM	389	CG2	THR	A	84	85.080	25.468	-18.954	1.00	60.25	C
ATOM	390	C	THR	A	84	83.309	22.938	-18.310	1.00	58.33	C
ATOM	391	O	THR	A	84	82.139	22.816	-17.930	1.00	58.41	O
ATOM	392	N	ARG	A	85	84.356	22.576	-17.572	1.00	56.14	N
ATOM	393	CA	ARG	A	85	84.198	22.026	-16.231	1.00	53.98	C
ATOM	394	CB	ARG	A	85	85.445	21.223	-15.844	1.00	54.58	C
ATOM	395	CG	ARG	A	85	85.227	20.243	-14.703	1.00	56.25	C
ATOM	396	CD	ARG	A	85	86.028	18.945	-14.819	1.00	58.89	C
ATOM	397	NE	ARG	A	85	85.870	18.099	-13.630	1.00	60.27	N
ATOM	398	CZ	ARG	A	85	84.879	17.226	-13.445	1.00	60.85	C
ATOM	399	NH1	ARG	A	85	83.933	17.065	-14.370	1.00	61.04	N
ATOM	400	NH2	ARG	A	85	84.834	16.506	-12.329	1.00	60.48	N
ATOM	401	C	ARG	A	85	83.906	23.130	-15.200	1.00	51.86	C
ATOM	402	O	ARG	A	85	84.789	23.931	-14.865	1.00	51.74	O
ATOM	403	N	VAL	A	86	82.659	23.172	-14.721	1.00	48.87	N
ATOM	404	CA	VAL	A	86	82.224	24.121	-13.680	1.00	45.97	C
ATOM	405	CB	VAL	A	86	81.335	25.276	-14.251	1.00	46.05	C
ATOM	406	CG1	VAL	A	86	82.074	26.064	-15.322	1.00	46.41	C
ATOM	407	CG2	VAL	A	86	80.008	24.755	-14.781	1.00	45.90	C
ATOM	408	C	VAL	A	86	81.462	23.409	-12.553	1.00	43.56	C
ATOM	409	O	VAL	A	86	80.984	22.292	-12.750	1.00	43.24	O
ATOM	410	N	PRO	A	87	81.345	24.040	-11.380	1.00	41.11	N
ATOM	411	CA	PRO	A	87	80.494	23.495	-10.314	1.00	39.00	C

ATOM	412	CB	PRO	A	87	80.654	24.499	-9.158	1.00	39.06	C
ATOM	413	CG	PRO	A	87	81.251	25.719	-9.759	1.00	40.31	C
ATOM	414	CD	PRO	A	87	82.015	25.287	-10.966	1.00	40.95	C
ATOM	415	C	PRO	A	87	79.037	23.413	-10.755	1.00	36.73	C
ATOM	416	O	PRO	A	87	78.567	24.258	-11.535	1.00	35.64	O
ATOM	417	N	MET	A	88	78.343	22.391	-10.255	1.00	34.56	N
ATOM	418	CA	MET	A	88	76.936	22.171	-10.564	1.00	32.47	C
ATOM	419	CB	MET	A	88	76.408	20.950	-9.799	1.00	33.23	C
ATOM	420	CG	MET	A	88	75.047	20.407	-10.263	1.00	36.09	C
ATOM	421	SD	MET	A	88	74.917	19.957	-12.033	1.00	43.02	S
ATOM	422	CE	MET	A	88	76.260	18.799	-12.218	1.00	41.30	C
ATOM	423	C	MET	A	88	76.110	23.423	-10.274	1.00	30.24	C
ATOM	424	O	MET	A	88	75.169	23.717	-11.006	1.00	29.10	O
ATOM	425	N	GLU	A	89	76.487	24.169	-9.231	1.00	28.21	N
ATOM	426	CA	GLU	A	89	75.773	25.392	-8.843	1.00	26.55	C
ATOM	427	CB	GLU	A	89	76.393	26.043	-7.576	1.00	26.83	C
ATOM	428	CG	GLU	A	89	75.711	27.347	-7.134	1.00	27.21	C
ATOM	429	CD	GLU	A	89	75.939	27.733	-5.670	1.00	29.78	C
ATOM	430	OE1	GLU	A	89	76.956	27.292	-5.073	1.00	29.01	O
ATOM	431	OE2	GLU	A	89	75.080	28.483	-5.118	1.00	29.29	O
ATOM	432	C	GLU	A	89	75.669	26.392	-10.000	1.00	25.41	C
ATOM	433	O	GLU	A	89	74.609	26.988	-10.223	1.00	25.07	O
ATOM	434	N	VAL	A	90	76.761	26.566	-10.744	1.00	24.25	N
ATOM	435	CA	VAL	A	90	76.747	27.435	-11.927	1.00	23.34	C
ATOM	436	CB	VAL	A	90	78.193	27.717	-12.452	1.00	23.97	C
ATOM	437	CG1	VAL	A	90	78.178	28.460	-13.796	1.00	23.00	C
ATOM	438	CG2	VAL	A	90	78.989	28.530	-11.411	1.00	23.11	C
ATOM	439	C	VAL	A	90	75.822	26.881	-13.020	1.00	22.89	C
ATOM	440	O	VAL	A	90	75.002	27.622	-13.570	1.00	22.78	O
ATOM	441	N	VAL	A	91	75.926	25.579	-13.305	1.00	22.51	N
ATOM	442	CA	VAL	A	91	75.048	24.917	-14.293	1.00	22.19	C
ATOM	443	CB	VAL	A	91	75.316	23.382	-14.399	1.00	22.50	C
ATOM	444	CG1	VAL	A	91	74.265	22.688	-15.314	1.00	22.61	C
ATOM	445	CG2	VAL	A	91	76.688	23.116	-14.934	1.00	22.68	C
ATOM	446	C	VAL	A	91	73.569	25.143	-13.965	1.00	21.66	C
ATOM	447	O	VAL	A	91	72.783	25.594	-14.807	1.00	20.36	O
ATOM	448	N	LEU	A	92	73.215	24.856	-12.715	1.00	21.61	N
ATOM	449	CA	LEU	A	92	71.833	24.963	-12.256	1.00	21.57	C
ATOM	450	CB	LEU	A	92	71.682	24.326	-10.873	1.00	21.14	C
ATOM	451	CG	LEU	A	92	72.112	22.854	-10.778	1.00	21.50	C
ATOM	452	CD1	LEU	A	92	71.945	22.365	-9.349	1.00	20.58	C
ATOM	453	CD2	LEU	A	92	71.378	21.928	-11.767	1.00	18.41	C
ATOM	454	C	LEU	A	92	71.331	26.408	-12.255	1.00	21.79	C
ATOM	455	O	LEU	A	92	70.212	26.671	-12.706	1.00	21.50	O
ATOM	456	N	LEU	A	93	72.159	27.332	-11.764	1.00	22.36	N
ATOM	457	CA	LEU	A	93	71.808	28.755	-11.756	1.00	23.34	C
ATOM	458	CB	LEU	A	93	72.861	29.584	-11.018	1.00	23.50	C
ATOM	459	CG	LEU	A	93	72.714	29.608	-9.482	1.00	24.22	C
ATOM	460	CD1	LEU	A	93	73.985	30.131	-8.852	1.00	23.74	C
ATOM	461	CD2	LEU	A	93	71.493	30.431	-9.048	1.00	22.10	C
ATOM	462	C	LEU	A	93	71.594	29.301	-13.162	1.00	23.97	C
ATOM	463	O	LEU	A	93	70.642	30.037	-13.409	1.00	23.67	O
ATOM	464	N	LYS	A	94	72.468	28.922	-14.088	1.00	24.87	N
ATOM	465	CA	LYS	A	94	72.265	29.290	-15.491	1.00	26.26	C
ATOM	466	CB	LYS	A	94	73.448	28.847	-16.356	1.00	26.36	C
ATOM	467	CG	LYS	A	94	74.664	29.745	-16.166	1.00	29.54	C
ATOM	468	CD	LYS	A	94	75.932	29.132	-16.750	1.00	34.13	C
ATOM	469	CE	LYS	A	94	76.210	29.633	-18.167	1.00	36.90	C
ATOM	470	NZ	LYS	A	94	76.658	31.059	-18.181	1.00	39.00	N
ATOM	471	C	LYS	A	94	70.946	28.761	-16.045	1.00	26.31	C
ATOM	472	O	LYS	A	94	70.240	29.481	-16.756	1.00	26.21	O
ATOM	473	N	LYS	A	95	70.610	27.515	-15.712	1.00	26.64	N
ATOM	474	CA	LYS	A	95	69.356	26.916	-16.172	1.00	28.04	C
ATOM	475	CB	LYS	A	95	69.295	25.427	-15.824	1.00	27.38	C
ATOM	476	CG	LYS	A	95	70.096	24.557	-16.777	1.00	28.63	C
ATOM	477	CD	LYS	A	95	70.218	23.114	-16.294	1.00	29.42	C
ATOM	478	CE	LYS	A	95	68.891	22.361	-16.392	1.00	30.74	C
ATOM	479	NZ	LYS	A	95	68.513	22.039	-17.803	1.00	31.02	N
ATOM	480	C	LYS	A	95	68.096	27.657	-15.674	1.00	28.66	C

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ATOM    481  O   LYS A  95      67.088  27.707 -16.379  1.00 28.72           O
ATOM    482  N   VAL A  96      68.167  28.239 -14.480  1.00 30.05           N
ATOM    483  CA  VAL A  96      67.017  28.940 -13.899  1.00 31.67           C
ATOM    484  CB  VAL A  96      66.818  28.631 -12.383  1.00 31.32           C
ATOM    485  CG1 VAL A  96      66.594  27.139 -12.159  1.00 30.44           C
ATOM    486  CG2 VAL A  96      67.978  29.149 -11.546  1.00 29.93           C
ATOM    487  C   VAL A  96      66.997  30.458 -14.119  1.00 33.63           C
ATOM    488  O   VAL A  96      65.999  31.112 -13.783  1.00 33.80           O
ATOM    489  N   SER A  97      68.074  31.018 -14.676  1.00 35.26           N
ATOM    490  CA  SER A  97      68.109  32.455 -14.979  1.00 37.17           C
ATOM    491  CB  SER A  97      69.490  32.907 -15.483  1.00 37.37           C
ATOM    492  OG  SER A  97      69.844  32.265 -16.699  1.00 38.96           O
ATOM    493  C   SER A  97      67.009  32.865 -15.962  1.00 38.05           C
ATOM    494  O   SER A  97      66.797  32.223 -16.996  1.00 38.07           O
ATOM    495  N   SER A  98      66.302  33.934 -15.603  1.00 39.50           N
ATOM    496  CA  SER A  98      65.224  34.521 -16.409  1.00 40.49           C
ATOM    497  CB  SER A  98      64.109  33.499 -16.685  1.00 40.48           C
ATOM    498  OG  SER A  98      63.105  33.547 -15.681  1.00 41.42           O
ATOM    499  C   SER A  98      64.671  35.738 -15.656  1.00 40.82           C
ATOM    500  O   SER A  98      65.177  36.091 -14.582  1.00 41.27           O
ATOM    501  N   GLY A  99      63.632  36.364 -16.210  1.00 40.95           N
ATOM    502  CA  GLY A  99      63.015  37.535 -15.602  1.00 40.62           C
ATOM    503  C   GLY A  99      62.281  37.294 -14.283  1.00 40.18           C
ATOM    504  O   GLY A  99      61.912  38.263 -13.600  1.00 40.34           O
ATOM    505  N   PHE A 100      62.056  36.019 -13.942  1.00 39.30           N
ATOM    506  CA  PHE A 100      61.391  35.628 -12.694  1.00 38.13           C
ATOM    507  CB  PHE A 100      61.038  34.135 -12.709  1.00 38.35           C
ATOM    508  CG  PHE A 100      60.296  33.656 -11.471  1.00 37.90           C
ATOM    509  CD1 PHE A 100      59.100  34.258 -11.069  1.00 36.99           C
ATOM    510  CE1 PHE A 100      58.411  33.801  -9.924  1.00 37.18           C
ATOM    511  CZ  PHE A 100      58.922  32.727  -9.177  1.00 35.96           C
ATOM    512  CE2 PHE A 100      60.108  32.116  -9.573  1.00 35.95           C
ATOM    513  CD2 PHE A 100      60.792  32.585 -10.718  1.00 37.98           C
ATOM    514  C   PHE A 100      62.266  35.944 -11.491  1.00 37.35           C
ATOM    515  O   PHE A 100      63.365  35.409 -11.354  1.00 37.45           O
ATOM    516  N   SER A 101      61.768  36.814 -10.620  1.00 36.17           N
ATOM    517  CA  SER A 101      62.534  37.263  -9.468  1.00 35.23           C
ATOM    518  CB  SER A 101      62.048  38.647  -9.003  1.00 35.81           C
ATOM    519  OG  SER A 101      60.697  38.612  -8.570  1.00 37.04           O
ATOM    520  C   SER A 101      62.571  36.280  -8.291  1.00 33.45           C
ATOM    521  O   SER A 101      63.260  36.544  -7.295  1.00 33.93           O
ATOM    522  N   GLY A 102      61.856  35.157  -8.402  1.00 31.13           N
ATOM    523  CA  GLY A 102      61.760  34.190  -7.310  1.00 28.02           C
ATOM    524  C   GLY A 102      63.026  33.377  -7.066  1.00 26.06           C
ATOM    525  O   GLY A 102      63.183  32.736  -6.040  1.00 24.79           O
ATOM    526  N   VAL A 103      63.936  33.396  -8.030  1.00 25.16           N
ATOM    527  CA  VAL A 103      65.213  32.726  -7.877  1.00 24.40           C
ATOM    528  CB  VAL A 103      65.377  31.540  -8.863  1.00 24.34           C
ATOM    529  CG1 VAL A 103      66.675  30.797  -8.585  1.00 25.25           C
ATOM    530  CG2 VAL A 103      64.214  30.567  -8.737  1.00 23.66           C
ATOM    531  C   VAL A 103      66.300  33.759  -8.104  1.00 24.50           C
ATOM    532  O   VAL A 103      66.217  34.566  -9.040  1.00 24.27           O
ATOM    533  N   ILE A 104      67.303  33.744  -7.232  1.00 23.78           N
ATOM    534  CA  ILE A 104      68.477  34.576  -7.383  1.00 24.18           C
ATOM    535  CB  ILE A 104      69.526  34.185  -6.324  1.00 24.30           C
ATOM    536  CG1 ILE A 104      70.384  35.394  -5.954  1.00 23.11           C
ATOM    537  CD1 ILE A 104      69.581  36.449  -5.162  1.00 22.00           C
ATOM    538  CG2 ILE A 104      70.327  32.934  -6.766  1.00 23.91           C
ATOM    539  C   ILE A 104      69.083  34.483  -8.789  1.00 24.77           C
ATOM    540  O   ILE A 104      69.188  33.403  -9.366  1.00 25.02           O
ATOM    541  N   ARG A 105      69.479  35.619  -9.337  1.00 25.08           N
ATOM    542  CA  ARG A 105      70.070  35.622 -10.667  1.00 26.17           C
ATOM    543  CB  ARG A 105      69.566  36.833 -11.454  1.00 27.31           C
ATOM    544  CG  ARG A 105      70.349  37.173 -12.714  1.00 32.33           C
ATOM    545  CD  ARG A 105      69.728  38.311 -13.536  1.00 39.80           C
ATOM    546  NE  ARG A 105      68.331  38.040 -13.891  1.00 45.22           N
ATOM    547  CZ  ARG A 105      67.573  38.838 -14.646  1.00 47.93           C
ATOM    548  NH1 ARG A 105      68.062  39.976 -15.139  1.00 48.73           N
ATOM    549  NH2 ARG A 105      66.319  38.498 -14.908  1.00 48.97           N
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ATOM    550  C   ARG A 105      71.593  35.590 -10.594  1.00 25.19           C
ATOM    551  O   ARG A 105      72.211  36.402  -9.885  1.00 24.65           O
ATOM    552  N   LEU A 106      72.188  34.634 -11.304  1.00 24.85           N
ATOM    553  CA  LEU A 106      73.642  34.609 -11.499  1.00 24.90           C
ATOM    554  CB  LEU A 106      74.136  33.223 -11.918  1.00 24.41           C
ATOM    555  CG  LEU A 106      75.651  33.073 -12.127  1.00 24.89           C
ATOM    556  CD1 LEU A 106      76.449  33.148 -10.796  1.00 24.67           C
ATOM    557  CD2 LEU A 106      75.961  31.790 -12.871  1.00 23.97           C
ATOM    558  C   LEU A 106      74.004  35.639 -12.554  1.00 25.16           C
ATOM    559  O   LEU A 106      73.536  35.565 -13.695  1.00 25.41           O
ATOM    560  N   LEU A 107      74.825  36.604 -12.163  1.00 25.22           N
ATOM    561  CA  LEU A 107      75.217  37.703 -13.046  1.00 25.72           C
ATOM    562  CB  LEU A 107      75.427  38.991 -12.240  1.00 25.54           C
ATOM    563  CG  LEU A 107      74.167  39.501 -11.524  1.00 25.95           C
ATOM    564  CD1 LEU A 107      74.478  40.685 -10.620  1.00 25.00           C
ATOM    565  CD2 LEU A 107      73.067  39.868 -12.525  1.00 27.51           C
ATOM    566  C   LEU A 107      76.465  37.363 -13.847  1.00 25.66           C
ATOM    567  O   LEU A 107      76.553  37.678 -15.040  1.00 25.68           O
ATOM    568  N   ASP A 108      77.420  36.717 -13.177  1.00 25.47           N
ATOM    569  CA  ASP A 108      78.699  36.333 -13.762  1.00 25.47           C
ATOM    570  CB  ASP A 108      79.624  37.557 -13.872  1.00 25.78           C
ATOM    571  CG  ASP A 108      80.569  37.485 -15.071  1.00 27.00           C
ATOM    572  OD1 ASP A 108      80.828  36.385 -15.610  1.00 27.45           O
ATOM    573  OD2 ASP A 108      81.111  38.501 -15.537  1.00 29.70           O
ATOM    574  C   ASP A 108      79.358  35.308 -12.856  1.00 25.21           C
ATOM    575  O   ASP A 108      78.938  35.119 -11.711  1.00 23.96           O
ATOM    576  N   TRP A 109      80.405  34.669 -13.369  1.00 25.09           N
ATOM    577  CA  TRP A 109      81.235  33.785 -12.565  1.00 25.83           C
ATOM    578  CB  TRP A 109      80.668  32.360 -12.565  1.00 26.03           C
ATOM    579  CG  TRP A 109      80.690  31.729 -13.918  1.00 27.82           C
ATOM    580  CD1 TRP A 109      79.727  31.818 -14.883  1.00 28.39           C
ATOM    581  NE1 TRP A 109      80.102  31.102 -15.995  1.00 30.13           N
ATOM    582  CE2 TRP A 109      81.332  30.539 -15.770  1.00 30.67           C
ATOM    583  CD2 TRP A 109      81.732  30.914 -14.465  1.00 29.83           C
ATOM    584  CE3 TRP A 109      82.970  30.460 -13.987  1.00 30.76           C
ATOM    585  CZ3 TRP A 109      83.758  29.664 -14.809  1.00 32.48           C
ATOM    586  CH2 TRP A 109      83.334  29.313 -16.107  1.00 33.06           C
ATOM    587  CZ2 TRP A 109      82.126  29.739 -16.602  1.00 32.39           C
ATOM    588  C   TRP A 109      82.689  33.808 -13.045  1.00 26.10           C
ATOM    589  O   TRP A 109      82.973  34.170 -14.191  1.00 25.61           O
ATOM    590  N   PHE A 110      83.599  33.425 -12.155  1.00 26.36           N
ATOM    591  CA  PHE A 110      85.028  33.407 -12.449  1.00 26.90           C
ATOM    592  CB  PHE A 110      85.734  34.607 -11.796  1.00 27.07           C
ATOM    593  CG  PHE A 110      85.249  35.945 -12.285  1.00 28.66           C
ATOM    594  CD1 PHE A 110      85.909  36.602 -13.330  1.00 30.61           C
ATOM    595  CE1 PHE A 110      85.464  37.851 -13.785  1.00 31.43           C
ATOM    596  CZ  PHE A 110      84.344  38.446 -13.195  1.00 31.46           C
ATOM    597  CE2 PHE A 110      83.679  37.795 -12.153  1.00 30.52           C
ATOM    598  CD2 PHE A 110      84.140  36.556 -11.701  1.00 28.63           C
ATOM    599  C   PHE A 110      85.646  32.117 -11.924  1.00 27.02           C
ATOM    600  O   PHE A 110      85.227  31.591 -10.879  1.00 26.50           O
ATOM    601  N   GLU A 111      86.638  31.614 -12.655  1.00 26.99           N
ATOM    602  CA  GLU A 111      87.454  30.500 -12.201  1.00 27.50           C
ATOM    603  CB  GLU A 111      87.683  29.476 -13.323  1.00 27.99           C
ATOM    604  CG  GLU A 111      88.309  28.179 -12.828  1.00 28.36           C
ATOM    605  CD  GLU A 111      88.468  27.116 -13.894  1.00 29.75           C
ATOM    606  OE1 GLU A 111      87.864  27.215 -14.989  1.00 31.47           O
ATOM    607  OE2 GLU A 111      89.206  26.154 -13.622  1.00 30.33           O
ATOM    608  C   GLU A 111      88.796  31.023 -11.696  1.00 27.98           C
ATOM    609  O   GLU A 111      89.415  31.891 -12.310  1.00 28.26           O
ATOM    610  N   ARG A 112      89.225  30.490 -10.560  1.00 28.31           N
ATOM    611  CA  ARG A 112      90.541  30.760 -10.004  1.00 28.18           C
ATOM    612  CB  ARG A 112      90.403  31.378  -8.614  1.00 28.37           C
ATOM    613  CG  ARG A 112      90.263  32.883  -8.622  1.00 27.57           C
ATOM    614  CD  ARG A 112      89.828  33.452  -7.293  1.00 27.27           C
ATOM    615  NE  ARG A 112      89.976  34.899  -7.282  1.00 26.93           N
ATOM    616  CZ  ARG A 112      89.758  35.671  -6.233  1.00 27.51           C
ATOM    617  NH1 ARG A 112      89.360  35.146  -5.079  1.00 28.76           N
ATOM    618  NH2 ARG A 112      89.932  36.979  -6.339  1.00 26.92           N
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ATOM	619	C	ARG A 112	91.255	29.413	-9.933	1.00	28.60	C
ATOM	620	O	ARG A 112	90.627	28.379	-10.197	1.00	28.00	O
ATOM	621	N	PRO A 113	92.556	29.402	-9.616	1.00	28.77	N
ATOM	622	CA	PRO A 113	93.282	28.129	-9.517	1.00	28.93	C
ATOM	623	CB	PRO A 113	94.697	28.557	-9.102	1.00	29.22	C
ATOM	624	CG	PRO A 113	94.817	29.977	-9.608	1.00	29.25	C
ATOM	625	CD	PRO A 113	93.444	30.560	-9.383	1.00	28.81	C
ATOM	626	C	PRO A 113	92.642	27.163	-8.505	1.00	28.63	C
ATOM	627	O	PRO A 113	92.473	25.982	-8.829	1.00	28.81	O
ATOM	628	N	ASP A 114	92.239	27.664	-7.340	1.00	28.09	N
ATOM	629	CA	ASP A 114	91.740	26.800	-6.269	1.00	27.57	C
ATOM	630	CB	ASP A 114	92.605	26.991	-5.020	1.00	28.11	C
ATOM	631	CG	ASP A 114	94.078	26.644	-5.272	1.00	30.45	C
ATOM	632	OD1	ASP A 114	94.959	27.360	-4.740	1.00	31.83	O
ATOM	633	OD2	ASP A 114	94.438	25.680	-5.998	1.00	30.94	O
ATOM	634	C	ASP A 114	90.252	26.962	-5.921	1.00	26.62	C
ATOM	635	O	ASP A 114	89.754	26.323	-4.980	1.00	26.49	O
ATOM	636	N	SER A 115	89.549	27.806	-6.677	1.00	25.25	N
ATOM	637	CA	SER A 115	88.150	28.130	-6.382	1.00	23.81	C
ATOM	638	CB	SER A 115	88.100	29.182	-5.276	1.00	23.83	C
ATOM	639	OG	SER A 115	88.650	30.403	-5.733	1.00	22.52	O
ATOM	640	C	SER A 115	87.352	28.653	-7.586	1.00	23.20	C
ATOM	641	O	SER A 115	87.917	28.964	-8.639	1.00	22.61	O
ATOM	642	N	PHE A 116	86.039	28.761	-7.400	1.00	22.13	N
ATOM	643	CA	PHE A 116	85.175	29.515	-8.306	1.00	21.81	C
ATOM	644	CB	PHE A 116	84.074	28.627	-8.901	1.00	21.79	C
ATOM	645	CG	PHE A 116	84.578	27.655	-9.921	1.00	22.56	C
ATOM	646	CD1	PHE A 116	85.096	26.425	-9.532	1.00	23.50	C
ATOM	647	CE1	PHE A 116	85.581	25.515	-10.487	1.00	25.19	C
ATOM	648	CZ	PHE A 116	85.550	25.846	-11.835	1.00	24.86	C
ATOM	649	CE2	PHE A 116	85.032	27.080	-12.230	1.00	25.05	C
ATOM	650	CD2	PHE A 116	84.551	27.974	-11.271	1.00	24.09	C
ATOM	651	C	PHE A 116	84.556	30.678	-7.553	1.00	21.29	C
ATOM	652	O	PHE A 116	84.349	30.605	-6.341	1.00	21.62	O
ATOM	653	N	VAL A 117	84.280	31.757	-8.275	1.00	20.75	N
ATOM	654	CA	VAL A 117	83.674	32.944	-7.707	1.00	19.94	C
ATOM	655	CB	VAL A 117	84.628	34.134	-7.791	1.00	20.10	C
ATOM	656	CG1	VAL A 117	84.036	35.341	-7.089	1.00	19.06	C
ATOM	657	CG2	VAL A 117	86.019	33.768	-7.189	1.00	20.50	C
ATOM	658	C	VAL A 117	82.399	33.242	-8.489	1.00	19.85	C
ATOM	659	O	VAL A 117	82.441	33.393	-9.713	1.00	20.09	O
ATOM	660	N	LEU A 118	81.276	33.327	-7.785	1.00	19.32	N
ATOM	661	CA	LEU A 118	79.981	33.584	-8.400	1.00	19.32	C
ATOM	662	CB	LEU A 118	78.936	32.565	-7.912	1.00	19.30	C
ATOM	663	CG	LEU A 118	78.914	31.157	-8.510	1.00	20.91	C
ATOM	664	CD1	LEU A 118	80.203	30.381	-8.224	1.00	23.74	C
ATOM	665	CD2	LEU A 118	77.741	30.382	-7.949	1.00	22.22	C
ATOM	666	C	LEU A 118	79.514	34.981	-8.051	1.00	19.31	C
ATOM	667	O	LEU A 118	79.574	35.387	-6.887	1.00	19.13	O
ATOM	668	N	ILE A 119	79.048	35.715	-9.062	1.00	19.23	N
ATOM	669	CA	ILE A 119	78.521	37.053	-8.860	1.00	19.06	C
ATOM	670	CB	ILE A 119	79.093	38.062	-9.898	1.00	19.52	C
ATOM	671	CG1	ILE A 119	80.627	37.931	-10.022	1.00	19.59	C
ATOM	672	CD1	ILE A 119	81.434	38.222	-8.736	1.00	19.03	C
ATOM	673	CG2	ILE A 119	78.652	39.509	-9.557	1.00	18.88	C
ATOM	674	C	ILE A 119	77.008	36.958	-8.938	1.00	19.43	C
ATOM	675	O	ILE A 119	76.446	36.592	-9.977	1.00	19.01	O
ATOM	676	N	LEU A 120	76.358	37.266	-7.823	1.00	19.78	N
ATOM	677	CA	LEU A 120	74.913	37.097	-7.683	1.00	20.66	C
ATOM	678	CB	LEU A 120	74.609	36.193	-6.483	1.00	20.51	C
ATOM	679	CG	LEU A 120	75.197	34.788	-6.594	1.00	21.71	C
ATOM	680	CD1	LEU A 120	75.218	34.103	-5.236	1.00	23.12	C
ATOM	681	CD2	LEU A 120	74.403	33.967	-7.591	1.00	22.78	C
ATOM	682	C	LEU A 120	74.253	38.436	-7.455	1.00	20.91	C
ATOM	683	O	LEU A 120	74.853	39.319	-6.848	1.00	20.71	O
ATOM	684	N	GLU A 121	73.015	38.588	-7.919	1.00	21.58	N
ATOM	685	CA	GLU A 121	72.238	39.775	-7.581	1.00	22.82	C
ATOM	686	CB	GLU A 121	70.883	39.780	-8.308	1.00	23.93	C
ATOM	687	CG	GLU A 121	69.759	39.096	-7.559	1.00	26.70	C

ATOM	688	CD	GLU	A	121	68.493	38.950	-8.387	1.00	30.59	C
ATOM	689	OE1	GLU	A	121	67.830	39.973	-8.654	1.00	33.17	O
ATOM	690	OE2	GLU	A	121	68.159	37.811	-8.759	1.00	31.26	O
ATOM	691	C	GLU	A	121	72.062	39.836	-6.065	1.00	22.52	C
ATOM	692	O	GLU	A	121	72.087	38.800	-5.391	1.00	22.12	O
ATOM	693	N	ARG	A	122	71.908	41.043	-5.533	1.00	22.16	N
ATOM	694	CA	ARG	A	122	71.677	41.212	-4.105	1.00	22.66	C
ATOM	695	CB	ARG	A	122	72.977	41.620	-3.390	1.00	21.96	C
ATOM	696	CG	ARG	A	122	72.814	41.952	-1.920	1.00	21.41	C
ATOM	697	CD	ARG	A	122	74.128	42.195	-1.161	1.00	21.79	C
ATOM	698	NE	ARG	A	122	74.932	43.293	-1.726	1.00	20.54	N
ATOM	699	CZ	ARG	A	122	74.781	44.581	-1.418	1.00	21.80	C
ATOM	700	NH1	ARG	A	122	73.860	44.973	-0.543	1.00	21.45	N
ATOM	701	NH2	ARG	A	122	75.568	45.489	-1.977	1.00	23.39	N
ATOM	702	C	ARG	A	122	70.575	42.249	-3.864	1.00	23.50	C
ATOM	703	O	ARG	A	122	70.764	43.419	-4.156	1.00	23.59	O
ATOM	704	N	PRO	A	123	69.429	41.818	-3.330	1.00	24.57	N
ATOM	705	CA	PRO	A	123	68.384	42.756	-2.888	1.00	25.12	C
ATOM	706	CB	PRO	A	123	67.233	41.832	-2.448	1.00	25.10	C
ATOM	707	CG	PRO	A	123	67.552	40.494	-3.044	1.00	25.14	C
ATOM	708	CD	PRO	A	123	69.047	40.411	-3.109	1.00	24.18	C
ATOM	709	C	PRO	A	123	68.860	43.599	-1.703	1.00	25.82	C
ATOM	710	O	PRO	A	123	69.678	43.129	-0.900	1.00	25.56	O
ATOM	711	N	GLU	A	124	68.358	44.830	-1.607	1.00	26.56	N
ATOM	712	CA	GLU	A	124	68.738	45.750	-0.533	1.00	27.26	C
ATOM	713	CB	GLU	A	124	69.952	46.591	-0.958	1.00	27.95	C
ATOM	714	CG	GLU	A	124	70.730	47.274	0.171	1.00	30.91	C
ATOM	715	CD	GLU	A	124	71.867	48.140	-0.367	1.00	35.36	C
ATOM	716	OE1	GLU	A	124	71.616	48.930	-1.311	1.00	37.56	O
ATOM	717	OE2	GLU	A	124	73.017	48.036	0.134	1.00	36.68	O
ATOM	718	C	GLU	A	124	67.544	46.649	-0.201	1.00	26.82	C
ATOM	719	O	GLU	A	124	67.053	47.358	-1.078	1.00	27.29	O
ATOM	720	N	PRO	A	125	67.061	46.617	1.045	1.00	25.92	N
ATOM	721	CA	PRO	A	125	67.599	45.755	2.101	1.00	24.79	C
ATOM	722	CB	PRO	A	125	67.062	46.403	3.373	1.00	24.95	C
ATOM	723	CG	PRO	A	125	65.759	46.993	2.960	1.00	24.96	C
ATOM	724	CD	PRO	A	125	65.936	47.437	1.530	1.00	25.81	C
ATOM	725	C	PRO	A	125	67.095	44.316	1.989	1.00	23.97	C
ATOM	726	O	PRO	A	125	66.109	44.040	1.287	1.00	23.35	O
ATOM	727	N	VAL	A	126	67.789	43.412	2.670	1.00	23.02	N
ATOM	728	CA	VAL	A	126	67.507	41.987	2.583	1.00	22.32	C
ATOM	729	CB	VAL	A	126	68.333	41.305	1.439	1.00	22.37	C
ATOM	730	CG1	VAL	A	126	69.815	41.129	1.837	1.00	21.96	C
ATOM	731	CG2	VAL	A	126	67.732	39.971	1.028	1.00	22.11	C
ATOM	732	C	VAL	A	126	67.809	41.342	3.925	1.00	22.20	C
ATOM	733	O	VAL	A	126	68.600	41.866	4.723	1.00	22.19	O
ATOM	734	N	GLN	A	127	67.159	40.209	4.166	1.00	21.35	N
ATOM	735	CA	GLN	A	127	67.429	39.378	5.323	1.00	20.84	C
ATOM	736	CB	GLN	A	127	66.653	39.883	6.540	1.00	20.45	C
ATOM	737	CG	GLN	A	127	66.866	39.053	7.796	1.00	20.49	C
ATOM	738	CD	GLN	A	127	66.156	39.632	8.999	1.00	22.00	C
ATOM	739	OE1	GLN	A	127	64.953	39.891	8.944	1.00	22.10	O
ATOM	740	NE2	GLN	A	127	66.892	39.842	10.082	1.00	20.41	N
ATOM	741	C	GLN	A	127	66.996	37.952	4.963	1.00	20.56	C
ATOM	742	O	GLN	A	127	65.917	37.760	4.392	1.00	20.00	O
ATOM	743	N	ASP	A	128	67.845	36.967	5.250	1.00	19.63	N
ATOM	744	CA	ASP	A	128	67.454	35.593	5.008	1.00	19.54	C
ATOM	745	CB	ASP	A	128	68.672	34.650	4.844	1.00	19.72	C
ATOM	746	CG	ASP	A	128	69.276	34.181	6.158	1.00	21.27	C
ATOM	747	OD1	ASP	A	128	68.578	34.093	7.189	1.00	22.90	O
ATOM	748	OD2	ASP	A	128	70.480	33.843	6.237	1.00	24.10	O
ATOM	749	C	ASP	A	128	66.381	35.126	6.016	1.00	19.14	C
ATOM	750	O	ASP	A	128	66.220	35.724	7.079	1.00	18.98	O
ATOM	751	N	LEU	A	129	65.642	34.077	5.658	1.00	18.65	N
ATOM	752	CA	LEU	A	129	64.485	33.651	6.429	1.00	18.28	C
ATOM	753	CB	LEU	A	129	63.611	32.662	5.619	1.00	17.80	C
ATOM	754	CG	LEU	A	129	62.291	32.181	6.245	1.00	17.80	C
ATOM	755	CD1	LEU	A	129	61.344	33.350	6.565	1.00	16.86	C
ATOM	756	CD2	LEU	A	129	61.591	31.180	5.327	1.00	15.45	C

ATOM	757	C	LEU	A	129	64.861	33.096	7.804	1.00	18.57	C
ATOM	758	O	LEU	A	129	64.095	33.220	8.760	1.00	18.46	O
ATOM	759	N	PHE	A	130	66.047	32.503	7.908	1.00	18.90	N
ATOM	760	CA	PHE	A	130	66.545	32.032	9.200	1.00	19.18	C
ATOM	761	CB	PHE	A	130	67.887	31.311	9.033	1.00	19.86	C
ATOM	762	CG	PHE	A	130	68.531	30.931	10.339	1.00	22.10	C
ATOM	763	CD1	PHE	A	130	69.471	31.764	10.933	1.00	23.65	C
ATOM	764	CE1	PHE	A	130	70.069	31.423	12.155	1.00	26.57	C
ATOM	765	CZ	PHE	A	130	69.712	30.232	12.792	1.00	25.84	C
ATOM	766	CE2	PHE	A	130	68.765	29.398	12.206	1.00	26.84	C
ATOM	767	CD2	PHE	A	130	68.179	29.748	10.982	1.00	24.38	C
ATOM	768	C	PHE	A	130	66.704	33.176	10.203	1.00	19.08	C
ATOM	769	O	PHE	A	130	66.287	33.060	11.374	1.00	17.75	O
ATOM	770	N	ASP	A	131	67.316	34.274	9.753	1.00	19.37	N
ATOM	771	CA	ASP	A	131	67.489	35.442	10.622	1.00	20.03	C
ATOM	772	CB	ASP	A	131	68.375	36.505	9.966	1.00	20.64	C
ATOM	773	CG	ASP	A	131	69.836	36.090	9.894	1.00	23.72	C
ATOM	774	OD1	ASP	A	131	70.258	35.197	10.671	1.00	28.11	O
ATOM	775	OD2	ASP	A	131	70.642	36.603	9.084	1.00	27.01	O
ATOM	776	C	ASP	A	131	66.136	36.030	10.947	1.00	19.62	C
ATOM	777	O	ASP	A	131	65.868	36.368	12.086	1.00	19.32	O
ATOM	778	N	PHE	A	132	65.275	36.133	9.936	1.00	19.50	N
ATOM	779	CA	PHE	A	132	63.969	36.758	10.094	1.00	19.48	C
ATOM	780	CB	PHE	A	132	63.233	36.740	8.754	1.00	19.50	C
ATOM	781	CG	PHE	A	132	61.939	37.481	8.749	1.00	20.08	C
ATOM	782	CD1	PHE	A	132	61.906	38.839	8.455	1.00	21.55	C
ATOM	783	CE1	PHE	A	132	60.704	39.535	8.433	1.00	22.42	C
ATOM	784	CZ	PHE	A	132	59.506	38.861	8.680	1.00	22.64	C
ATOM	785	CE2	PHE	A	132	59.522	37.505	8.962	1.00	21.42	C
ATOM	786	CD2	PHE	A	132	60.734	36.814	8.991	1.00	21.38	C
ATOM	787	C	PHE	A	132	63.186	36.015	11.167	1.00	20.30	C
ATOM	788	O	PHE	A	132	62.643	36.642	12.088	1.00	20.08	O
ATOM	789	N	ILE	A	133	63.131	34.682	11.064	1.00	20.79	N
ATOM	790	CA	ILE	A	133	62.411	33.875	12.064	1.00	21.52	C
ATOM	791	CB	ILE	A	133	62.195	32.429	11.583	1.00	21.38	C
ATOM	792	CG1	ILE	A	133	61.215	32.402	10.402	1.00	19.84	C
ATOM	793	CD1	ILE	A	133	61.200	31.104	9.665	1.00	16.74	C
ATOM	794	CG2	ILE	A	133	61.665	31.539	12.747	1.00	21.31	C
ATOM	795	C	ILE	A	133	63.097	33.868	13.438	1.00	22.84	C
ATOM	796	O	ILE	A	133	62.430	33.825	14.472	1.00	22.75	O
ATOM	797	N	THR	A	134	64.423	33.888	13.446	1.00	23.77	N
ATOM	798	CA	THR	A	134	65.167	34.000	14.696	1.00	25.24	C
ATOM	799	CB	THR	A	134	66.683	33.972	14.427	1.00	24.97	C
ATOM	800	OG1	THR	A	134	67.056	32.682	13.921	1.00	24.99	O
ATOM	801	CG2	THR	A	134	67.486	34.101	15.735	1.00	25.41	C
ATOM	802	C	THR	A	134	64.779	35.286	15.433	1.00	26.05	C
ATOM	803	O	THR	A	134	64.514	35.271	16.636	1.00	26.27	O
ATOM	804	N	GLU	A	135	64.728	36.386	14.693	1.00	27.17	N
ATOM	805	CA	GLU	A	135	64.424	37.693	15.268	1.00	28.48	C
ATOM	806	CB	GLU	A	135	64.830	38.807	14.302	1.00	28.91	C
ATOM	807	CG	GLU	A	135	66.282	39.221	14.449	1.00	32.87	C
ATOM	808	CD	GLU	A	135	66.702	40.288	13.450	1.00	37.37	C
ATOM	809	OE1	GLU	A	135	65.813	41.022	12.939	1.00	38.58	O
ATOM	810	OE2	GLU	A	135	67.927	40.383	13.177	1.00	38.32	O
ATOM	811	C	GLU	A	135	62.958	37.853	15.657	1.00	28.36	C
ATOM	812	O	GLU	A	135	62.656	38.416	16.710	1.00	27.93	O
ATOM	813	N	ARG	A	136	62.056	37.345	14.817	1.00	27.83	N
ATOM	814	CA	ARG	A	136	60.635	37.631	14.983	1.00	27.91	C
ATOM	815	CB	ARG	A	136	60.022	38.109	13.657	1.00	28.19	C
ATOM	816	CG	ARG	A	136	60.551	39.487	13.244	1.00	30.84	C
ATOM	817	CD	ARG	A	136	60.046	40.034	11.909	1.00	33.40	C
ATOM	818	NE	ARG	A	136	58.583	40.081	11.805	1.00	35.56	N
ATOM	819	CZ	ARG	A	136	57.907	40.978	11.081	1.00	35.76	C
ATOM	820	NH1	ARG	A	136	58.556	41.923	10.403	1.00	35.79	N
ATOM	821	NH2	ARG	A	136	56.580	40.938	11.041	1.00	34.21	N
ATOM	822	C	ARG	A	136	59.836	36.488	15.594	1.00	26.86	C
ATOM	823	O	ARG	A	136	58.683	36.677	15.980	1.00	27.36	O
ATOM	824	N	GLY	A	137	60.452	35.316	15.713	1.00	25.61	N
ATOM	825	CA	GLY	A	137	59.754	34.134	16.187	1.00	24.72	C

ATOM	826	C	GLY	A	137	58.763	33.584	15.156	1.00	24.39	C
ATOM	827	O	GLY	A	137	58.796	33.952	13.969	1.00	23.90	O
ATOM	828	N	ALA	A	138	57.880	32.699	15.615	1.00	23.04	N
ATOM	829	CA	ALA	A	138	56.864	32.089	14.760	1.00	22.25	C
ATOM	830	CB	ALA	A	138	55.895	31.269	15.612	1.00	22.29	C
ATOM	831	C	ALA	A	138	56.101	33.152	13.968	1.00	22.02	C
ATOM	832	O	ALA	A	138	55.694	34.174	14.523	1.00	21.11	O
ATOM	833	N	LEU	A	139	55.914	32.906	12.671	1.00	20.97	N
ATOM	834	CA	LEU	A	139	55.223	33.860	11.814	1.00	20.45	C
ATOM	835	CB	LEU	A	139	55.673	33.676	10.358	1.00	19.75	C
ATOM	836	CG	LEU	A	139	57.194	33.668	10.121	1.00	19.78	C
ATOM	837	CD1	LEU	A	139	57.509	33.578	8.624	1.00	17.80	C
ATOM	838	CD2	LEU	A	139	57.871	34.908	10.772	1.00	19.37	C
ATOM	839	C	LEU	A	139	53.706	33.707	11.938	1.00	20.32	C
ATOM	840	O	LEU	A	139	53.209	32.589	12.007	1.00	20.36	O
ATOM	841	N	GLN	A	140	52.979	34.828	11.950	1.00	19.81	N
ATOM	842	CA	GLN	A	140	51.530	34.796	11.751	1.00	19.77	C
ATOM	843	CB	GLN	A	140	50.958	36.210	11.624	1.00	20.35	C
ATOM	844	CG	GLN	A	140	50.938	37.006	12.913	1.00	24.46	C
ATOM	845	CD	GLN	A	140	50.666	38.484	12.674	1.00	30.48	C
ATOM	846	OE1	GLN	A	140	49.836	38.846	11.827	1.00	32.68	O
ATOM	847	NE2	GLN	A	140	51.357	39.343	13.421	1.00	32.67	N
ATOM	848	C	GLN	A	140	51.211	34.035	10.469	1.00	18.78	C
ATOM	849	O	GLN	A	140	51.957	34.118	9.494	1.00	17.03	O
ATOM	850	N	GLU	A	141	50.088	33.325	10.453	1.00	18.57	N
ATOM	851	CA	GLU	A	141	49.769	32.482	9.296	1.00	18.81	C
ATOM	852	CB	GLU	A	141	48.563	31.588	9.579	1.00	18.86	C
ATOM	853	CG	GLU	A	141	48.922	30.461	10.531	1.00	20.50	C
ATOM	854	CD	GLU	A	141	47.785	29.504	10.762	1.00	20.11	C
ATOM	855	OE1	GLU	A	141	47.107	29.151	9.779	1.00	20.79	O
ATOM	856	OE2	GLU	A	141	47.572	29.120	11.933	1.00	21.96	O
ATOM	857	C	GLU	A	141	49.605	33.235	7.970	1.00	18.75	C
ATOM	858	O	GLU	A	141	49.969	32.702	6.931	1.00	18.07	O
ATOM	859	N	GLU	A	142	49.048	34.454	8.002	1.00	18.37	N
ATOM	860	CA	GLU	A	142	48.939	35.263	6.787	1.00	18.46	C
ATOM	861	CB	GLU	A	142	48.216	36.589	7.078	1.00	18.72	C
ATOM	862	CG	GLU	A	142	48.076	37.515	5.889	1.00	20.48	C
ATOM	863	CD	GLU	A	142	47.411	38.836	6.241	1.00	24.11	C
ATOM	864	OE1	GLU	A	142	48.061	39.692	6.891	1.00	23.55	O
ATOM	865	OE2	GLU	A	142	46.232	39.017	5.851	1.00	25.93	O
ATOM	866	C	GLU	A	142	50.329	35.529	6.179	1.00	17.83	C
ATOM	867	O	GLU	A	142	50.506	35.530	4.959	1.00	17.80	O
ATOM	868	N	LEU	A	143	51.309	35.761	7.037	1.00	16.88	N
ATOM	869	CA	LEU	A	143	52.653	36.029	6.568	1.00	16.41	C
ATOM	870	CB	LEU	A	143	53.497	36.667	7.666	1.00	16.81	C
ATOM	871	CG	LEU	A	143	54.952	36.998	7.288	1.00	16.83	C
ATOM	872	CD1	LEU	A	143	54.999	37.909	6.049	1.00	15.94	C
ATOM	873	CD2	LEU	A	143	55.625	37.670	8.464	1.00	16.70	C
ATOM	874	C	LEU	A	143	53.307	34.749	6.057	1.00	15.72	C
ATOM	875	O	LEU	A	143	53.921	34.745	4.983	1.00	15.44	O
ATOM	876	N	ALA	A	144	53.173	33.670	6.824	1.00	14.81	N
ATOM	877	CA	ALA	A	144	53.692	32.364	6.404	1.00	14.61	C
ATOM	878	CB	ALA	A	144	53.444	31.327	7.470	1.00	14.33	C
ATOM	879	C	ALA	A	144	53.078	31.914	5.077	1.00	14.82	C
ATOM	880	O	ALA	A	144	53.754	31.270	4.253	1.00	14.19	O
ATOM	881	N	ARG	A	145	51.796	32.235	4.884	1.00	14.19	N
ATOM	882	CA	ARG	A	145	51.090	31.869	3.666	1.00	15.16	C
ATOM	883	CB	ARG	A	145	49.587	32.205	3.764	1.00	15.23	C
ATOM	884	CG	ARG	A	145	48.803	32.031	2.453	1.00	16.28	C
ATOM	885	CD	ARG	A	145	47.303	32.380	2.564	1.00	18.20	C
ATOM	886	NE	ARG	A	145	46.693	31.573	3.615	1.00	17.28	N
ATOM	887	CZ	ARG	A	145	46.238	32.049	4.761	1.00	17.72	C
ATOM	888	NH1	ARG	A	145	46.270	33.352	5.018	1.00	17.11	N
ATOM	889	NH2	ARG	A	145	45.747	31.212	5.657	1.00	18.63	N
ATOM	890	C	ARG	A	145	51.727	32.562	2.471	1.00	15.43	C
ATOM	891	O	ARG	A	145	52.034	31.917	1.470	1.00	16.61	O
ATOM	892	N	SER	A	146	51.941	33.868	2.578	1.00	15.08	N
ATOM	893	CA	SER	A	146	52.557	34.618	1.491	1.00	15.89	C
ATOM	894	CB	SER	A	146	52.558	36.114	1.823	1.00	15.77	C

ATOM	895	OG	SER	A	146	53.374	36.817	0.907	1.00	18.17	O
ATOM	896	C	SER	A	146	53.976	34.104	1.170	1.00	15.75	C
ATOM	897	O	SER	A	146	54.311	33.849	0.000	1.00	15.69	O
ATOM	898	N	PHE	A	147	54.777	33.926	2.220	1.00	15.20	N
ATOM	899	CA	PHE	A	147	56.145	33.423	2.104	1.00	15.40	C
ATOM	900	CB	PHE	A	147	56.801	33.392	3.487	1.00	15.25	C
ATOM	901	CG	PHE	A	147	57.345	34.724	3.939	1.00	16.31	C
ATOM	902	CD1	PHE	A	147	57.041	35.903	3.246	1.00	17.31	C
ATOM	903	CE1	PHE	A	147	57.552	37.121	3.663	1.00	18.81	C
ATOM	904	CZ	PHE	A	147	58.389	37.178	4.790	1.00	18.13	C
ATOM	905	CE2	PHE	A	147	58.696	36.017	5.480	1.00	17.81	C
ATOM	906	CD2	PHE	A	147	58.176	34.793	5.052	1.00	16.34	C
ATOM	907	C	PHE	A	147	56.195	32.024	1.483	1.00	14.94	C
ATOM	908	O	PHE	A	147	56.927	31.786	0.522	1.00	15.80	O
ATOM	909	N	PHE	A	148	55.407	31.114	2.033	1.00	14.80	N
ATOM	910	CA	PHE	A	148	55.354	29.733	1.549	1.00	15.37	C
ATOM	911	CB	PHE	A	148	54.409	28.887	2.418	1.00	14.71	C
ATOM	912	CG	PHE	A	148	54.574	27.399	2.224	1.00	14.42	C
ATOM	913	CD1	PHE	A	148	55.810	26.776	2.456	1.00	13.47	C
ATOM	914	CE1	PHE	A	148	55.962	25.379	2.277	1.00	10.13	C
ATOM	915	CZ	PHE	A	148	54.876	24.618	1.864	1.00	12.94	C
ATOM	916	CE2	PHE	A	148	53.635	25.237	1.625	1.00	14.02	C
ATOM	917	CD2	PHE	A	148	53.495	26.622	1.813	1.00	14.27	C
ATOM	918	C	PHE	A	148	54.898	29.648	0.089	1.00	15.20	C
ATOM	919	O	PHE	A	148	55.459	28.902	-0.703	1.00	14.97	O
ATOM	920	N	TRP	A	149	53.866	30.413	-0.253	1.00	15.54	N
ATOM	921	CA	TRP	A	149	53.393	30.477	-1.634	1.00	15.37	C
ATOM	922	CB	TRP	A	149	52.230	31.470	-1.739	1.00	15.34	C
ATOM	923	CG	TRP	A	149	51.671	31.606	-3.110	1.00	15.24	C
ATOM	924	CD1	TRP	A	149	52.070	32.494	-4.075	1.00	14.51	C
ATOM	925	NE1	TRP	A	149	51.301	32.333	-5.205	1.00	15.75	N
ATOM	926	CE2	TRP	A	149	50.394	31.326	-4.998	1.00	15.41	C
ATOM	927	CD2	TRP	A	149	50.595	30.845	-3.682	1.00	15.51	C
ATOM	928	CE3	TRP	A	149	49.766	29.804	-3.210	1.00	15.20	C
ATOM	929	CZ3	TRP	A	149	48.777	29.287	-4.064	1.00	14.40	C
ATOM	930	CH2	TRP	A	149	48.614	29.788	-5.376	1.00	15.19	C
ATOM	931	CZ2	TRP	A	149	49.405	30.804	-5.857	1.00	15.74	C
ATOM	932	C	TRP	A	149	54.516	30.881	-2.585	1.00	15.47	C
ATOM	933	O	TRP	A	149	54.709	30.266	-3.637	1.00	15.67	O
ATOM	934	N	GLN	A	150	55.267	31.913	-2.213	1.00	16.07	N
ATOM	935	CA	GLN	A	150	56.354	32.394	-3.063	1.00	16.16	C
ATOM	936	CB	GLN	A	150	56.926	33.704	-2.522	1.00	16.54	C
ATOM	937	CG	GLN	A	150	56.012	34.904	-2.760	1.00	17.72	C
ATOM	938	CD	GLN	A	150	56.654	36.188	-2.309	1.00	20.82	C
ATOM	939	OE1	GLN	A	150	57.668	36.594	-2.860	1.00	20.46	O
ATOM	940	NE2	GLN	A	150	56.078	36.825	-1.291	1.00	22.67	N
ATOM	941	C	GLN	A	150	57.470	31.366	-3.231	1.00	16.22	C
ATOM	942	O	GLN	A	150	58.068	31.271	-4.311	1.00	16.09	O
ATOM	943	N	VAL	A	151	57.747	30.613	-2.165	1.00	15.69	N
ATOM	944	CA	VAL	A	151	58.719	29.528	-2.219	1.00	15.67	C
ATOM	945	CB	VAL	A	151	58.973	28.914	-0.819	1.00	15.75	C
ATOM	946	CG1	VAL	A	151	59.838	27.661	-0.920	1.00	15.14	C
ATOM	947	CG2	VAL	A	151	59.648	29.950	0.087	1.00	14.26	C
ATOM	948	C	VAL	A	151	58.232	28.454	-3.186	1.00	15.73	C
ATOM	949	O	VAL	A	151	58.979	28.003	-4.048	1.00	15.25	O
ATOM	950	N	LEU	A	152	56.967	28.065	-3.046	1.00	16.29	N
ATOM	951	CA	LEU	A	152	56.348	27.138	-3.992	1.00	17.18	C
ATOM	952	CB	LEU	A	152	54.859	26.947	-3.658	1.00	17.37	C
ATOM	953	CG	LEU	A	152	54.467	25.690	-2.874	1.00	19.91	C
ATOM	954	CD1	LEU	A	152	54.643	24.445	-3.756	1.00	22.90	C
ATOM	955	CD2	LEU	A	152	55.236	25.494	-1.621	1.00	23.13	C
ATOM	956	C	LEU	A	152	56.512	27.572	-5.453	1.00	16.62	C
ATOM	957	O	LEU	A	152	56.889	26.765	-6.299	1.00	16.65	O
ATOM	958	N	GLU	A	153	56.217	28.841	-5.739	1.00	16.61	N
ATOM	959	CA	GLU	A	153	56.333	29.375	-7.096	1.00	16.62	C
ATOM	960	CB	GLU	A	153	55.832	30.827	-7.180	1.00	16.56	C
ATOM	961	CG	GLU	A	153	54.331	30.997	-6.968	1.00	17.23	C
ATOM	962	CD	GLU	A	153	53.514	30.514	-8.156	1.00	17.86	C
ATOM	963	OE1	GLU	A	153	53.901	30.807	-9.303	1.00	20.00	O

ATOM	964	OE2	GLU	A	153	52.487	29.843	-7.945	1.00	17.52	O
ATOM	965	C	GLU	A	153	57.777	29.297	-7.568	1.00	16.68	C
ATOM	966	O	GLU	A	153	58.038	28.986	-8.732	1.00	16.20	O
ATOM	967	N	ALA	A	154	58.712	29.559	-6.656	1.00	16.55	N
ATOM	968	CA	ALA	A	154	60.140	29.496	-6.992	1.00	16.97	C
ATOM	969	CB	ALA	A	154	61.004	30.188	-5.919	1.00	15.90	C
ATOM	970	C	ALA	A	154	60.621	28.063	-7.243	1.00	16.84	C
ATOM	971	O	ALA	A	154	61.345	27.818	-8.207	1.00	17.76	O
ATOM	972	N	VAL	A	155	60.218	27.126	-6.386	1.00	16.64	N
ATOM	973	CA	VAL	A	155	60.584	25.724	-6.564	1.00	16.78	C
ATOM	974	CB	VAL	A	155	60.201	24.871	-5.326	1.00	17.27	C
ATOM	975	CG1	VAL	A	155	60.395	23.386	-5.589	1.00	16.81	C
ATOM	976	CG2	VAL	A	155	61.032	25.313	-4.084	1.00	17.68	C
ATOM	977	C	VAL	A	155	59.958	25.163	-7.852	1.00	16.84	C
ATOM	978	O	VAL	A	155	60.621	24.445	-8.603	1.00	16.56	O
ATOM	979	N	ARG	A	156	58.690	25.491	-8.107	1.00	16.70	N
ATOM	980	CA	ARG	A	156	58.051	25.086	-9.374	1.00	17.03	C
ATOM	981	CB	ARG	A	156	56.603	25.570	-9.461	1.00	16.46	C
ATOM	982	CG	ARG	A	156	55.645	24.827	-8.564	1.00	17.08	C
ATOM	983	CD	ARG	A	156	54.201	25.302	-8.681	1.00	16.07	C
ATOM	984	NE	ARG	A	156	53.815	25.379	-10.087	1.00	15.86	N
ATOM	985	CZ	ARG	A	156	52.921	26.218	-10.591	1.00	16.05	C
ATOM	986	NH1	ARG	A	156	52.280	27.071	-9.805	1.00	14.03	N
ATOM	987	NH2	ARG	A	156	52.672	26.199	-11.895	1.00	15.89	N
ATOM	988	C	ARG	A	156	58.839	25.599	-10.573	1.00	17.05	C
ATOM	989	O	ARG	A	156	59.071	24.864	-11.529	1.00	17.34	O
ATOM	990	N	HIS	A	157	59.266	26.855	-10.522	1.00	17.35	N
ATOM	991	CA	HIS	A	157	60.090	27.397	-11.594	1.00	18.31	C
ATOM	992	CB	HIS	A	157	60.449	28.859	-11.330	1.00	18.48	C
ATOM	993	CG	HIS	A	157	61.374	29.443	-12.351	1.00	20.28	C
ATOM	994	ND1	HIS	A	157	62.696	29.733	-12.078	1.00	23.93	N
ATOM	995	CE1	HIS	A	157	63.262	30.241	-13.158	1.00	23.06	C
ATOM	996	NE2	HIS	A	157	62.356	30.288	-14.118	1.00	23.55	N
ATOM	997	CD2	HIS	A	157	61.168	29.796	-13.639	1.00	20.83	C
ATOM	998	C	HIS	A	157	61.361	26.559	-11.806	1.00	18.61	C
ATOM	999	O	HIS	A	157	61.691	26.199	-12.947	1.00	17.98	O
ATOM	1000	N	CYS	A	158	62.064	26.247	-10.715	1.00	18.74	N
ATOM	1001	CA	CYS	A	158	63.259	25.405	-10.800	1.00	19.66	C
ATOM	1002	CB	CYS	A	158	63.837	25.146	-9.413	1.00	19.79	C
ATOM	1003	SG	CYS	A	158	64.537	26.620	-8.683	1.00	22.60	S
ATOM	1004	C	CYS	A	158	62.979	24.077	-11.501	1.00	19.92	C
ATOM	1005	O	CYS	A	158	63.677	23.712	-12.447	1.00	20.10	O
ATOM	1006	N	HIS	A	159	61.955	23.365	-11.032	1.00	20.09	N
ATOM	1007	CA	HIS	A	159	61.580	22.085	-11.612	1.00	20.50	C
ATOM	1008	CB	HIS	A	159	60.484	21.410	-10.782	1.00	20.39	C
ATOM	1009	CG	HIS	A	159	60.934	20.995	-9.414	1.00	21.38	C
ATOM	1010	ND1	HIS	A	159	60.503	19.834	-8.814	1.00	22.95	N
ATOM	1011	CE1	HIS	A	159	61.055	19.727	-7.616	1.00	22.06	C
ATOM	1012	NE2	HIS	A	159	61.845	20.769	-7.426	1.00	21.41	N
ATOM	1013	CD2	HIS	A	159	61.790	21.577	-8.534	1.00	21.73	C
ATOM	1014	C	HIS	A	159	61.175	22.194	-13.092	1.00	20.62	C
ATOM	1015	O	HIS	A	159	61.558	21.340	-13.883	1.00	20.59	O
ATOM	1016	N	ASN	A	160	60.433	23.240	-13.463	1.00	20.97	N
ATOM	1017	CA	ASN	A	160	60.110	23.508	-14.882	1.00	21.47	C
ATOM	1018	CB	ASN	A	160	59.230	24.754	-15.042	1.00	21.81	C
ATOM	1019	CG	AASN	A	160	57.985	24.688	-14.251	0.50	22.71	C
ATOM	1020	CG	BASN	A	160	58.366	24.731	-16.318	0.50	21.42	C
ATOM	1021	OD1	AASN	A	160	57.565	25.688	-13.683	0.50	25.62	O
ATOM	1022	OD1	BASN	A	160	58.380	25.680	-17.103	0.50	21.10	O
ATOM	1023	ND2	AASN	A	160	57.364	23.518	-14.203	0.50	26.04	N
ATOM	1024	ND2	BASN	A	160	57.598	23.664	-16.506	0.50	19.99	N
ATOM	1025	C	ASN	A	160	61.353	23.728	-15.731	1.00	21.48	C
ATOM	1026	O	ASN	A	160	61.344	23.430	-16.925	1.00	21.00	O
ATOM	1027	N	CYS	A	161	62.404	24.278	-15.115	1.00	20.77	N
ATOM	1028	CA	CYS	A	161	63.691	24.462	-15.773	1.00	21.07	C
ATOM	1029	CB	CYS	A	161	64.395	25.716	-15.231	1.00	20.76	C
ATOM	1030	SG	CYS	A	161	63.499	27.235	-15.609	1.00	26.51	S
ATOM	1031	C	CYS	A	161	64.628	23.242	-15.665	1.00	20.01	C
ATOM	1032	O	CYS	A	161	65.791	23.329	-16.052	1.00	19.64	O

ATOM	1033	N	GLY	A	162	64.141	22.124	-15.130	1.00	18.99	N
ATOM	1034	CA	GLY	A	162	64.965	20.921	-15.005	1.00	18.24	C
ATOM	1035	C	GLY	A	162	65.968	20.898	-13.850	1.00	17.99	C
ATOM	1036	O	GLY	A	162	66.963	20.153	-13.878	1.00	16.70	O
ATOM	1037	N	VAL	A	163	65.696	21.678	-12.805	1.00	17.86	N
ATOM	1038	CA	VAL	A	163	66.634	21.799	-11.688	1.00	17.74	C
ATOM	1039	CB	VAL	A	163	67.173	23.251	-11.564	1.00	18.57	C
ATOM	1040	CG1	VAL	A	163	67.897	23.479	-10.215	1.00	17.79	C
ATOM	1041	CG2	VAL	A	163	68.078	23.608	-12.766	1.00	17.89	C
ATOM	1042	C	VAL	A	163	65.970	21.373	-10.374	1.00	17.54	C
ATOM	1043	O	VAL	A	163	64.851	21.780	-10.071	1.00	17.67	O
ATOM	1044	N	LEU	A	164	66.673	20.550	-9.612	1.00	17.14	N
ATOM	1045	CA	LEU	A	164	66.235	20.142	-8.288	1.00	17.15	C
ATOM	1046	CB	LEU	A	164	66.298	18.614	-8.170	1.00	17.23	C
ATOM	1047	CG	LEU	A	164	65.715	17.973	-6.909	1.00	18.35	C
ATOM	1048	CD1	LEU	A	164	64.183	18.038	-6.939	1.00	18.69	C
ATOM	1049	CD2	LEU	A	164	66.201	16.530	-6.783	1.00	15.82	C
ATOM	1050	C	LEU	A	164	67.151	20.802	-7.269	1.00	16.92	C
ATOM	1051	O	LEU	A	164	68.367	20.594	-7.305	1.00	17.02	O
ATOM	1052	N	HIS	A	165	66.574	21.583	-6.359	1.00	16.61	N
ATOM	1053	CA	HIS	A	165	67.356	22.378	-5.410	1.00	15.80	C
ATOM	1054	CB	HIS	A	165	66.462	23.440	-4.747	1.00	16.02	C
ATOM	1055	CG	HIS	A	165	67.212	24.444	-3.924	1.00	15.04	C
ATOM	1056	ND1	HIS	A	165	67.698	24.155	-2.668	1.00	13.63	N
ATOM	1057	CE1	HIS	A	165	68.311	25.218	-2.175	1.00	14.79	C
ATOM	1058	NE2	HIS	A	165	68.248	26.188	-3.071	1.00	16.20	N
ATOM	1059	CD2	HIS	A	165	67.571	25.726	-4.182	1.00	14.88	C
ATOM	1060	C	HIS	A	165	68.065	21.520	-4.352	1.00	16.12	C
ATOM	1061	O	HIS	A	165	69.281	21.692	-4.112	1.00	15.47	O
ATOM	1062	N	ARG	A	166	67.301	20.628	-3.708	1.00	15.81	N
ATOM	1063	CA	ARG	A	166	67.802	19.692	-2.685	1.00	16.34	C
ATOM	1064	CB	ARG	A	166	68.933	18.830	-3.231	1.00	16.34	C
ATOM	1065	CG	ARG	A	166	68.542	17.800	-4.282	1.00	17.58	C
ATOM	1066	CD	ARG	A	166	69.743	17.471	-5.131	1.00	23.63	C
ATOM	1067	NE	ARG	A	166	70.090	16.080	-5.010	1.00	27.91	N
ATOM	1068	CZ	ARG	A	166	71.277	15.551	-5.274	1.00	28.25	C
ATOM	1069	NH1	ARG	A	166	72.327	16.299	-5.636	1.00	26.61	N
ATOM	1070	NH2	ARG	A	166	71.404	14.246	-5.142	1.00	25.73	N
ATOM	1071	C	ARG	A	166	68.284	20.261	-1.348	1.00	17.04	C
ATOM	1072	O	ARG	A	166	68.778	19.491	-0.517	1.00	17.97	O
ATOM	1073	N	ASP	A	167	68.165	21.571	-1.127	1.00	16.44	N
ATOM	1074	CA	ASP	A	167	68.537	22.157	0.172	1.00	17.08	C
ATOM	1075	CB	ASP	A	167	70.018	22.615	0.164	1.00	16.76	C
ATOM	1076	CG	ASP	A	167	70.639	22.733	1.576	1.00	19.52	C
ATOM	1077	OD1	ASP	A	167	70.136	22.109	2.552	1.00	19.71	O
ATOM	1078	OD2	ASP	A	167	71.660	23.441	1.792	1.00	20.05	O
ATOM	1079	C	ASP	A	167	67.593	23.303	0.559	1.00	16.55	C
ATOM	1080	O	ASP	A	167	68.028	24.327	1.065	1.00	17.85	O
ATOM	1081	N	ILE	A	168	66.289	23.130	0.321	1.00	16.37	N
ATOM	1082	CA	ILE	A	168	65.304	24.165	0.643	1.00	15.43	C
ATOM	1083	CB	ILE	A	168	63.919	23.803	0.061	1.00	15.49	C
ATOM	1084	CG1	ILE	A	168	63.990	23.685	-1.467	1.00	15.11	C
ATOM	1085	CD1	ILE	A	168	62.816	22.891	-2.049	1.00	15.98	C
ATOM	1086	CG2	ILE	A	168	62.841	24.821	0.481	1.00	14.46	C
ATOM	1087	C	ILE	A	168	65.226	24.257	2.159	1.00	15.89	C
ATOM	1088	O	ILE	A	168	64.988	23.247	2.828	1.00	15.71	O
ATOM	1089	N	LYS	A	169	65.445	25.459	2.682	1.00	15.34	N
ATOM	1090	CA	LYS	A	169	65.458	25.724	4.116	1.00	15.97	C
ATOM	1091	CB	LYS	A	169	66.666	25.055	4.793	1.00	16.17	C
ATOM	1092	CG	LYS	A	169	68.018	25.601	4.321	1.00	18.35	C
ATOM	1093	CD	LYS	A	169	69.165	24.636	4.595	1.00	21.69	C
ATOM	1094	CE	LYS	A	169	69.449	24.497	6.073	1.00	23.35	C
ATOM	1095	NZ	LYS	A	169	70.883	24.061	6.239	1.00	24.28	N
ATOM	1096	C	LYS	A	169	65.542	27.234	4.314	1.00	15.57	C
ATOM	1097	O	LYS	A	169	65.954	27.971	3.392	1.00	15.50	O
ATOM	1098	N	ASP	A	170	65.213	27.676	5.526	1.00	15.04	N
ATOM	1099	CA	ASP	A	170	65.179	29.090	5.868	1.00	15.81	C
ATOM	1100	CB	ASP	A	170	64.849	29.284	7.358	1.00	15.73	C
ATOM	1101	CG	ASP	A	170	65.734	28.457	8.295	1.00	18.50	C

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ATOM   1102  OD1 ASP A 170      66.780  27.869   7.880  1.00 19.79           O
ATOM   1103  OD2 ASP A 170      65.450  28.361   9.509  1.00 21.07           O
ATOM   1104  C   ASP A 170      66.433  29.880   5.468  1.00 16.21           C
ATOM   1105  O   ASP A 170      66.321  30.954   4.874  1.00 16.22           O
ATOM   1106  N   GLU A 171      67.607  29.341   5.792  1.00 16.57           N
ATOM   1107  CA  GLU A 171      68.918  29.951   5.480  1.00 17.89           C
ATOM   1108  CB  GLU A 171      70.040  28.959   5.796  1.00 18.41           C
ATOM   1109  CG  GLU A 171      70.770  29.167   7.082  1.00 24.87           C
ATOM   1110  CD  GLU A 171      71.735  28.024   7.352  1.00 29.19           C
ATOM   1111  OE1 GLU A 171      72.124  27.876   8.521  1.00 34.95           O
ATOM   1112  OE2 GLU A 171      72.072  27.259   6.407  1.00 30.15           O
ATOM   1113  C   GLU A 171      69.096  30.224   3.998  1.00 16.68           C
ATOM   1114  O   GLU A 171      69.853  31.125   3.626  1.00 15.52           O
ATOM   1115  N   ASN A 172      68.468  29.391   3.171  1.00 15.92           N
ATOM   1116  CA  ASN A 172      68.601  29.487   1.707  1.00 15.37           C
ATOM   1117  CB  ASN A 172      68.806  28.111   1.093  1.00 14.94           C
ATOM   1118  CG  ASN A 172      70.122  27.517   1.493  1.00 15.14           C
ATOM   1119  OD1 ASN A 172      71.047  28.264   1.760  1.00 15.76           O
ATOM   1120  ND2 ASN A 172      70.218  26.188   1.567  1.00 13.68           N
ATOM   1121  C   ASN A 172      67.454  30.228   1.026  1.00 15.23           C
ATOM   1122  O   ASN A 172      67.198  30.038  -0.154  1.00 15.24           O
ATOM   1123  N   ILE A 173      66.799  31.102   1.778  1.00 15.43           N
ATOM   1124  CA  ILE A 173      65.714  31.920   1.252  1.00 15.78           C
ATOM   1125  CB  ILE A 173      64.350  31.416   1.775  1.00 15.76           C
ATOM   1126  CG1 ILE A 173      64.066  29.987   1.287  1.00 16.39           C
ATOM   1127  CD1 ILE A 173      62.948  29.264   2.080  1.00 14.60           C
ATOM   1128  CG2 ILE A 173      63.211  32.396   1.379  1.00 15.41           C
ATOM   1129  C   ILE A 173      65.947  33.363   1.701  1.00 15.85           C
ATOM   1130  O   ILE A 173      66.149  33.622   2.884  1.00 15.12           O
ATOM   1131  N   LEU A 174      65.914  34.285   0.741  1.00 16.29           N
ATOM   1132  CA  LEU A 174      66.139  35.707   0.992  1.00 16.81           C
ATOM   1133  CB  LEU A 174      67.035  36.307  -0.105  1.00 16.84           C
ATOM   1134  CG  LEU A 174      68.479  35.805  -0.189  1.00 17.08           C
ATOM   1135  CD1 LEU A 174      69.217  36.628  -1.214  1.00 16.20           C
ATOM   1136  CD2 LEU A 174      69.187  35.865   1.153  1.00 16.61           C
ATOM   1137  C   LEU A 174      64.816  36.419   0.956  1.00 17.35           C
ATOM   1138  O   LEU A 174      63.963  36.085   0.127  1.00 17.94           O
ATOM   1139  N   ILE A 175      64.641  37.387   1.850  1.00 17.74           N
ATOM   1140  CA  ILE A 175      63.470  38.255   1.833  1.00 18.68           C
ATOM   1141  CB  ILE A 175      62.818  38.360   3.226  1.00 18.50           C
ATOM   1142  CG1 ILE A 175      62.456  36.976   3.794  1.00 18.87           C
ATOM   1143  CD1 ILE A 175      62.302  36.995   5.327  1.00 18.86           C
ATOM   1144  CG2 ILE A 175      61.576  39.278   3.167  1.00 18.77           C
ATOM   1145  C   ILE A 175      63.902  39.649   1.389  1.00 19.58           C
ATOM   1146  O   ILE A 175      64.664  40.322   2.095  1.00 19.31           O
ATOM   1147  N   ASP A 176      63.412  40.074   0.228  1.00 20.23           N
ATOM   1148  CA  ASP A 176      63.581  41.449  -0.230  1.00 21.84           C
ATOM   1149  CB  ASP A 176      63.315  41.541  -1.739  1.00 22.01           C
ATOM   1150  CG  ASP A 176      63.414  42.967  -2.280  1.00 23.60           C
ATOM   1151  OD1 ASP A 176      63.243  43.920  -1.502  1.00 23.50           O
ATOM   1152  OD2 ASP A 176      63.625  43.217  -3.482  1.00 24.73           O
ATOM   1153  C   ASP A 176      62.588  42.286   0.587  1.00 22.79           C
ATOM   1154  O   ASP A 176      61.387  42.316   0.297  1.00 22.81           O
ATOM   1155  N   LEU A 177      63.102  42.924   1.634  1.00 23.58           N
ATOM   1156  CA  LEU A 177      62.271  43.537   2.660  1.00 24.93           C
ATOM   1157  CB  LEU A 177      63.132  44.012   3.835  1.00 25.33           C
ATOM   1158  CG  LEU A 177      63.764  42.908   4.700  1.00 25.91           C
ATOM   1159  CD1 LEU A 177      64.830  43.473   5.621  1.00 26.41           C
ATOM   1160  CD2 LEU A 177      62.715  42.118   5.504  1.00 27.00           C
ATOM   1161  C   LEU A 177      61.345  44.658   2.164  1.00 25.53           C
ATOM   1162  O   LEU A 177      60.231  44.789   2.661  1.00 26.29           O
ATOM   1163  N   ASN A 178      61.789  45.433   1.177  1.00 25.87           N
ATOM   1164  CA  ASN A 178      60.985  46.525   0.607  1.00 26.30           C
ATOM   1165  CB  ASN A 178      61.875  47.492  -0.187  1.00 26.74           C
ATOM   1166  CG  ASN A 178      62.544  48.534   0.690  1.00 28.73           C
ATOM   1167  OD1 ASN A 178      62.308  48.600   1.904  1.00 31.92           O
ATOM   1168  ND2 ASN A 178      63.382  49.361   0.078  1.00 30.86           N
ATOM   1169  C   ASN A 178      59.857  46.042  -0.307  1.00 26.01           C
ATOM   1170  O   ASN A 178      58.771  46.630  -0.338  1.00 25.84           O
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ATOM	1171	N	ARG	A	179	60.134	44.986	-1.066	1.00 25.22	N
ATOM	1172	CA	ARG	A	179	59.202	44.497	-2.073	1.00 25.06	C
ATOM	1173	CB	ARG	A	179	59.951	44.089	-3.340	1.00 25.43	C
ATOM	1174	CG	ARG	A	179	60.482	45.270	-4.157	1.00 26.18	C
ATOM	1175	CD	ARG	A	179	61.170	44.845	-5.426	1.00 29.81	C
ATOM	1176	NE	ARG	A	179	61.712	45.951	-6.219	1.00 33.67	N
ATOM	1177	CZ	ARG	A	179	60.987	46.869	-6.859	1.00 35.31	C
ATOM	1178	NH1	ARG	A	179	59.658	46.854	-6.805	1.00 36.83	N
ATOM	1179	NH2	ARG	A	179	61.598	47.816	-7.559	1.00 36.82	N
ATOM	1180	C	ARG	A	179	58.330	43.355	-1.574	1.00 24.41	C
ATOM	1181	O	ARG	A	179	57.345	43.004	-2.221	1.00 24.91	O
ATOM	1182	N	GLY	A	180	58.675	42.786	-0.421	1.00 23.59	N
ATOM	1183	CA	GLY	A	180	57.977	41.611	0.083	1.00 22.56	C
ATOM	1184	C	GLY	A	180	58.160	40.359	-0.779	1.00 21.90	C
ATOM	1185	O	GLY	A	180	57.320	39.456	-0.754	1.00 21.19	O
ATOM	1186	N	GLU	A	181	59.263	40.310	-1.524	1.00 21.18	N
ATOM	1187	CA	GLU	A	181	59.542	39.216	-2.462	1.00 21.26	C
ATOM	1188	CB	GLU	A	181	60.001	39.767	-3.815	1.00 20.99	C
ATOM	1189	CG	GLU	A	181	58.883	40.426	-4.598	1.00 22.33	C
ATOM	1190	CD	GLU	A	181	59.360	41.165	-5.827	1.00 24.38	C
ATOM	1191	OE1	GLU	A	181	60.493	40.911	-6.310	1.00 25.63	O
ATOM	1192	OE2	GLU	A	181	58.578	42.011	-6.317	1.00 26.99	O
ATOM	1193	C	GLU	A	181	60.613	38.281	-1.928	1.00 20.80	C
ATOM	1194	O	GLU	A	181	61.659	38.735	-1.467	1.00 20.59	O
ATOM	1195	N	LEU	A	182	60.348	36.979	-2.002	1.00 20.60	N
ATOM	1196	CA	LEU	A	182	61.297	35.963	-1.555	1.00 20.56	C
ATOM	1197	CB	LEU	A	182	60.570	34.791	-0.891	1.00 20.37	C
ATOM	1198	CG	LEU	A	182	60.517	34.821	0.631	1.00 21.15	C
ATOM	1199	CD1	LEU	A	182	59.818	36.090	1.096	1.00 22.41	C
ATOM	1200	CD2	LEU	A	182	59.801	33.559	1.145	1.00 19.08	C
ATOM	1201	C	LEU	A	182	62.118	35.439	-2.725	1.00 20.73	C
ATOM	1202	O	LEU	A	182	61.612	35.341	-3.849	1.00 20.32	O
ATOM	1203	N	LYS	A	183	63.372	35.096	-2.442	1.00 20.55	N
ATOM	1204	CA	LYS	A	183	64.313	34.617	-3.448	1.00 20.89	C
ATOM	1205	CB	LYS	A	183	65.374	35.692	-3.759	1.00 21.35	C
ATOM	1206	CG	LYS	A	183	64.883	36.741	-4.750	1.00 24.94	C
ATOM	1207	CD	LYS	A	183	65.757	37.973	-4.773	1.00 26.84	C
ATOM	1208	CE	LYS	A	183	65.777	38.639	-6.149	1.00 30.89	C
ATOM	1209	NZ	LYS	A	183	64.436	38.886	-6.765	1.00 30.16	N
ATOM	1210	C	LYS	A	183	65.005	33.373	-2.927	1.00 19.72	C
ATOM	1211	O	LYS	A	183	65.572	33.384	-1.844	1.00 19.28	O
ATOM	1212	N	LEU	A	184	64.960	32.317	-3.725	1.00 18.78	N
ATOM	1213	CA	LEU	A	184	65.689	31.088	-3.462	1.00 18.80	C
ATOM	1214	CB	LEU	A	184	65.057	29.957	-4.278	1.00 18.65	C
ATOM	1215	CG	LEU	A	184	65.182	28.479	-3.925	1.00 22.15	C
ATOM	1216	CD1	LEU	A	184	64.840	28.132	-2.445	1.00 22.78	C
ATOM	1217	CD2	LEU	A	184	64.302	27.643	-4.894	1.00 19.46	C
ATOM	1218	C	LEU	A	184	67.166	31.270	-3.827	1.00 17.97	C
ATOM	1219	O	LEU	A	184	67.500	31.813	-4.895	1.00 17.51	O
ATOM	1220	N	ILE	A	185	68.048	30.840	-2.932	1.00 16.83	N
ATOM	1221	CA	ILE	A	185	69.482	30.849	-3.204	1.00 16.25	C
ATOM	1222	CB	ILE	A	185	70.215	31.922	-2.348	1.00 16.56	C
ATOM	1223	CG1	ILE	A	185	69.892	31.720	-0.859	1.00 15.91	C
ATOM	1224	CD1	ILE	A	185	70.811	32.451	0.107	1.00 16.54	C
ATOM	1225	CG2	ILE	A	185	69.924	33.333	-2.865	1.00 15.65	C
ATOM	1226	C	ILE	A	185	70.098	29.504	-2.880	1.00 16.22	C
ATOM	1227	O	ILE	A	185	69.411	28.607	-2.380	1.00 16.13	O
ATOM	1228	N	ASP	A	186	71.409	29.408	-3.127	1.00 15.92	N
ATOM	1229	CA	ASP	A	186	72.254	28.263	-2.788	1.00 15.84	C
ATOM	1230	CB	ASP	A	186	72.344	28.039	-1.269	1.00 16.13	C
ATOM	1231	CG	ASP	A	186	73.351	26.972	-0.898	1.00 15.73	C
ATOM	1232	OD1	ASP	A	186	73.977	26.372	-1.791	1.00 17.28	O
ATOM	1233	OD2	ASP	A	186	73.571	26.621	0.268	1.00 16.60	O
ATOM	1234	C	ASP	A	186	71.875	26.980	-3.505	1.00 17.14	C
ATOM	1235	O	ASP	A	186	71.185	26.128	-2.968	1.00 17.68	O
ATOM	1236	N	PHE	A	187	72.372	26.828	-4.721	1.00 17.98	N
ATOM	1237	CA	PHE	A	187	72.163	25.603	-5.459	1.00 19.11	C
ATOM	1238	CB	PHE	A	187	71.813	25.935	-6.905	1.00 19.00	C
ATOM	1239	CG	PHE	A	187	70.462	26.572	-7.042	1.00 18.98	C

ATOM	1240	CD1	PHE	A	187	70.277	27.914	-6.731	1.00	17.58	C
ATOM	1241	CE1	PHE	A	187	69.010	28.508	-6.832	1.00	19.96	C
ATOM	1242	CZ	PHE	A	187	67.917	27.743	-7.260	1.00	19.45	C
ATOM	1243	CE2	PHE	A	187	68.094	26.402	-7.575	1.00	18.98	C
ATOM	1244	CD2	PHE	A	187	69.366	25.817	-7.452	1.00	19.42	C
ATOM	1245	C	PHE	A	187	73.367	24.669	-5.342	1.00	19.81	C
ATOM	1246	O	PHE	A	187	73.540	23.776	-6.162	1.00	20.32	O
ATOM	1247	N	GLY	A	188	74.157	24.864	-4.285	1.00	20.15	N
ATOM	1248	CA	GLY	A	188	75.355	24.074	-4.027	1.00	20.64	C
ATOM	1249	C	GLY	A	188	75.130	22.581	-3.824	1.00	20.89	C
ATOM	1250	O	GLY	A	188	76.061	21.795	-4.008	1.00	20.70	O
ATOM	1251	N	SER	A	189	73.904	22.186	-3.460	1.00	20.61	N
ATOM	1252	CA	SER	A	189	73.585	20.774	-3.205	1.00	20.36	C
ATOM	1253	CB	SER	A	189	72.891	20.598	-1.843	1.00	20.68	C
ATOM	1254	OG	SER	A	189	73.701	21.035	-0.766	1.00	20.77	O
ATOM	1255	C	SER	A	189	72.668	20.218	-4.276	1.00	20.23	C
ATOM	1256	O	SER	A	189	72.229	19.079	-4.181	1.00	19.67	O
ATOM	1257	N	GLY	A	190	72.359	21.040	-5.273	1.00	19.66	N
ATOM	1258	CA	GLY	A	190	71.362	20.701	-6.256	1.00	20.11	C
ATOM	1259	C	GLY	A	190	71.779	19.655	-7.282	1.00	20.35	C
ATOM	1260	O	GLY	A	190	72.924	19.203	-7.309	1.00	20.22	O
ATOM	1261	N	ALA	A	191	70.830	19.271	-8.122	1.00	19.81	N
ATOM	1262	CA	ALA	A	191	71.085	18.339	-9.201	1.00	20.13	C
ATOM	1263	CB	ALA	A	191	70.902	16.875	-8.722	1.00	20.04	C
ATOM	1264	C	ALA	A	191	70.130	18.652	-10.323	1.00	20.23	C
ATOM	1265	O	ALA	A	191	69.126	19.344	-10.122	1.00	20.11	O
ATOM	1266	N	LEU	A	192	70.446	18.144	-11.512	1.00	20.33	N
ATOM	1267	CA	LEU	A	192	69.504	18.154	-12.617	1.00	20.48	C
ATOM	1268	CB	LEU	A	192	70.160	17.538	-13.870	1.00	20.65	C
ATOM	1269	CG	LEU	A	192	71.394	18.241	-14.460	1.00	21.30	C
ATOM	1270	CD1	LEU	A	192	72.025	17.441	-15.650	1.00	24.01	C
ATOM	1271	CD2	LEU	A	192	71.028	19.649	-14.922	1.00	20.92	C
ATOM	1272	C	LEU	A	192	68.301	17.329	-12.171	1.00	20.62	C
ATOM	1273	O	LEU	A	192	68.472	16.302	-11.520	1.00	20.87	O
ATOM	1274	N	LEU	A	193	67.092	17.787	-12.488	1.00	20.82	N
ATOM	1275	CA	LEU	A	193	65.883	17.033	-12.163	1.00	20.67	C
ATOM	1276	CB	LEU	A	193	64.626	17.901	-12.333	1.00	20.90	C
ATOM	1277	CG	LEU	A	193	63.271	17.308	-11.915	1.00	21.37	C
ATOM	1278	CD1	LEU	A	193	63.216	16.979	-10.428	1.00	19.30	C
ATOM	1279	CD2	LEU	A	193	62.103	18.226	-12.303	1.00	23.02	C
ATOM	1280	C	LEU	A	193	65.770	15.784	-13.042	1.00	20.94	C
ATOM	1281	O	LEU	A	193	66.005	15.837	-14.250	1.00	20.46	O
ATOM	1282	N	LYS	A	194	65.403	14.666	-12.423	1.00	20.70	N
ATOM	1283	CA	LYS	A	194	65.191	13.411	-13.140	1.00	20.09	C
ATOM	1284	CB	LYS	A	194	66.464	12.559	-13.094	1.00	20.03	C
ATOM	1285	CG	LYS	A	194	66.780	11.998	-11.717	1.00	18.07	C
ATOM	1286	CD	LYS	A	194	68.169	11.391	-11.691	1.00	19.71	C
ATOM	1287	CE	LYS	A	194	68.381	10.652	-10.385	1.00	20.42	C
ATOM	1288	NZ	LYS	A	194	69.586	9.789	-10.403	1.00	19.70	N
ATOM	1289	C	LYS	A	194	64.025	12.658	-12.505	1.00	19.94	C
ATOM	1290	O	LYS	A	194	63.669	12.913	-11.349	1.00	19.51	O
ATOM	1291	N	ASP	A	195	63.456	11.722	-13.260	1.00	19.71	N
ATOM	1292	CA	ASP	A	195	62.308	10.943	-12.808	1.00	19.96	C
ATOM	1293	CB	ASP	A	195	61.352	10.706	-13.972	1.00	20.12	C
ATOM	1294	CG	ASP	A	195	60.843	12.005	-14.573	1.00	21.01	C
ATOM	1295	OD1	ASP	A	195	60.213	12.792	-13.832	1.00	21.96	O
ATOM	1296	OD2	ASP	A	195	61.028	12.311	-15.770	1.00	22.33	O
ATOM	1297	C	ASP	A	195	62.684	9.613	-12.166	1.00	20.21	C
ATOM	1298	O	ASP	A	195	61.811	8.866	-11.740	1.00	20.16	O
ATOM	1299	N	THR	A	196	63.979	9.324	-12.111	1.00	20.34	N
ATOM	1300	CA	THR	A	196	64.459	8.086	-11.519	1.00	20.80	C
ATOM	1301	CB	THR	A	196	65.550	7.433	-12.402	1.00	20.79	C
ATOM	1302	OG1	THR	A	196	66.489	8.431	-12.832	1.00	19.71	O
ATOM	1303	CG2	THR	A	196	64.942	6.891	-13.701	1.00	20.94	C
ATOM	1304	C	THR	A	196	64.997	8.357	-10.132	1.00	21.32	C
ATOM	1305	O	THR	A	196	65.059	9.515	-9.686	1.00	21.17	O
ATOM	1306	N	VAL	A	197	65.387	7.290	-9.447	1.00	21.71	N
ATOM	1307	CA	VAL	A	197	65.741	7.385	-8.039	1.00	22.75	C
ATOM	1308	CB	VAL	A	197	65.661	5.983	-7.364	1.00	22.95	C

ATOM	1309	CG1	VAL	A	197	66.823	5.098	-7.798	1.00	24.30	C
ATOM	1310	CG2	VAL	A	197	65.592	6.094	-5.849	1.00	23.66	C
ATOM	1311	C	VAL	A	197	67.102	8.074	-7.834	1.00	22.86	C
ATOM	1312	O	VAL	A	197	68.044	7.862	-8.611	1.00	23.08	O
ATOM	1313	N	TYR	A	198	67.176	8.939	-6.823	1.00	22.60	N
ATOM	1314	CA	TYR	A	198	68.441	9.506	-6.375	1.00	22.42	C
ATOM	1315	CB	TYR	A	198	68.242	10.922	-5.829	1.00	21.98	C
ATOM	1316	CG	TYR	A	198	67.927	11.966	-6.869	1.00	19.83	C
ATOM	1317	CD1	TYR	A	198	66.610	12.197	-7.262	1.00	18.45	C
ATOM	1318	CE1	TYR	A	198	66.301	13.147	-8.205	1.00	16.56	C
ATOM	1319	CZ	TYR	A	198	67.307	13.909	-8.772	1.00	17.06	C
ATOM	1320	OH	TYR	A	198	66.949	14.848	-9.713	1.00	15.18	O
ATOM	1321	CE2	TYR	A	198	68.641	13.708	-8.410	1.00	16.87	C
ATOM	1322	CD2	TYR	A	198	68.942	12.732	-7.455	1.00	18.51	C
ATOM	1323	C	TYR	A	198	69.010	8.631	-5.266	1.00	22.99	C
ATOM	1324	O	TYR	A	198	68.273	8.209	-4.363	1.00	22.53	O
ATOM	1325	N	THR	A	199	70.314	8.370	-5.337	1.00	23.94	N
ATOM	1326	CA	THR	A	199	71.034	7.617	-4.302	1.00	25.22	C
ATOM	1327	CB	THR	A	199	71.694	6.331	-4.880	1.00	25.19	C
ATOM	1328	OG1	THR	A	199	72.604	6.688	-5.923	1.00	25.62	O
ATOM	1329	CG2	THR	A	199	70.681	5.427	-5.571	1.00	25.21	C
ATOM	1330	C	THR	A	199	72.111	8.475	-3.635	1.00	26.00	C
ATOM	1331	O	THR	A	199	72.881	7.982	-2.818	1.00	25.92	O
ATOM	1332	N	ASP	A	200	72.170	9.752	-4.007	1.00	27.25	N
ATOM	1333	CA	ASP	A	200	73.121	10.694	-3.424	1.00	28.69	C
ATOM	1334	CB	ASP	A	200	74.132	11.197	-4.477	1.00	29.29	C
ATOM	1335	CG	ASP	A	200	73.490	12.085	-5.559	1.00	32.11	C
ATOM	1336	OD1	ASP	A	200	73.879	13.277	-5.649	1.00	34.36	O
ATOM	1337	OD2	ASP	A	200	72.609	11.686	-6.370	1.00	34.31	O
ATOM	1338	C	ASP	A	200	72.374	11.855	-2.788	1.00	28.79	C
ATOM	1339	O	ASP	A	200	71.327	12.278	-3.283	1.00	28.34	O
ATOM	1340	N	PHE	A	201	72.904	12.350	-1.677	1.00	29.39	N
ATOM	1341	CA	PHE	A	201	72.328	13.501	-1.000	1.00	30.23	C
ATOM	1342	CB	PHE	A	201	71.140	13.077	-0.140	1.00	29.94	C
ATOM	1343	CG	PHE	A	201	70.534	14.196	0.660	1.00	28.00	C
ATOM	1344	CD1	PHE	A	201	69.676	15.109	0.062	1.00	27.14	C
ATOM	1345	CE1	PHE	A	201	69.104	16.143	0.791	1.00	27.27	C
ATOM	1346	CZ	PHE	A	201	69.381	16.266	2.148	1.00	27.00	C
ATOM	1347	CE2	PHE	A	201	70.244	15.357	2.763	1.00	28.69	C
ATOM	1348	CD2	PHE	A	201	70.811	14.322	2.012	1.00	28.58	C
ATOM	1349	C	PHE	A	201	73.381	14.192	-0.146	1.00	31.40	C
ATOM	1350	O	PHE	A	201	74.097	13.542	0.614	1.00	31.87	O
ATOM	1351	N	ASP	A	202	73.449	15.512	-0.274	1.00	32.09	N
ATOM	1352	CA	ASP	A	202	74.428	16.314	0.432	1.00	33.18	C
ATOM	1353	CB	ASP	A	202	75.581	16.677	-0.510	1.00	34.28	C
ATOM	1354	CG	ASP	A	202	76.918	16.282	0.054	1.00	37.84	C
ATOM	1355	OD1	ASP	A	202	77.292	15.090	-0.089	1.00	42.28	O
ATOM	1356	OD2	ASP	A	202	77.655	17.087	0.671	1.00	41.24	O
ATOM	1357	C	ASP	A	202	73.823	17.576	1.024	1.00	32.23	C
ATOM	1358	O	ASP	A	202	74.550	18.471	1.451	1.00	32.66	O
ATOM	1359	N	GLY	A	203	72.494	17.648	1.049	1.00	31.25	N
ATOM	1360	CA	GLY	A	203	71.801	18.764	1.677	1.00	29.41	C
ATOM	1361	C	GLY	A	203	71.721	18.616	3.189	1.00	28.69	C
ATOM	1362	O	GLY	A	203	72.489	17.863	3.792	1.00	28.32	O
ATOM	1363	N	THR	A	204	70.770	19.324	3.800	1.00	28.21	N
ATOM	1364	CA	THR	A	204	70.628	19.353	5.257	1.00	27.26	C
ATOM	1365	CB	THR	A	204	69.950	20.656	5.702	1.00	26.96	C
ATOM	1366	OG1	THR	A	204	70.654	21.769	5.142	1.00	26.09	O
ATOM	1367	CG2	THR	A	204	70.103	20.855	7.222	1.00	25.58	C
ATOM	1368	C	THR	A	204	69.847	18.152	5.776	1.00	27.62	C
ATOM	1369	O	THR	A	204	68.680	17.948	5.397	1.00	27.26	O
ATOM	1370	N	ARG	A	205	70.483	17.391	6.670	1.00	27.57	N
ATOM	1371	CA	ARG	A	205	69.928	16.139	7.173	1.00	27.70	C
ATOM	1372	CB	ARG	A	205	70.881	15.491	8.193	1.00	28.59	C
ATOM	1373	CG	ARG	A	205	70.306	14.238	8.883	1.00	31.06	C
ATOM	1374	CD	ARG	A	205	71.326	13.172	9.299	1.00	34.02	C
ATOM	1375	NE	ARG	A	205	71.717	12.397	8.132	1.00	37.36	N
ATOM	1376	CZ	ARG	A	205	71.619	11.073	7.997	1.00	37.19	C
ATOM	1377	NH1	ARG	A	205	71.156	10.302	8.970	1.00	36.97	N

ATOM	1378	NH2	ARG	A	205	71.995	10.523	6.856	1.00	36.80	N
ATOM	1379	C	ARG	A	205	68.508	16.270	7.748	1.00	27.42	C
ATOM	1380	O	ARG	A	205	67.600	15.482	7.393	1.00	27.39	O
ATOM	1381	N	VAL	A	206	68.323	17.271	8.611	1.00	26.15	N
ATOM	1382	CA	VAL	A	206	67.088	17.452	9.368	1.00	24.94	C
ATOM	1383	CB	VAL	A	206	67.268	18.408	10.593	1.00	25.07	C
ATOM	1384	CG1	VAL	A	206	68.149	17.763	11.651	1.00	24.65	C
ATOM	1385	CG2	VAL	A	206	67.842	19.792	10.167	1.00	23.92	C
ATOM	1386	C	VAL	A	206	65.986	17.956	8.455	1.00	25.16	C
ATOM	1387	O	VAL	A	206	64.835	18.077	8.883	1.00	25.56	O
ATOM	1388	N	TYR	A	207	66.343	18.226	7.195	1.00	24.00	N
ATOM	1389	CA	TYR	A	207	65.363	18.533	6.169	1.00	23.56	C
ATOM	1390	CB	TYR	A	207	65.792	19.777	5.388	1.00	23.98	C
ATOM	1391	CG	TYR	A	207	65.472	21.091	6.067	1.00	23.10	C
ATOM	1392	CD1	TYR	A	207	66.274	21.587	7.101	1.00	22.69	C
ATOM	1393	CE1	TYR	A	207	65.980	22.819	7.722	1.00	24.39	C
ATOM	1394	CZ	TYR	A	207	64.884	23.551	7.277	1.00	27.17	C
ATOM	1395	OH	TYR	A	207	64.556	24.776	7.844	1.00	30.13	O
ATOM	1396	CE2	TYR	A	207	64.080	23.064	6.243	1.00	25.83	C
ATOM	1397	CD2	TYR	A	207	64.382	21.851	5.647	1.00	24.73	C
ATOM	1398	C	TYR	A	207	65.141	17.371	5.198	1.00	22.93	C
ATOM	1399	O	TYR	A	207	64.299	17.469	4.285	1.00	22.62	O
ATOM	1400	N	SER	A	208	65.906	16.292	5.382	1.00	21.96	N
ATOM	1401	CA	SER	A	208	65.849	15.131	4.487	1.00	21.81	C
ATOM	1402	CB	SER	A	208	67.203	14.408	4.432	1.00	22.13	C
ATOM	1403	OG	SER	A	208	67.426	13.650	5.611	1.00	23.96	O
ATOM	1404	C	SER	A	208	64.738	14.139	4.876	1.00	20.92	C
ATOM	1405	O	SER	A	208	64.427	13.970	6.062	1.00	20.62	O
ATOM	1406	N	PRO	A	209	64.177	13.466	3.873	1.00	19.97	N
ATOM	1407	CA	PRO	A	209	62.999	12.620	4.067	1.00	19.59	C
ATOM	1408	CB	PRO	A	209	62.467	12.452	2.639	1.00	19.55	C
ATOM	1409	CG	PRO	A	209	63.689	12.524	1.774	1.00	19.80	C
ATOM	1410	CD	PRO	A	209	64.644	13.447	2.470	1.00	19.85	C
ATOM	1411	C	PRO	A	209	63.380	11.269	4.690	1.00	19.33	C
ATOM	1412	O	PRO	A	209	64.554	10.867	4.623	1.00	19.13	O
ATOM	1413	N	PRO	A	210	62.415	10.592	5.304	1.00	18.92	N
ATOM	1414	CA	PRO	A	210	62.668	9.300	5.961	1.00	19.08	C
ATOM	1415	CB	PRO	A	210	61.301	8.921	6.557	1.00	18.83	C
ATOM	1416	CG	PRO	A	210	60.302	9.737	5.821	1.00	19.11	C
ATOM	1417	CD	PRO	A	210	61.006	11.018	5.435	1.00	18.89	C
ATOM	1418	C	PRO	A	210	63.164	8.203	5.012	1.00	19.74	C
ATOM	1419	O	PRO	A	210	63.892	7.324	5.476	1.00	19.91	O
ATOM	1420	N	GLU	A	211	62.796	8.256	3.732	1.00	19.73	N
ATOM	1421	CA	GLU	A	211	63.273	7.278	2.766	1.00	20.85	C
ATOM	1422	CB	GLU	A	211	62.461	7.323	1.451	1.00	20.53	C
ATOM	1423	CG	GLU	A	211	62.554	8.649	0.684	1.00	20.57	C
ATOM	1424	CD	GLU	A	211	61.446	9.651	1.014	1.00	20.44	C
ATOM	1425	OE1	GLU	A	211	60.905	9.640	2.143	1.00	21.24	O
ATOM	1426	OE2	GLU	A	211	61.122	10.474	0.132	1.00	19.92	O
ATOM	1427	C	GLU	A	211	64.782	7.446	2.532	1.00	21.48	C
ATOM	1428	O	GLU	A	211	65.491	6.465	2.284	1.00	21.77	O
ATOM	1429	N	TRP	A	212	65.269	8.683	2.624	1.00	21.85	N
ATOM	1430	CA	TRP	A	212	66.702	8.917	2.576	1.00	22.59	C
ATOM	1431	CB	TRP	A	212	67.059	10.402	2.439	1.00	21.76	C
ATOM	1432	CG	TRP	A	212	68.537	10.610	2.665	1.00	23.30	C
ATOM	1433	CD1	TRP	A	212	69.128	11.209	3.745	1.00	23.54	C
ATOM	1434	NE1	TRP	A	212	70.497	11.187	3.610	1.00	24.29	N
ATOM	1435	CE2	TRP	A	212	70.828	10.556	2.441	1.00	23.65	C
ATOM	1436	CD2	TRP	A	212	69.618	10.169	1.817	1.00	22.66	C
ATOM	1437	CE3	TRP	A	212	69.684	9.497	0.589	1.00	22.34	C
ATOM	1438	CZ3	TRP	A	212	70.944	9.227	0.028	1.00	23.22	C
ATOM	1439	CH2	TRP	A	212	72.129	9.621	0.680	1.00	23.33	C
ATOM	1440	CZ2	TRP	A	212	72.093	10.288	1.882	1.00	24.31	C
ATOM	1441	C	TRP	A	212	67.375	8.324	3.814	1.00	22.99	C
ATOM	1442	O	TRP	A	212	68.368	7.609	3.695	1.00	23.46	O
ATOM	1443	N	ILE	A	213	66.812	8.611	4.986	1.00	23.54	N
ATOM	1444	CA	ILE	A	213	67.375	8.166	6.265	1.00	24.57	C
ATOM	1445	CB	ILE	A	213	66.566	8.729	7.468	1.00	24.25	C
ATOM	1446	CG1	ILE	A	213	66.550	10.265	7.469	1.00	24.58	C

ATOM	1447	CD1	ILE	A	213	67.945	10.927	7.479	1.00	24.84	C
ATOM	1448	CG2	ILE	A	213	67.143	8.217	8.788	1.00	24.24	C
ATOM	1449	C	ILE	A	213	67.480	6.646	6.350	1.00	25.27	C
ATOM	1450	O	ILE	A	213	68.523	6.113	6.741	1.00	25.42	O
ATOM	1451	N	ARG	A	214	66.409	5.963	5.955	1.00	26.19	N
ATOM	1452	CA	ARG	A	214	66.330	4.508	6.035	1.00	27.54	C
ATOM	1453	CB	ARG	A	214	64.873	4.052	6.126	1.00	27.97	C
ATOM	1454	CG	ARG	A	214	64.138	4.599	7.344	1.00	31.59	C
ATOM	1455	CD	ARG	A	214	62.621	4.436	7.296	1.00	37.14	C
ATOM	1456	NE	ARG	A	214	62.201	3.037	7.213	1.00	40.55	N
ATOM	1457	CZ	ARG	A	214	62.233	2.167	8.219	1.00	43.40	C
ATOM	1458	NH1	ARG	A	214	62.672	2.525	9.423	1.00	44.08	N
ATOM	1459	NH2	ARG	A	214	61.823	0.919	8.018	1.00	44.82	N
ATOM	1460	C	ARG	A	214	67.018	3.787	4.877	1.00	27.77	C
ATOM	1461	O	ARG	A	214	67.799	2.869	5.113	1.00	27.88	O
ATOM	1462	N	TYR	A	215	66.731	4.195	3.641	1.00	27.94	N
ATOM	1463	CA	TYR	A	215	67.151	3.428	2.460	1.00	28.52	C
ATOM	1464	CB	TYR	A	215	65.931	2.983	1.642	1.00	28.63	C
ATOM	1465	CG	TYR	A	215	64.788	2.478	2.486	1.00	30.63	C
ATOM	1466	CD1	TYR	A	215	64.884	1.262	3.177	1.00	32.35	C
ATOM	1467	CE1	TYR	A	215	63.832	0.800	3.965	1.00	33.17	C
ATOM	1468	CZ	TYR	A	215	62.674	1.560	4.063	1.00	34.20	C
ATOM	1469	OH	TYR	A	215	61.625	1.121	4.834	1.00	36.84	O
ATOM	1470	CE2	TYR	A	215	62.556	2.764	3.390	1.00	33.32	C
ATOM	1471	CD2	TYR	A	215	63.610	3.217	2.607	1.00	32.43	C
ATOM	1472	C	TYR	A	215	68.143	4.128	1.539	1.00	28.30	C
ATOM	1473	O	TYR	A	215	68.551	3.558	0.531	1.00	28.64	O
ATOM	1474	N	HIS	A	216	68.520	5.360	1.870	1.00	27.98	N
ATOM	1475	CA	HIS	A	216	69.431	6.133	1.027	1.00	27.92	C
ATOM	1476	CB	HIS	A	216	70.866	5.574	1.125	1.00	28.78	C
ATOM	1477	CG	HIS	A	216	71.628	6.080	2.315	1.00	32.47	C
ATOM	1478	ND1	HIS	A	216	72.993	5.922	2.453	1.00	36.05	N
ATOM	1479	CE1	HIS	A	216	73.386	6.479	3.587	1.00	37.27	C
ATOM	1480	NE2	HIS	A	216	72.328	6.997	4.187	1.00	36.76	N
ATOM	1481	CD2	HIS	A	216	71.217	6.761	3.413	1.00	35.02	C
ATOM	1482	C	HIS	A	216	68.936	6.268	-0.435	1.00	26.74	C
ATOM	1483	O	HIS	A	216	69.728	6.295	-1.383	1.00	26.90	O
ATOM	1484	N	ARG	A	217	67.616	6.360	-0.592	1.00	25.13	N
ATOM	1485	CA	ARG	A	217	66.964	6.461	-1.892	1.00	24.20	C
ATOM	1486	CB	ARG	A	217	66.380	5.106	-2.341	1.00	24.35	C
ATOM	1487	CG	ARG	A	217	67.373	3.964	-2.525	1.00	27.36	C
ATOM	1488	CD	ARG	A	217	66.718	2.584	-2.668	1.00	31.36	C
ATOM	1489	NE	ARG	A	217	66.048	2.433	-3.958	1.00	34.40	N
ATOM	1490	CZ	ARG	A	217	66.633	1.967	-5.061	1.00	36.63	C
ATOM	1491	NH1	ARG	A	217	67.909	1.595	-5.043	1.00	36.66	N
ATOM	1492	NH2	ARG	A	217	65.943	1.879	-6.190	1.00	37.21	N
ATOM	1493	C	ARG	A	217	65.808	7.429	-1.749	1.00	22.74	C
ATOM	1494	O	ARG	A	217	65.124	7.420	-0.729	1.00	23.06	O
ATOM	1495	N	TYR	A	218	65.580	8.240	-2.777	1.00	20.60	N
ATOM	1496	CA	TYR	A	218	64.445	9.141	-2.824	1.00	18.74	C
ATOM	1497	CB	TYR	A	218	64.674	10.371	-1.917	1.00	18.22	C
ATOM	1498	CG	TYR	A	218	65.867	11.216	-2.299	1.00	16.94	C
ATOM	1499	CD1	TYR	A	218	67.160	10.880	-1.870	1.00	15.03	C
ATOM	1500	CE1	TYR	A	218	68.265	11.679	-2.220	1.00	14.80	C
ATOM	1501	CZ	TYR	A	218	68.064	12.802	-3.020	1.00	15.81	C
ATOM	1502	OH	TYR	A	218	69.125	13.594	-3.393	1.00	16.21	O
ATOM	1503	CE2	TYR	A	218	66.790	13.145	-3.453	1.00	15.34	C
ATOM	1504	CD2	TYR	A	218	65.705	12.355	-3.093	1.00	15.11	C
ATOM	1505	C	TYR	A	218	64.212	9.584	-4.267	1.00	18.07	C
ATOM	1506	O	TYR	A	218	65.112	9.486	-5.102	1.00	17.75	O
ATOM	1507	N	HIS	A	219	63.006	10.075	-4.545	1.00	17.04	N
ATOM	1508	CA	HIS	A	219	62.721	10.757	-5.811	1.00	16.74	C
ATOM	1509	CB	HIS	A	219	61.430	10.231	-6.440	1.00	16.49	C
ATOM	1510	CG	HIS	A	219	61.547	8.819	-6.917	1.00	18.35	C
ATOM	1511	ND1	HIS	A	219	61.677	8.489	-8.253	1.00	18.97	N
ATOM	1512	CE1	HIS	A	219	61.791	7.179	-8.368	1.00	17.84	C
ATOM	1513	NE2	HIS	A	219	61.763	6.650	-7.157	1.00	19.10	N
ATOM	1514	CD2	HIS	A	219	61.621	7.653	-6.230	1.00	16.82	C
ATOM	1515	C	HIS	A	219	62.651	12.255	-5.551	1.00	16.15	C

ATOM	1516	O	HIS	A	219	62.346	12.681	-4.438	1.00 15.76	O
ATOM	1517	N	GLY	A	220	62.938	13.048	-6.576	1.00 16.23	N
ATOM	1518	CA	GLY	A	220	63.172	14.462	-6.384	1.00 16.70	C
ATOM	1519	C	GLY	A	220	61.992	15.217	-5.807	1.00 16.87	C
ATOM	1520	O	GLY	A	220	62.110	15.886	-4.788	1.00 16.14	O
ATOM	1521	N	ARG	A	221	60.848	15.097	-6.469	1.00 17.28	N
ATOM	1522	CA	ARG	A	221	59.691	15.923	-6.150	1.00 17.64	C
ATOM	1523	CB	ARG	A	221	58.590	15.746	-7.185	1.00 18.45	C
ATOM	1524	CG	ARG	A	221	59.002	16.190	-8.578	1.00 23.24	C
ATOM	1525	CD	ARG	A	221	58.156	15.591	-9.697	1.00 28.55	C
ATOM	1526	NE	ARG	A	221	58.705	15.933	-11.013	1.00 32.56	N
ATOM	1527	CZ	ARG	A	221	59.512	15.147	-11.720	1.00 35.42	C
ATOM	1528	NH1	ARG	A	221	59.879	13.956	-11.241	1.00 36.89	N
ATOM	1529	NH2	ARG	A	221	59.943	15.539	-12.920	1.00 35.53	N
ATOM	1530	C	ARG	A	221	59.155	15.652	-4.764	1.00 16.82	C
ATOM	1531	O	ARG	A	221	58.922	16.596	-4.015	1.00 16.95	O
ATOM	1532	N	SER	A	222	58.981	14.374	-4.417	1.00 15.97	N
ATOM	1533	CA	SER	A	222	58.439	14.002	-3.111	1.00 15.37	C
ATOM	1534	CB	SER	A	222	58.036	12.510	-3.066	1.00 15.54	C
ATOM	1535	OG	SER	A	222	59.136	11.654	-3.333	1.00 15.91	O
ATOM	1536	C	SER	A	222	59.396	14.347	-1.971	1.00 14.74	C
ATOM	1537	O	SER	A	222	58.963	14.684	-0.874	1.00 14.86	O
ATOM	1538	N	ALA	A	223	60.694	14.270	-2.225	1.00 14.48	N
ATOM	1539	CA	ALA	A	223	61.686	14.738	-1.253	1.00 14.36	C
ATOM	1540	CB	ALA	A	223	63.081	14.313	-1.677	1.00 14.45	C
ATOM	1541	C	ALA	A	223	61.619	16.266	-1.091	1.00 14.53	C
ATOM	1542	O	ALA	A	223	61.718	16.779	0.030	1.00 14.59	O
ATOM	1543	N	ALA	A	224	61.441	16.982	-2.205	1.00 13.88	N
ATOM	1544	CA	ALA	A	224	61.310	18.444	-2.169	1.00 13.96	C
ATOM	1545	CB	ALA	A	224	61.174	19.032	-3.591	1.00 13.04	C
ATOM	1546	C	ALA	A	224	60.116	18.832	-1.296	1.00 13.72	C
ATOM	1547	O	ALA	A	224	60.220	19.713	-0.462	1.00 14.14	O
ATOM	1548	N	VAL	A	225	59.001	18.123	-1.470	1.00 14.13	N
ATOM	1549	CA	VAL	A	225	57.776	18.363	-0.704	1.00 13.34	C
ATOM	1550	CB	VAL	A	225	56.602	17.517	-1.301	1.00 13.99	C
ATOM	1551	CG1	VAL	A	225	55.370	17.457	-0.352	1.00 11.55	C
ATOM	1552	CG2	VAL	A	225	56.236	18.063	-2.701	1.00 12.97	C
ATOM	1553	C	VAL	A	225	57.986	18.076	0.778	1.00 14.00	C
ATOM	1554	O	VAL	A	225	57.513	18.820	1.650	1.00 14.66	O
ATOM	1555	N	TRP	A	226	58.695	16.996	1.087	1.00 13.82	N
ATOM	1556	CA	TRP	A	226	59.037	16.751	2.481	1.00 14.22	C
ATOM	1557	CB	TRP	A	226	59.908	15.501	2.626	1.00 14.10	C
ATOM	1558	CG	TRP	A	226	60.362	15.305	4.045	1.00 14.21	C
ATOM	1559	CD1	TRP	A	226	61.444	15.888	4.651	1.00 13.01	C
ATOM	1560	NE1	TRP	A	226	61.516	15.488	5.961	1.00 13.97	N
ATOM	1561	CE2	TRP	A	226	60.473	14.643	6.231	1.00 13.33	C
ATOM	1562	CD2	TRP	A	226	59.723	14.510	5.046	1.00 14.66	C
ATOM	1563	CE3	TRP	A	226	58.583	13.683	5.063	1.00 14.53	C
ATOM	1564	CZ3	TRP	A	226	58.254	13.024	6.238	1.00 14.25	C
ATOM	1565	CH2	TRP	A	226	59.020	13.173	7.395	1.00 14.22	C
ATOM	1566	CZ2	TRP	A	226	60.132	13.981	7.415	1.00 15.55	C
ATOM	1567	C	TRP	A	226	59.763	17.976	3.062	1.00 13.86	C
ATOM	1568	O	TRP	A	226	59.406	18.468	4.136	1.00 14.16	O
ATOM	1569	N	SER	A	227	60.764	18.485	2.349	1.00 13.20	N
ATOM	1570	CA	SER	A	227	61.522	19.610	2.875	1.00 13.52	C
ATOM	1571	CB	SER	A	227	62.793	19.886	2.043	1.00 13.28	C
ATOM	1572	OG	SER	A	227	62.448	20.474	0.803	1.00 12.96	O
ATOM	1573	C	SER	A	227	60.634	20.845	2.967	1.00 13.72	C
ATOM	1574	O	SER	A	227	60.848	21.702	3.816	1.00 13.60	O
ATOM	1575	N	LEU	A	228	59.614	20.917	2.110	1.00 13.17	N
ATOM	1576	CA	LEU	A	228	58.673	22.028	2.171	1.00 13.14	C
ATOM	1577	CB	LEU	A	228	57.807	22.105	0.891	1.00 12.32	C
ATOM	1578	CG	LEU	A	228	58.606	22.646	-0.297	1.00 11.69	C
ATOM	1579	CD1	LEU	A	228	57.931	22.321	-1.659	1.00 13.88	C
ATOM	1580	CD2	LEU	A	228	58.893	24.135	-0.171	1.00 10.58	C
ATOM	1581	C	LEU	A	228	57.801	21.968	3.427	1.00 12.15	C
ATOM	1582	O	LEU	A	228	57.489	22.990	4.020	1.00 12.32	O
ATOM	1583	N	GLY	A	229	57.405	20.766	3.811	1.00 12.02	N
ATOM	1584	CA	GLY	A	229	56.693	20.556	5.056	1.00 12.19	C

ATOM	1585	C	GLY A 229	57.512	20.973	6.281	1.00	12.64	C
ATOM	1586	O	GLY A 229	56.968	21.560	7.224	1.00	12.42	O
ATOM	1587	N	ILE A 230	58.811	20.662	6.269	1.00	13.07	N
ATOM	1588	CA	ILE A 230	59.718	21.050	7.357	1.00	13.99	C
ATOM	1589	CB	ILE A 230	61.145	20.421	7.133	1.00	13.90	C
ATOM	1590	CG1	ILE A 230	61.067	18.894	7.053	1.00	13.25	C
ATOM	1591	CD1	ILE A 230	60.622	18.243	8.368	1.00	11.51	C
ATOM	1592	CG2	ILE A 230	62.118	20.815	8.272	1.00	14.90	C
ATOM	1593	C	ILE A 230	59.785	22.587	7.409	1.00	14.39	C
ATOM	1594	O	ILE A 230	59.686	23.211	8.488	1.00	14.11	O
ATOM	1595	N	LEU A 231	59.915	23.182	6.222	1.00	14.04	N
ATOM	1596	CA	LEU A 231	59.961	24.620	6.083	1.00	14.10	C
ATOM	1597	CB	LEU A 231	60.197	24.995	4.609	1.00	14.16	C
ATOM	1598	CG	LEU A 231	60.121	26.508	4.330	1.00	15.24	C
ATOM	1599	CD1	LEU A 231	61.292	27.224	4.967	1.00	15.13	C
ATOM	1600	CD2	LEU A 231	60.075	26.778	2.838	1.00	15.78	C
ATOM	1601	C	LEU A 231	58.688	25.299	6.615	1.00	14.01	C
ATOM	1602	O	LEU A 231	58.775	26.270	7.382	1.00	13.50	O
ATOM	1603	N	LEU A 232	57.515	24.796	6.217	1.00	13.22	N
ATOM	1604	CA	LEU A 232	56.256	25.394	6.644	1.00	13.16	C
ATOM	1605	CB	LEU A 232	55.031	24.750	5.949	1.00	13.56	C
ATOM	1606	CG	LEU A 232	53.653	25.362	6.282	1.00	12.22	C
ATOM	1607	CD1	LEU A 232	53.627	26.902	6.159	1.00	13.83	C
ATOM	1608	CD2	LEU A 232	52.521	24.721	5.419	1.00	11.85	C
ATOM	1609	C	LEU A 232	56.112	25.294	8.164	1.00	13.79	C
ATOM	1610	O	LEU A 232	55.723	26.269	8.817	1.00	14.65	O
ATOM	1611	N	TYR A 233	56.445	24.133	8.723	1.00	13.34	N
ATOM	1612	CA	TYR A 233	56.407	23.940	10.175	1.00	13.68	C
ATOM	1613	CB	TYR A 233	56.870	22.524	10.551	1.00	12.73	C
ATOM	1614	CG	TYR A 233	56.786	22.263	12.044	1.00	14.51	C
ATOM	1615	CD1	TYR A 233	57.791	22.713	12.908	1.00	14.02	C
ATOM	1616	CE1	TYR A 233	57.728	22.487	14.266	1.00	13.74	C
ATOM	1617	CZ	TYR A 233	56.647	21.796	14.798	1.00	15.95	C
ATOM	1618	OH	TYR A 233	56.590	21.586	16.169	1.00	17.38	O
ATOM	1619	CE2	TYR A 233	55.630	21.352	13.978	1.00	15.69	C
ATOM	1620	CD2	TYR A 233	55.705	21.588	12.594	1.00	14.19	C
ATOM	1621	C	TYR A 233	57.296	24.989	10.855	1.00	14.14	C
ATOM	1622	O	TYR A 233	56.893	25.639	11.837	1.00	14.22	O
ATOM	1623	N	ASP A 234	58.497	25.162	10.304	1.00	14.64	N
ATOM	1624	CA	ASP A 234	59.462	26.128	10.820	1.00	14.70	C
ATOM	1625	CB	ASP A 234	60.741	26.074	9.986	1.00	15.23	C
ATOM	1626	CG	ASP A 234	61.806	27.031	10.482	1.00	17.95	C
ATOM	1627	OD1	ASP A 234	62.134	27.038	11.693	1.00	17.66	O
ATOM	1628	OD2	ASP A 234	62.372	27.815	9.707	1.00	23.64	O
ATOM	1629	C	ASP A 234	58.902	27.550	10.842	1.00	15.14	C
ATOM	1630	O	ASP A 234	59.130	28.304	11.808	1.00	14.44	O
ATOM	1631	N	MET A 235	58.177	27.921	9.782	1.00	14.52	N
ATOM	1632	CA	MET A 235	57.585	29.248	9.679	1.00	15.77	C
ATOM	1633	CB	MET A 235	56.946	29.472	8.300	1.00	15.95	C
ATOM	1634	CG	MET A 235	57.955	29.567	7.157	1.00	19.29	C
ATOM	1635	SD	MET A 235	57.147	30.105	5.616	1.00	23.96	S
ATOM	1636	CE	MET A 235	56.577	28.752	5.093	1.00	24.70	C
ATOM	1637	C	MET A 235	56.535	29.503	10.756	1.00	15.44	C
ATOM	1638	O	MET A 235	56.551	30.545	11.395	1.00	15.28	O
ATOM	1639	N	VAL A 236	55.622	28.557	10.944	1.00	15.79	N
ATOM	1640	CA	VAL A 236	54.480	28.780	11.845	1.00	16.11	C
ATOM	1641	CB	VAL A 236	53.169	28.062	11.349	1.00	16.48	C
ATOM	1642	CG1	VAL A 236	52.709	28.622	9.995	1.00	15.52	C
ATOM	1643	CG2	VAL A 236	53.327	26.521	11.277	1.00	14.68	C
ATOM	1644	C	VAL A 236	54.808	28.422	13.295	1.00	17.29	C
ATOM	1645	O	VAL A 236	54.084	28.833	14.220	1.00	17.67	O
ATOM	1646	N	CYS A 237	55.901	27.673	13.503	1.00	17.50	N
ATOM	1647	CA	CYS A 237	56.276	27.261	14.863	1.00	18.98	C
ATOM	1648	CB	CYS A 237	56.400	25.735	14.986	1.00	18.51	C
ATOM	1649	SG	CYS A 237	54.825	24.891	14.842	1.00	22.03	S
ATOM	1650	C	CYS A 237	57.548	27.914	15.366	1.00	18.98	C
ATOM	1651	O	CYS A 237	57.788	27.936	16.562	1.00	18.75	O
ATOM	1652	N	GLY A 238	58.359	28.443	14.452	1.00	19.38	N
ATOM	1653	CA	GLY A 238	59.584	29.125	14.835	1.00	20.34	C

ATOM	1654	C	GLY	A	238	60.776	28.206	14.966	1.00	21.28	C
ATOM	1655	O	GLY	A	238	61.871	28.677	15.269	1.00	21.63	O
ATOM	1656	N	ASP	A	239	60.572	26.906	14.743	1.00	21.89	N
ATOM	1657	CA	ASP	A	239	61.662	25.904	14.741	1.00	23.14	C
ATOM	1658	CB	ASP	A	239	62.038	25.466	16.161	1.00	24.31	C
ATOM	1659	CG	ASP	A	239	63.557	25.367	16.363	1.00	28.93	C
ATOM	1660	OD1	ASP	A	239	64.268	24.729	15.530	1.00	31.83	O
ATOM	1661	OD2	ASP	A	239	64.126	25.919	17.333	1.00	34.08	O
ATOM	1662	C	ASP	A	239	61.271	24.671	13.918	1.00	22.10	C
ATOM	1663	O	ASP	A	239	60.110	24.508	13.582	1.00	22.05	O
ATOM	1664	N	ILE	A	240	62.241	23.823	13.590	1.00	21.41	N
ATOM	1665	CA	ILE	A	240	61.995	22.616	12.803	1.00	21.20	C
ATOM	1666	CB	ILE	A	240	63.299	22.130	12.119	1.00	21.27	C
ATOM	1667	CG1	ILE	A	240	64.418	21.934	13.162	1.00	22.95	C
ATOM	1668	CD1	ILE	A	240	65.727	21.359	12.604	1.00	24.55	C
ATOM	1669	CG2	ILE	A	240	63.711	23.113	11.020	1.00	22.14	C
ATOM	1670	C	ILE	A	240	61.390	21.516	13.687	1.00	21.05	C
ATOM	1671	O	ILE	A	240	61.628	21.507	14.896	1.00	20.43	O
ATOM	1672	N	PRO	A	241	60.596	20.610	13.112	1.00	21.20	N
ATOM	1673	CA	PRO	A	241	59.885	19.609	13.924	1.00	22.14	C
ATOM	1674	CB	PRO	A	241	58.818	19.070	12.967	1.00	22.34	C
ATOM	1675	CG	PRO	A	241	59.418	19.243	11.581	1.00	20.54	C
ATOM	1676	CD	PRO	A	241	60.303	20.461	11.670	1.00	21.11	C
ATOM	1677	C	PRO	A	241	60.762	18.466	14.413	1.00	23.21	C
ATOM	1678	O	PRO	A	241	60.432	17.885	15.443	1.00	23.48	O
ATOM	1679	N	PHE	A	242	61.843	18.143	13.699	1.00	24.34	N
ATOM	1680	CA	PHE	A	242	62.625	16.949	13.999	1.00	25.31	C
ATOM	1681	CB	PHE	A	242	62.503	15.894	12.881	1.00	24.74	C
ATOM	1682	CG	PHE	A	242	61.097	15.596	12.440	1.00	22.55	C
ATOM	1683	CD1	PHE	A	242	60.115	15.212	13.354	1.00	21.74	C
ATOM	1684	CE1	PHE	A	242	58.812	14.916	12.923	1.00	21.18	C
ATOM	1685	CZ	PHE	A	242	58.489	15.011	11.556	1.00	21.06	C
ATOM	1686	CE2	PHE	A	242	59.467	15.392	10.642	1.00	20.29	C
ATOM	1687	CD2	PHE	A	242	60.763	15.672	11.088	1.00	21.16	C
ATOM	1688	C	PHE	A	242	64.099	17.286	14.169	1.00	27.27	C
ATOM	1689	O	PHE	A	242	64.671	18.038	13.370	1.00	27.35	O
ATOM	1690	N	GLU	A	243	64.716	16.692	15.186	1.00	29.13	N
ATOM	1691	CA	GLU	A	243	66.149	16.849	15.428	1.00	31.65	C
ATOM	1692	CB	GLU	A	243	66.404	17.361	16.849	1.00	32.51	C
ATOM	1693	CG	GLU	A	243	65.779	18.723	17.153	1.00	37.83	C
ATOM	1694	CD	GLU	A	243	66.521	19.895	16.505	1.00	43.98	C
ATOM	1695	OE1	GLU	A	243	66.675	19.903	15.260	1.00	46.61	O
ATOM	1696	OE2	GLU	A	243	66.941	20.824	17.241	1.00	46.61	O
ATOM	1697	C	GLU	A	243	66.951	15.568	15.187	1.00	31.62	C
ATOM	1698	O	GLU	A	243	68.096	15.630	14.759	1.00	32.81	O
ATOM	1699	N	HIS	A	244	66.361	14.409	15.454	1.00	31.55	N
ATOM	1700	CA	HIS	A	244	67.089	13.146	15.307	1.00	31.42	C
ATOM	1701	CB	HIS	A	244	67.187	12.423	16.650	1.00	32.01	C
ATOM	1702	CG	HIS	A	244	67.774	13.265	17.738	1.00	34.56	C
ATOM	1703	ND1	HIS	A	244	67.014	13.790	18.763	1.00	36.67	N
ATOM	1704	CE1	HIS	A	244	67.791	14.502	19.561	1.00	37.86	C
ATOM	1705	NE2	HIS	A	244	69.026	14.462	19.087	1.00	37.93	N
ATOM	1706	CD2	HIS	A	244	69.041	13.697	17.945	1.00	36.34	C
ATOM	1707	C	HIS	A	244	66.482	12.235	14.243	1.00	30.37	C
ATOM	1708	O	HIS	A	244	65.279	12.327	13.941	1.00	29.56	O
ATOM	1709	N	ASP	A	245	67.326	11.360	13.689	1.00	29.19	N
ATOM	1710	CA	ASP	A	245	66.909	10.373	12.691	1.00	28.54	C
ATOM	1711	CB	ASP	A	245	68.005	9.315	12.473	1.00	28.34	C
ATOM	1712	CG	ASP	A	245	69.208	9.853	11.726	1.00	28.71	C
ATOM	1713	OD1	ASP	A	245	69.183	11.016	11.252	1.00	28.60	O
ATOM	1714	OD2	ASP	A	245	70.242	9.174	11.572	1.00	30.07	O
ATOM	1715	C	ASP	A	245	65.624	9.670	13.103	1.00	28.04	C
ATOM	1716	O	ASP	A	245	64.724	9.485	12.284	1.00	27.65	O
ATOM	1717	N	GLU	A	246	65.566	9.292	14.381	1.00	27.40	N
ATOM	1718	CA	GLU	A	246	64.451	8.563	14.978	1.00	27.37	C
ATOM	1719	CB	GLU	A	246	64.743	8.286	16.468	1.00	28.11	C
ATOM	1720	CG	GLU	A	246	65.942	7.369	16.736	1.00	32.49	C
ATOM	1721	CD	GLU	A	246	67.302	8.072	16.650	1.00	37.16	C
ATOM	1722	OE1	GLU	A	246	67.413	9.255	17.037	1.00	39.44	O

ATOM	1723	OE2	GLU	A	246	68.276	7.434	16.191	1.00	40.05	O
ATOM	1724	C	GLU	A	246	63.128	9.318	14.844	1.00	26.19	C
ATOM	1725	O	GLU	A	246	62.087	8.720	14.570	1.00	25.74	O
ATOM	1726	N	GLU	A	247	63.178	10.630	15.054	1.00	24.84	N
ATOM	1727	CA	GLU	A	247	61.997	11.473	14.925	1.00	24.64	C
ATOM	1728	CB	GLU	A	247	62.228	12.861	15.550	1.00	24.76	C
ATOM	1729	CG	GLU	A	247	62.600	12.823	17.029	1.00	27.07	C
ATOM	1730	CD	GLU	A	247	63.106	14.164	17.539	1.00	31.82	C
ATOM	1731	OE1	GLU	A	247	63.956	14.804	16.873	1.00	31.23	O
ATOM	1732	OE2	GLU	A	247	62.653	14.582	18.623	1.00	35.62	O
ATOM	1733	C	GLU	A	247	61.573	11.592	13.458	1.00	23.43	C
ATOM	1734	O	GLU	A	247	60.388	11.491	13.151	1.00	22.84	O
ATOM	1735	N	ILE	A	248	62.546	11.782	12.563	1.00	22.82	N
ATOM	1736	CA	ILE	A	248	62.269	11.827	11.119	1.00	22.09	C
ATOM	1737	CB	ILE	A	248	63.555	12.106	10.284	1.00	22.33	C
ATOM	1738	CG1	ILE	A	248	64.103	13.506	10.594	1.00	21.24	C
ATOM	1739	CD1	ILE	A	248	65.557	13.692	10.191	1.00	23.01	C
ATOM	1740	CG2	ILE	A	248	63.273	11.965	8.767	1.00	21.11	C
ATOM	1741	C	ILE	A	248	61.567	10.547	10.665	1.00	22.18	C
ATOM	1742	O	ILE	A	248	60.512	10.608	10.038	1.00	21.20	O
ATOM	1743	N	ILE	A	249	62.144	9.396	11.016	1.00	22.55	N
ATOM	1744	CA	ILE	A	249	61.595	8.083	10.646	1.00	23.21	C
ATOM	1745	CB	ILE	A	249	62.539	6.943	11.136	1.00	23.49	C
ATOM	1746	CG1	ILE	A	249	63.856	6.947	10.348	1.00	24.43	C
ATOM	1747	CD1	ILE	A	249	64.971	6.114	11.041	1.00	26.84	C
ATOM	1748	CG2	ILE	A	249	61.853	5.562	11.051	1.00	24.03	C
ATOM	1749	C	ILE	A	249	60.175	7.875	11.200	1.00	23.18	C
ATOM	1750	O	ILE	A	249	59.312	7.314	10.520	1.00	22.99	O
ATOM	1751	N	ARG	A	250	59.943	8.318	12.435	1.00	23.13	N
ATOM	1752	CA	ARG	A	250	58.614	8.204	13.044	1.00	23.60	C
ATOM	1753	CB	ARG	A	250	58.679	8.421	14.562	1.00	23.56	C
ATOM	1754	CG	ARG	A	250	57.356	8.162	15.290	1.00	24.55	C
ATOM	1755	CD	ARG	A	250	57.504	7.770	16.760	1.00	24.93	C
ATOM	1756	NE	ARG	A	250	56.208	7.638	17.430	1.00	25.45	N
ATOM	1757	CZ	ARG	A	250	55.636	8.594	18.168	1.00	25.98	C
ATOM	1758	NH1	ARG	A	250	56.234	9.770	18.349	1.00	24.37	N
ATOM	1759	NH2	ARG	A	250	54.459	8.373	18.733	1.00	26.41	N
ATOM	1760	C	ARG	A	250	57.621	9.159	12.375	1.00	23.56	C
ATOM	1761	O	ARG	A	250	56.468	8.802	12.165	1.00	23.53	O
ATOM	1762	N	GLY	A	251	58.089	10.357	12.022	1.00	23.63	N
ATOM	1763	CA	GLY	A	251	57.282	11.334	11.314	1.00	24.56	C
ATOM	1764	C	GLY	A	251	56.082	11.864	12.096	1.00	25.30	C
ATOM	1765	O	GLY	A	251	55.074	12.248	11.496	1.00	25.76	O
ATOM	1766	N	GLN	A	252	56.177	11.877	13.423	1.00	25.26	N
ATOM	1767	CA	GLN	A	252	55.082	12.373	14.263	1.00	25.84	C
ATOM	1768	CB	GLN	A	252	55.005	11.603	15.593	1.00	26.06	C
ATOM	1769	CG	GLN	A	252	53.796	11.937	16.488	1.00	29.12	C
ATOM	1770	CD	GLN	A	252	52.439	11.649	15.837	1.00	32.13	C
ATOM	1771	OE1	GLN	A	252	51.537	12.506	15.854	1.00	31.35	O
ATOM	1772	NE2	GLN	A	252	52.292	10.448	15.264	1.00	32.42	N
ATOM	1773	C	GLN	A	252	55.271	13.863	14.504	1.00	25.11	C
ATOM	1774	O	GLN	A	252	56.310	14.303	15.008	1.00	24.98	O
ATOM	1775	N	VAL	A	253	54.265	14.634	14.123	1.00	24.33	N
ATOM	1776	CA	VAL	A	253	54.351	16.085	14.196	1.00	24.36	C
ATOM	1777	CB	VAL	A	253	53.751	16.750	12.922	1.00	24.24	C
ATOM	1778	CG1	VAL	A	253	53.971	18.240	12.948	1.00	24.73	C
ATOM	1779	CG2	VAL	A	253	54.356	16.124	11.647	1.00	24.87	C
ATOM	1780	C	VAL	A	253	53.601	16.576	15.431	1.00	23.69	C
ATOM	1781	O	VAL	A	253	52.427	16.275	15.602	1.00	23.22	O
ATOM	1782	N	PHE	A	254	54.297	17.321	16.278	1.00	23.14	N
ATOM	1783	CA	PHE	A	254	53.683	17.993	17.403	1.00	23.19	C
ATOM	1784	CB	PHE	A	254	54.295	17.481	18.702	1.00	22.64	C
ATOM	1785	CG	APHE	A	254	53.868	18.247	19.912	0.70	21.91	C
ATOM	1786	CG	BPHE	A	254	53.915	16.067	18.997	0.30	22.47	C
ATOM	1787	CD1	APHE	A	254	52.711	17.897	20.596	0.70	20.57	C
ATOM	1788	CD1	BPHE	A	254	54.877	15.073	19.055	0.30	21.39	C
ATOM	1789	CE1	APHE	A	254	52.308	18.608	21.724	0.70	18.82	C
ATOM	1790	CE1	BPHE	A	254	54.517	13.772	19.304	0.30	20.97	C
ATOM	1791	CZ	APHE	A	254	53.054	19.677	22.163	0.70	20.33	C

ATOM	1792	CZ BPHE	A 254	53.180	13.445	19.476	0.30	21.52	C
ATOM	1793	CE2APHE	A 254	54.214	20.045	21.486	0.70	20.58	C
ATOM	1794	CE2BPHE	A 254	52.207	14.421	19.400	0.30	21.67	C
ATOM	1795	CD2APHE	A 254	54.615	19.333	20.369	0.70	21.56	C
ATOM	1796	CD2BPHE	A 254	52.574	15.720	19.157	0.30	21.61	C
ATOM	1797	C PHE	A 254	53.789	19.507	17.295	1.00	23.65	C
ATOM	1798	O PHE	A 254	54.876	20.055	17.059	1.00	23.03	O
ATOM	1799	N PHE	A 255	52.652	20.173	17.475	1.00	24.25	N
ATOM	1800	CA PHE	A 255	52.600	21.636	17.448	1.00	24.57	C
ATOM	1801	CB PHE	A 255	51.367	22.117	16.705	1.00	24.07	C
ATOM	1802	CG PHE	A 255	51.421	21.819	15.250	1.00	22.93	C
ATOM	1803	CD1 PHE	A 255	51.972	22.743	14.368	1.00	20.88	C
ATOM	1804	CE1 PHE	A 255	52.048	22.466	13.018	1.00	18.91	C
ATOM	1805	CZ PHE	A 255	51.585	21.254	12.540	1.00	20.61	C
ATOM	1806	CE2 PHE	A 255	51.047	20.307	13.426	1.00	19.19	C
ATOM	1807	CD2 PHE	A 255	50.974	20.595	14.762	1.00	19.54	C
ATOM	1808	C PHE	A 255	52.668	22.239	18.830	1.00	25.43	C
ATOM	1809	O PHE	A 255	51.839	21.958	19.691	1.00	25.30	O
ATOM	1810	N ARG	A 256	53.701	23.057	19.015	1.00	26.64	N
ATOM	1811	CA ARG	A 256	54.026	23.713	20.274	1.00	27.50	C
ATOM	1812	CB ARG	A 256	55.556	23.791	20.412	1.00	28.35	C
ATOM	1813	CG ARG	A 256	56.282	24.268	19.116	1.00	31.19	C
ATOM	1814	CD ARG	A 256	57.825	24.203	19.164	1.00	35.66	C
ATOM	1815	NE ARG	A 256	58.346	23.171	18.257	1.00	38.13	N
ATOM	1816	CZ ARG	A 256	59.580	22.660	18.298	1.00	40.12	C
ATOM	1817	NH1 ARG	A 256	60.466	23.080	19.204	1.00	40.47	N
ATOM	1818	NH2 ARG	A 256	59.930	21.716	17.431	1.00	38.85	N
ATOM	1819	C ARG	A 256	53.444	25.122	20.255	1.00	27.08	C
ATOM	1820	O ARG	A 256	53.389	25.807	21.279	1.00	27.90	O
ATOM	1821	N GLN	A 257	53.023	25.546	19.068	1.00	26.07	N
ATOM	1822	CA GLN	A 257	52.369	26.834	18.871	1.00	25.36	C
ATOM	1823	CB GLN	A 257	53.126	27.643	17.803	1.00	25.81	C
ATOM	1824	CG GLN	A 257	54.514	28.095	18.215	1.00	29.91	C
ATOM	1825	CD GLN	A 257	54.493	29.381	19.019	1.00	35.63	C
ATOM	1826	OE1 GLN	A 257	53.596	30.222	18.846	1.00	37.93	O
ATOM	1827	NE2 GLN	A 257	55.480	29.545	19.901	1.00	37.58	N
ATOM	1828	C GLN	A 257	50.931	26.611	18.399	1.00	23.15	C
ATOM	1829	O GLN	A 257	50.618	25.574	17.821	1.00	22.57	O
ATOM	1830	N ARG	A 258	50.072	27.593	18.633	1.00	21.04	N
ATOM	1831	CA ARG	A 258	48.726	27.571	18.079	1.00	19.58	C
ATOM	1832	CB ARG	A 258	47.862	28.674	18.683	1.00	19.69	C
ATOM	1833	CG ARG	A 258	46.355	28.438	18.509	1.00	21.79	C
ATOM	1834	CD ARG	A 258	45.834	28.809	17.134	1.00	24.81	C
ATOM	1835	NE ARG	A 258	44.538	28.195	16.847	1.00	26.49	N
ATOM	1836	CZ ARG	A 258	43.844	28.395	15.725	1.00	27.04	C
ATOM	1837	NH1 ARG	A 258	44.316	29.200	14.757	1.00	27.33	N
ATOM	1838	NH2 ARG	A 258	42.677	27.789	15.570	1.00	25.64	N
ATOM	1839	C ARG	A 258	48.811	27.738	16.564	1.00	18.78	C
ATOM	1840	O ARG	A 258	49.282	28.759	16.074	1.00	18.29	O
ATOM	1841	N VAL	A 259	48.367	26.716	15.843	1.00	17.49	N
ATOM	1842	CA VAL	A 259	48.404	26.682	14.389	1.00	17.02	C
ATOM	1843	CB VAL	A 259	49.533	25.733	13.879	1.00	16.57	C
ATOM	1844	CG1 VAL	A 259	49.472	25.544	12.361	1.00	15.19	C
ATOM	1845	CG2 VAL	A 259	50.929	26.259	14.310	1.00	17.98	C
ATOM	1846	C VAL	A 259	47.043	26.171	13.920	1.00	16.99	C
ATOM	1847	O VAL	A 259	46.541	25.190	14.460	1.00	16.43	O
ATOM	1848	N SER	A 260	46.451	26.843	12.930	1.00	17.02	N
ATOM	1849	CA SER	A 260	45.141	26.451	12.398	1.00	17.31	C
ATOM	1850	CB SER	A 260	44.687	27.398	11.273	1.00	17.29	C
ATOM	1851	OG SER	A 260	45.399	27.137	10.073	1.00	17.50	O
ATOM	1852	C SER	A 260	45.145	25.005	11.916	1.00	17.62	C
ATOM	1853	O SER	A 260	46.182	24.484	11.518	1.00	17.40	O
ATOM	1854	N SER	A 261	43.974	24.367	11.957	1.00	17.98	N
ATOM	1855	CA SER	A 261	43.820	22.972	11.559	1.00	18.43	C
ATOM	1856	CB SER	A 261	42.398	22.499	11.855	1.00	18.46	C
ATOM	1857	OG SER	A 261	42.169	22.473	13.254	1.00	19.59	O
ATOM	1858	C SER	A 261	44.118	22.748	10.082	1.00	18.64	C
ATOM	1859	O SER	A 261	44.630	21.694	9.701	1.00	18.31	O
ATOM	1860	N GLU	A 262	43.780	23.729	9.256	1.00	19.27	N

ATOM	1861	CA	GLU	A	262	44.102	23.659	7.829	1.00	20.49	C
ATOM	1862	CB	GLU	A	262	43.461	24.807	7.058	1.00	21.45	C
ATOM	1863	CG	GLU	A	262	42.033	24.525	6.627	1.00	27.18	C
ATOM	1864	CD	GLU	A	262	41.304	25.782	6.184	1.00	35.25	C
ATOM	1865	OE1	GLU	A	262	41.928	26.645	5.498	1.00	38.82	O
ATOM	1866	OE2	GLU	A	262	40.101	25.915	6.522	1.00	39.29	O
ATOM	1867	C	GLU	A	262	45.615	23.663	7.614	1.00	19.31	C
ATOM	1868	O	GLU	A	262	46.131	22.851	6.853	1.00	18.98	O
ATOM	1869	N	CYS	A	263	46.318	24.561	8.297	1.00	18.97	N
ATOM	1870	CA	CYS	A	263	47.785	24.596	8.196	1.00	18.66	C
ATOM	1871	CB	CYS	A	263	48.359	25.805	8.937	1.00	18.56	C
ATOM	1872	SG	CYS	A	263	50.133	26.031	8.731	1.00	18.69	S
ATOM	1873	C	CYS	A	263	48.385	23.275	8.703	1.00	18.45	C
ATOM	1874	O	CYS	A	263	49.223	22.664	8.024	1.00	18.06	O
ATOM	1875	N	GLN	A	264	47.932	22.827	9.873	1.00	18.01	N
ATOM	1876	CA	GLN	A	264	48.389	21.553	10.434	1.00	18.32	C
ATOM	1877	CB	GLN	A	264	47.650	21.210	11.748	1.00	17.97	C
ATOM	1878	CG	GLN	A	264	48.085	22.034	12.955	1.00	18.25	C
ATOM	1879	CD	GLN	A	264	47.598	21.447	14.282	1.00	20.77	C
ATOM	1880	OE1	GLN	A	264	47.359	20.240	14.382	1.00	19.45	O
ATOM	1881	NE2	GLN	A	264	47.464	22.299	15.304	1.00	19.10	N
ATOM	1882	C	GLN	A	264	48.191	20.419	9.424	1.00	18.18	C
ATOM	1883	O	GLN	A	264	49.068	19.581	9.252	1.00	18.03	O
ATOM	1884	N	HIS	A	265	47.033	20.405	8.768	1.00	18.36	N
ATOM	1885	CA	HIS	A	265	46.712	19.366	7.805	1.00	19.15	C
ATOM	1886	CB	HIS	A	265	45.269	19.505	7.310	1.00	19.80	C
ATOM	1887	CG	HIS	A	265	44.890	18.474	6.295	1.00	23.71	C
ATOM	1888	ND1	HIS	A	265	45.147	18.627	4.948	1.00	27.52	N
ATOM	1889	CE1	HIS	A	265	44.712	17.562	4.294	1.00	28.98	C
ATOM	1890	NE2	HIS	A	265	44.190	16.720	5.170	1.00	29.95	N
ATOM	1891	CD2	HIS	A	265	44.294	17.264	6.430	1.00	27.50	C
ATOM	1892	C	HIS	A	265	47.701	19.383	6.624	1.00	18.47	C
ATOM	1893	O	HIS	A	265	48.219	18.340	6.236	1.00	17.33	O
ATOM	1894	N	LEU	A	266	47.973	20.577	6.089	1.00	17.86	N
ATOM	1895	CA	LEU	A	266	48.891	20.717	4.968	1.00	17.70	C
ATOM	1896	CB	LEU	A	266	48.925	22.167	4.440	1.00	17.79	C
ATOM	1897	CG	LEU	A	266	49.889	22.490	3.277	1.00	16.98	C
ATOM	1898	CD1	LEU	A	266	49.700	21.533	2.080	1.00	16.25	C
ATOM	1899	CD2	LEU	A	266	49.731	23.941	2.832	1.00	16.33	C
ATOM	1900	C	LEU	A	266	50.282	20.225	5.372	1.00	17.61	C
ATOM	1901	O	LEU	A	266	50.906	19.443	4.642	1.00	17.30	O
ATOM	1902	N	ILE	A	267	50.741	20.639	6.555	1.00	17.19	N
ATOM	1903	CA	ILE	A	267	52.072	20.263	7.023	1.00	16.80	C
ATOM	1904	CB	ILE	A	267	52.425	20.934	8.385	1.00	16.67	C
ATOM	1905	CG1	ILE	A	267	52.702	22.433	8.196	1.00	15.36	C
ATOM	1906	CD1	ILE	A	267	52.656	23.273	9.494	1.00	14.12	C
ATOM	1907	CG2	ILE	A	267	53.626	20.245	9.024	1.00	15.66	C
ATOM	1908	C	ILE	A	267	52.173	18.753	7.137	1.00	17.49	C
ATOM	1909	O	ILE	A	267	53.119	18.156	6.618	1.00	16.97	O
ATOM	1910	N	ARG	A	268	51.178	18.140	7.783	1.00	17.52	N
ATOM	1911	CA	ARG	A	268	51.165	16.692	7.997	1.00	18.02	C
ATOM	1912	CB	ARG	A	268	49.990	16.302	8.907	1.00	18.56	C
ATOM	1913	CG	ARG	A	268	50.240	16.587	10.386	1.00	20.63	C
ATOM	1914	CD	ARG	A	268	49.234	15.899	11.331	1.00	25.57	C
ATOM	1915	NE	ARG	A	268	48.912	16.743	12.487	1.00	29.85	N
ATOM	1916	CZ	ARG	A	268	49.629	16.737	13.585	1.00	31.14	C
ATOM	1917	NH1	ARG	A	268	50.663	15.929	13.648	1.00	34.34	N
ATOM	1918	NH2	ARG	A	268	49.331	17.507	14.615	1.00	30.34	N
ATOM	1919	C	ARG	A	268	51.104	15.910	6.668	1.00	17.59	C
ATOM	1920	O	ARG	A	268	51.676	14.833	6.544	1.00	16.65	O
ATOM	1921	N	TRP	A	269	50.397	16.470	5.693	1.00	17.56	N
ATOM	1922	CA	TRP	A	269	50.336	15.913	4.341	1.00	18.04	C
ATOM	1923	CB	TRP	A	269	49.340	16.717	3.490	1.00	18.77	C
ATOM	1924	CG	TRP	A	269	48.810	15.979	2.265	1.00	21.08	C
ATOM	1925	CD1	TRP	A	269	49.030	14.662	1.914	1.00	22.56	C
ATOM	1926	NE1	TRP	A	269	48.387	14.372	0.730	1.00	24.35	N
ATOM	1927	CE2	TRP	A	269	47.716	15.491	0.301	1.00	23.34	C
ATOM	1928	CD2	TRP	A	269	47.957	16.522	1.248	1.00	22.70	C
ATOM	1929	CE3	TRP	A	269	47.377	17.781	1.033	1.00	23.10	C

ATOM	1930	CZ3	TRP	A	269	46.576	17.970	-0.102	1.00	24.93	C
ATOM	1931	CH2	TRP	A	269	46.351	16.922	-1.014	1.00	24.84	C
ATOM	1932	CZ2	TRP	A	269	46.911	15.679	-0.829	1.00	23.75	C
ATOM	1933	C	TRP	A	269	51.711	15.906	3.667	1.00	17.27	C
ATOM	1934	O	TRP	A	269	52.137	14.870	3.149	1.00	16.99	O
ATOM	1935	N	CYS	A	270	52.400	17.056	3.687	1.00	16.34	N
ATOM	1936	CA	CYS	A	270	53.759	17.173	3.134	1.00	16.21	C
ATOM	1937	CB	CYS	A	270	54.294	18.607	3.275	1.00	15.97	C
ATOM	1938	SG	CYS	A	270	53.427	19.842	2.287	1.00	16.89	S
ATOM	1939	C	CYS	A	270	54.742	16.241	3.824	1.00	16.04	C
ATOM	1940	O	CYS	A	270	55.711	15.774	3.195	1.00	15.33	O
ATOM	1941	N	LEU	A	271	54.488	15.978	5.112	1.00	15.59	N
ATOM	1942	CA	LEU	A	271	55.357	15.124	5.907	1.00	16.36	C
ATOM	1943	CB	LEU	A	271	55.574	15.727	7.304	1.00	15.90	C
ATOM	1944	CG	LEU	A	271	56.248	17.116	7.361	1.00	16.31	C
ATOM	1945	CD1	LEU	A	271	56.473	17.592	8.793	1.00	13.91	C
ATOM	1946	CD2	LEU	A	271	57.590	17.113	6.570	1.00	14.64	C
ATOM	1947	C	LEU	A	271	54.861	13.667	6.010	1.00	16.92	C
ATOM	1948	O	LEU	A	271	55.190	12.969	6.976	1.00	17.11	O
ATOM	1949	N	ALA	A	272	54.085	13.217	5.021	1.00	17.22	N
ATOM	1950	CA	ALA	A	272	53.627	11.819	4.971	1.00	18.16	C
ATOM	1951	CB	ALA	A	272	52.691	11.581	3.798	1.00	18.05	C
ATOM	1952	C	ALA	A	272	54.839	10.921	4.852	1.00	18.59	C
ATOM	1953	O	ALA	A	272	55.768	11.216	4.083	1.00	18.17	O
ATOM	1954	N	LEU	A	273	54.835	9.835	5.621	1.00	19.19	N
ATOM	1955	CA	LEU	A	273	55.953	8.894	5.630	1.00	19.94	C
ATOM	1956	CB	LEU	A	273	55.754	7.832	6.728	1.00	20.56	C
ATOM	1957	CG	LEU	A	273	56.079	8.298	8.162	1.00	21.18	C
ATOM	1958	CD1	LEU	A	273	55.894	7.176	9.193	1.00	21.79	C
ATOM	1959	CD2	LEU	A	273	57.491	8.889	8.262	1.00	20.34	C
ATOM	1960	C	LEU	A	273	56.178	8.254	4.258	1.00	20.58	C
ATOM	1961	O	LEU	A	273	57.322	8.138	3.800	1.00	20.82	O
ATOM	1962	N	ARG	A	274	55.090	7.849	3.605	1.00	20.78	N
ATOM	1963	CA	ARG	A	274	55.164	7.292	2.259	1.00	21.86	C
ATOM	1964	CB	ARG	A	274	53.968	6.373	1.955	1.00	22.23	C
ATOM	1965	CG	ARG	A	274	53.714	5.266	2.975	1.00	27.91	C
ATOM	1966	CD	ARG	A	274	52.588	4.263	2.576	1.00	35.10	C
ATOM	1967	NE	ARG	A	274	52.637	3.917	1.150	1.00	40.44	N
ATOM	1968	CZ	ARG	A	274	51.914	2.962	0.564	1.00	44.04	C
ATOM	1969	NH1	ARG	A	274	51.061	2.223	1.275	1.00	45.20	N
ATOM	1970	NH2	ARG	A	274	52.047	2.741	-0.742	1.00	44.81	N
ATOM	1971	C	ARG	A	274	55.226	8.418	1.227	1.00	20.85	C
ATOM	1972	O	ARG	A	274	54.312	9.249	1.157	1.00	20.77	O
ATOM	1973	N	PRO	A	275	56.297	8.452	0.435	1.00	20.06	N
ATOM	1974	CA	PRO	A	275	56.479	9.502	-0.576	1.00	20.15	C
ATOM	1975	CB	PRO	A	275	57.684	9.007	-1.384	1.00	19.41	C
ATOM	1976	CG	PRO	A	275	58.448	8.169	-0.409	1.00	19.87	C
ATOM	1977	CD	PRO	A	275	57.432	7.509	0.469	1.00	20.03	C
ATOM	1978	C	PRO	A	275	55.245	9.709	-1.474	1.00	20.50	C
ATOM	1979	O	PRO	A	275	54.842	10.860	-1.692	1.00	20.44	O
ATOM	1980	N	SER	A	276	54.650	8.618	-1.966	1.00	20.58	N
ATOM	1981	CA	SER	A	276	53.454	8.693	-2.811	1.00	20.56	C
ATOM	1982	CB	SER	A	276	53.146	7.323	-3.430	1.00	20.69	C
ATOM	1983	OG	SER	A	276	52.516	6.487	-2.479	1.00	22.25	O
ATOM	1984	C	SER	A	276	52.219	9.234	-2.067	1.00	20.21	C
ATOM	1985	O	SER	A	276	51.232	9.612	-2.697	1.00	20.43	O
ATOM	1986	N	ASP	A	277	52.264	9.266	-0.737	1.00	19.88	N
ATOM	1987	CA	ASP	A	277	51.173	9.875	0.027	1.00	19.72	C
ATOM	1988	CB	ASP	A	277	51.093	9.311	1.443	1.00	19.57	C
ATOM	1989	CG	ASP	A	277	50.404	7.945	1.501	1.00	21.58	C
ATOM	1990	OD1	ASP	A	277	49.751	7.540	0.504	1.00	20.40	O
ATOM	1991	OD2	ASP	A	277	50.470	7.222	2.522	1.00	21.84	O
ATOM	1992	C	ASP	A	277	51.266	11.407	0.085	1.00	19.39	C
ATOM	1993	O	ASP	A	277	50.295	12.068	0.483	1.00	20.39	O
ATOM	1994	N	ARG	A	278	52.413	11.962	-0.308	1.00	18.14	N
ATOM	1995	CA	ARG	A	278	52.633	13.408	-0.252	1.00	17.60	C
ATOM	1996	CB	ARG	A	278	54.137	13.740	-0.277	1.00	17.19	C
ATOM	1997	CG	ARG	A	278	54.859	13.330	1.009	1.00	16.29	C
ATOM	1998	CD	ARG	A	278	56.388	13.456	0.995	1.00	15.61	C

ATOM	1999	NE	ARG	A	278	56.954	12.458	1.908	1.00	15.33	N
ATOM	2000	CZ	ARG	A	278	58.152	11.885	1.769	1.00	15.76	C
ATOM	2001	NH1	ARG	A	278	58.965	12.239	0.770	1.00	13.75	N
ATOM	2002	NH2	ARG	A	278	58.541	10.966	2.649	1.00	13.90	N
ATOM	2003	C	ARG	A	278	51.908	14.104	-1.391	1.00	17.58	C
ATOM	2004	O	ARG	A	278	51.716	13.506	-2.466	1.00	17.77	O
ATOM	2005	N	PRO	A	279	51.508	15.357	-1.166	1.00	16.97	N
ATOM	2006	CA	PRO	A	279	50.820	16.142	-2.192	1.00	16.86	C
ATOM	2007	CB	PRO	A	279	50.364	17.387	-1.415	1.00	17.33	C
ATOM	2008	CG	PRO	A	279	51.426	17.533	-0.313	1.00	16.46	C
ATOM	2009	CD	PRO	A	279	51.685	16.125	0.088	1.00	16.42	C
ATOM	2010	C	PRO	A	279	51.768	16.573	-3.290	1.00	17.64	C
ATOM	2011	O	PRO	A	279	52.967	16.757	-3.021	1.00	17.91	O
ATOM	2012	N	THR	A	280	51.245	16.735	-4.507	1.00	17.35	N
ATOM	2013	CA	THR	A	280	51.998	17.353	-5.593	1.00	17.56	C
ATOM	2014	CB	THR	A	280	51.284	17.108	-6.937	1.00	17.70	C
ATOM	2015	OG1	THR	A	280	49.989	17.716	-6.885	1.00	18.13	O
ATOM	2016	CG2	THR	A	280	50.976	15.600	-7.152	1.00	18.27	C
ATOM	2017	C	THR	A	280	52.048	18.864	-5.326	1.00	18.09	C
ATOM	2018	O	THR	A	280	51.342	19.358	-4.427	1.00	18.12	O
ATOM	2019	N	PHE	A	281	52.838	19.600	-6.113	1.00	18.50	N
ATOM	2020	CA	PHE	A	281	52.870	21.066	-6.000	1.00	19.56	C
ATOM	2021	CB	PHE	A	281	53.863	21.702	-6.994	1.00	19.97	C
ATOM	2022	CG	PHE	A	281	55.322	21.369	-6.721	1.00	22.52	C
ATOM	2023	CD1	PHE	A	281	55.834	21.383	-5.433	1.00	25.27	C
ATOM	2024	CE1	PHE	A	281	57.198	21.070	-5.177	1.00	26.96	C
ATOM	2025	CZ	PHE	A	281	58.040	20.748	-6.235	1.00	29.27	C
ATOM	2026	CE2	PHE	A	281	57.535	20.748	-7.553	1.00	28.17	C
ATOM	2027	CD2	PHE	A	281	56.183	21.061	-7.781	1.00	26.44	C
ATOM	2028	C	PHE	A	281	51.474	21.656	-6.211	1.00	19.44	C
ATOM	2029	O	PHE	A	281	51.064	22.559	-5.481	1.00	19.75	O
ATOM	2030	N	GLU	A	282	50.742	21.119	-7.188	1.00	18.94	N
ATOM	2031	CA	GLU	A	282	49.396	21.592	-7.492	1.00	19.12	C
ATOM	2032	CB	GLU	A	282	48.851	20.940	-8.787	1.00	19.45	C
ATOM	2033	CG	GLU	A	282	47.360	21.133	-9.034	1.00	21.47	C
ATOM	2034	CD	GLU	A	282	46.874	20.578	-10.387	1.00	26.22	C
ATOM	2035	OE1	GLU	A	282	47.449	19.584	-10.886	1.00	26.51	O
ATOM	2036	OE2	GLU	A	282	45.901	21.136	-10.951	1.00	25.95	O
ATOM	2037	C	GLU	A	282	48.454	21.369	-6.307	1.00	18.61	C
ATOM	2038	O	GLU	A	282	47.648	22.248	-5.986	1.00	18.93	O
ATOM	2039	N	GLU	A	283	48.558	20.219	-5.640	1.00	17.63	N
ATOM	2040	CA	GLU	A	283	47.693	19.956	-4.485	1.00	17.55	C
ATOM	2041	CB	GLU	A	283	47.744	18.489	-4.076	1.00	17.90	C
ATOM	2042	CG	GLU	A	283	46.951	17.556	-4.989	1.00	18.94	C
ATOM	2043	CD	GLU	A	283	47.298	16.099	-4.752	1.00	21.25	C
ATOM	2044	OE1	GLU	A	283	48.463	15.806	-4.453	1.00	21.74	O
ATOM	2045	OE2	GLU	A	283	46.399	15.240	-4.852	1.00	26.34	O
ATOM	2046	C	GLU	A	283	47.994	20.850	-3.277	1.00	16.99	C
ATOM	2047	O	GLU	A	283	47.090	21.208	-2.519	1.00	16.78	O
ATOM	2048	N	ILE	A	284	49.260	21.208	-3.109	1.00	16.34	N
ATOM	2049	CA	ILE	A	284	49.645	22.147	-2.057	1.00	16.23	C
ATOM	2050	CB	ILE	A	284	51.182	22.296	-1.977	1.00	15.68	C
ATOM	2051	CG1	ILE	A	284	51.837	20.997	-1.492	1.00	15.14	C
ATOM	2052	CD1	ILE	A	284	53.373	20.968	-1.576	1.00	13.98	C
ATOM	2053	CG2	ILE	A	284	51.552	23.488	-1.074	1.00	15.67	C
ATOM	2054	C	ILE	A	284	49.003	23.507	-2.320	1.00	16.48	C
ATOM	2055	O	ILE	A	284	48.371	24.076	-1.447	1.00	16.43	O
ATOM	2056	N	GLN	A	285	49.162	24.009	-3.539	1.00	16.57	N
ATOM	2057	CA	GLN	A	285	48.677	25.335	-3.872	1.00	17.32	C
ATOM	2058	CB	GLN	A	285	49.376	25.867	-5.124	1.00	16.61	C
ATOM	2059	CG	GLN	A	285	50.848	26.173	-4.858	1.00	16.82	C
ATOM	2060	CD	GLN	A	285	51.485	26.941	-5.984	1.00	16.61	C
ATOM	2061	OE1	GLN	A	285	51.643	26.408	-7.087	1.00	16.49	O
ATOM	2062	NE2	GLN	A	285	51.822	28.204	-5.731	1.00	12.74	N
ATOM	2063	C	GLN	A	285	47.153	25.426	-3.998	1.00	17.59	C
ATOM	2064	O	GLN	A	285	46.596	26.520	-3.882	1.00	17.62	O
ATOM	2065	N	ASN	A	286	46.495	24.292	-4.231	1.00	17.76	N
ATOM	2066	CA	ASN	A	286	45.038	24.227	-4.189	1.00	18.67	C
ATOM	2067	CB	ASN	A	286	44.507	23.196	-5.199	1.00	19.01	C

ATOM	2068	CG	ASN	A	286	44.599	23.683	-6.644	1.00	20.31	C
ATOM	2069	OD1	ASN	A	286	44.581	24.890	-6.923	1.00	21.12	O
ATOM	2070	ND2	ASN	A	286	44.697	22.746	-7.566	1.00	21.21	N
ATOM	2071	C	ASN	A	286	44.473	23.948	-2.787	1.00	19.15	C
ATOM	2072	O	ASN	A	286	43.253	23.959	-2.585	1.00	18.66	O
ATOM	2073	N	HIS	A	287	45.362	23.711	-1.820	1.00	19.57	N
ATOM	2074	CA	HIS	A	287	44.943	23.402	-0.455	1.00	19.96	C
ATOM	2075	CB	HIS	A	287	46.161	23.008	0.398	1.00	20.42	C
ATOM	2076	CG	HIS	A	287	45.811	22.535	1.776	1.00	20.16	C
ATOM	2077	ND1	HIS	A	287	45.771	21.201	2.120	1.00	21.24	N
ATOM	2078	CE1	HIS	A	287	45.417	21.085	3.388	1.00	20.50	C
ATOM	2079	NE2	HIS	A	287	45.224	22.298	3.878	1.00	21.14	N
ATOM	2080	CD2	HIS	A	287	45.469	23.220	2.891	1.00	19.59	C
ATOM	2081	C	HIS	A	287	44.212	24.613	0.140	1.00	20.17	C
ATOM	2082	O	HIS	A	287	44.585	25.753	-0.140	1.00	20.09	O
ATOM	2083	N	PRO	A	288	43.154	24.375	0.921	1.00	20.64	N
ATOM	2084	CA	PRO	A	288	42.399	25.468	1.540	1.00	20.94	C
ATOM	2085	CB	PRO	A	288	41.409	24.741	2.463	1.00	21.25	C
ATOM	2086	CG	PRO	A	288	41.229	23.429	1.836	1.00	21.49	C
ATOM	2087	CD	PRO	A	288	42.549	23.063	1.215	1.00	20.84	C
ATOM	2088	C	PRO	A	288	43.263	26.449	2.323	1.00	20.62	C
ATOM	2089	O	PRO	A	288	42.995	27.641	2.242	1.00	21.00	O
ATOM	2090	N	TRP	A	289	44.290	25.982	3.027	1.00	20.44	N
ATOM	2091	CA	TRP	A	289	45.144	26.903	3.785	1.00	20.73	C
ATOM	2092	CB	TRP	A	289	46.165	26.169	4.668	1.00	19.78	C
ATOM	2093	CG	TRP	A	289	46.932	27.139	5.535	1.00	18.93	C
ATOM	2094	CD1	TRP	A	289	46.469	27.795	6.646	1.00	17.79	C
ATOM	2095	NE1	TRP	A	289	47.450	28.617	7.152	1.00	17.69	N
ATOM	2096	CE2	TRP	A	289	48.560	28.535	6.348	1.00	17.45	C
ATOM	2097	CD2	TRP	A	289	48.265	27.614	5.316	1.00	16.35	C
ATOM	2098	CE3	TRP	A	289	49.252	27.348	4.352	1.00	16.19	C
ATOM	2099	CZ3	TRP	A	289	50.488	27.992	4.453	1.00	14.25	C
ATOM	2100	CH2	TRP	A	289	50.753	28.894	5.498	1.00	15.51	C
ATOM	2101	CZ2	TRP	A	289	49.805	29.181	6.453	1.00	16.21	C
ATOM	2102	C	TRP	A	289	45.868	27.924	2.897	1.00	21.43	C
ATOM	2103	O	TRP	A	289	46.219	29.005	3.371	1.00	21.35	O
ATOM	2104	N	MET	A	290	46.081	27.575	1.627	1.00	22.16	N
ATOM	2105	CA	MET	A	290	46.795	28.432	0.672	1.00	23.41	C
ATOM	2106	CB	MET	A	290	47.570	27.561	-0.328	1.00	23.44	C
ATOM	2107	CG	MET	A	290	48.631	26.687	0.341	1.00	23.18	C
ATOM	2108	SD	MET	A	290	50.289	27.282	-0.016	1.00	24.31	S
ATOM	2109	CE	MET	A	290	50.282	28.805	0.810	1.00	21.67	C
ATOM	2110	C	MET	A	290	45.935	29.456	-0.093	1.00	24.66	C
ATOM	2111	O	MET	A	290	46.465	30.229	-0.901	1.00	24.82	O
ATOM	2112	N	GLN	A	291	44.627	29.472	0.161	1.00	25.63	N
ATOM	2113	CA	GLN	A	291	43.725	30.390	-0.541	1.00	27.47	C
ATOM	2114	CB	GLN	A	291	42.263	29.932	-0.399	1.00	28.12	C
ATOM	2115	CG	GLN	A	291	41.931	28.612	-1.133	1.00	30.95	C
ATOM	2116	CD	GLN	A	291	42.797	28.376	-2.378	1.00	35.68	C
ATOM	2117	OE1	GLN	A	291	42.599	29.038	-3.414	1.00	37.06	O
ATOM	2118	NE2	GLN	A	291	43.766	27.441	-2.277	1.00	34.40	N
ATOM	2119	C	GLN	A	291	43.879	31.844	-0.094	1.00	27.73	C
ATOM	2120	O	GLN	A	291	44.222	32.122	1.059	1.00	28.09	O
ATOM	2121	N	ASP	A	292	43.651	32.765	-1.026	1.00	28.22	N
ATOM	2122	CA	ASP	A	292	43.678	34.207	-0.750	1.00	28.34	C
ATOM	2123	CB	ASP	A	292	42.553	34.596	0.224	1.00	29.02	C
ATOM	2124	CG	ASP	A	292	41.176	34.236	-0.308	1.00	31.45	C
ATOM	2125	OD1	ASP	A	292	40.817	34.731	-1.402	1.00	33.30	O
ATOM	2126	OD2	ASP	A	292	40.400	33.452	0.291	1.00	34.49	O
ATOM	2127	C	ASP	A	292	45.027	34.718	-0.245	1.00	27.65	C
ATOM	2128	O	ASP	A	292	45.098	35.446	0.761	1.00	27.28	O
ATOM	2129	N	VAL	A	293	46.094	34.334	-0.946	1.00	26.88	N
ATOM	2130	CA	VAL	A	293	47.429	34.808	-0.622	1.00	25.72	C
ATOM	2131	CB	VAL	A	293	48.538	34.025	-1.396	1.00	26.36	C
ATOM	2132	CG1	VAL	A	293	48.546	34.374	-2.881	1.00	26.33	C
ATOM	2133	CG2	VAL	A	293	49.912	34.299	-0.799	1.00	24.82	C
ATOM	2134	C	VAL	A	293	47.550	36.311	-0.877	1.00	25.50	C
ATOM	2135	O	VAL	A	293	47.007	36.824	-1.848	1.00	24.70	O
ATOM	2136	N	LEU	A	294	48.261	37.004	0.009	1.00	25.07	N

ATOM	2137	CA	LEU	A	294	48.630	38.392	-0.226	1.00	25.15	C
ATOM	2138	CB	LEU	A	294	49.280	38.998	1.017	1.00	24.83	C
ATOM	2139	CG	LEU	A	294	48.500	39.140	2.329	1.00	24.86	C
ATOM	2140	CD1	LEU	A	294	49.412	39.783	3.371	1.00	22.85	C
ATOM	2141	CD2	LEU	A	294	47.199	39.941	2.148	1.00	24.42	C
ATOM	2142	C	LEU	A	294	49.621	38.487	-1.384	1.00	25.66	C
ATOM	2143	O	LEU	A	294	50.437	37.585	-1.598	1.00	25.15	O
ATOM	2144	N	LEU	A	295	49.539	39.585	-2.128	1.00	26.06	N
ATOM	2145	CA	LEU	A	295	50.587	39.950	-3.071	1.00	26.73	C
ATOM	2146	CB	LEU	A	295	50.122	41.106	-3.981	1.00	27.23	C
ATOM	2147	CG	LEU	A	295	48.775	40.944	-4.717	1.00	29.21	C
ATOM	2148	CD1	LEU	A	295	48.330	42.237	-5.412	1.00	31.53	C
ATOM	2149	CD2	LEU	A	295	48.829	39.801	-5.721	1.00	31.44	C
ATOM	2150	C	LEU	A	295	51.841	40.337	-2.265	1.00	26.44	C
ATOM	2151	O	LEU	A	295	51.729	40.733	-1.103	1.00	25.11	O
ATOM	2152	N	PRO	A	296	53.028	40.170	-2.851	1.00	27.04	N
ATOM	2153	CA	PRO	A	296	54.277	40.535	-2.164	1.00	27.59	C
ATOM	2154	CB	PRO	A	296	55.331	40.358	-3.250	1.00	27.65	C
ATOM	2155	CG	PRO	A	296	54.772	39.247	-4.091	1.00	27.68	C
ATOM	2156	CD	PRO	A	296	53.292	39.564	-4.171	1.00	26.80	C
ATOM	2157	C	PRO	A	296	54.265	41.964	-1.623	1.00	28.49	C
ATOM	2158	O	PRO	A	296	54.608	42.151	-0.459	1.00	28.36	O
ATOM	2159	N	GLN	A	297	53.854	42.942	-2.430	1.00	29.34	N
ATOM	2160	CA	GLN	A	297	53.801	44.328	-1.960	1.00	30.65	C
ATOM	2161	CB	GLN	A	297	53.467	45.305	-3.102	1.00	31.10	C
ATOM	2162	CG	GLN	A	297	53.783	46.766	-2.787	1.00	33.83	C
ATOM	2163	CD	GLN	A	297	55.239	46.993	-2.374	1.00	37.47	C
ATOM	2164	OE1	GLN	A	297	56.158	46.742	-3.153	1.00	38.85	O
ATOM	2165	NE2	GLN	A	297	55.444	47.468	-1.147	1.00	39.03	N
ATOM	2166	C	GLN	A	297	52.830	44.490	-0.782	1.00	30.41	C
ATOM	2167	O	GLN	A	297	53.174	45.125	0.210	1.00	30.58	O
ATOM	2168	N	GLU	A	298	51.640	43.900	-0.891	1.00	30.38	N
ATOM	2169	CA	GLU	A	298	50.699	43.839	0.235	1.00	30.73	C
ATOM	2170	CB	GLU	A	298	49.479	42.981	-0.103	1.00	31.10	C
ATOM	2171	CG	GLU	A	298	48.534	43.558	-1.141	1.00	33.59	C
ATOM	2172	CD	GLU	A	298	47.270	42.722	-1.289	1.00	37.83	C
ATOM	2173	OE1	GLU	A	298	47.369	41.480	-1.435	1.00	36.99	O
ATOM	2174	OE2	GLU	A	298	46.166	43.313	-1.272	1.00	40.82	O
ATOM	2175	C	GLU	A	298	51.378	43.269	1.485	1.00	30.06	C
ATOM	2176	O	GLU	A	298	51.258	43.837	2.577	1.00	30.09	O
ATOM	2177	N	THR	A	299	52.096	42.156	1.301	1.00	28.83	N
ATOM	2178	CA	THR	A	299	52.857	41.496	2.360	1.00	27.61	C
ATOM	2179	CB	THR	A	299	53.619	40.265	1.782	1.00	27.45	C
ATOM	2180	OG1	THR	A	299	52.690	39.346	1.192	1.00	25.03	O
ATOM	2181	CG2	THR	A	299	54.269	39.447	2.897	1.00	26.87	C
ATOM	2182	C	THR	A	299	53.840	42.442	3.062	1.00	27.70	C
ATOM	2183	O	THR	A	299	53.890	42.487	4.289	1.00	27.42	O
ATOM	2184	N	ALA	A	300	54.626	43.177	2.278	1.00	27.78	N
ATOM	2185	CA	ALA	A	300	55.622	44.093	2.819	1.00	28.26	C
ATOM	2186	CB	ALA	A	300	56.517	44.627	1.706	1.00	28.09	C
ATOM	2187	C	ALA	A	300	54.972	45.250	3.588	1.00	28.73	C
ATOM	2188	O	ALA	A	300	55.444	45.636	4.658	1.00	28.08	O
ATOM	2189	N	GLU	A	301	53.884	45.785	3.040	1.00	29.58	N
ATOM	2190	CA	GLU	A	301	53.169	46.894	3.668	1.00	31.18	C
ATOM	2191	CB	GLU	A	301	52.063	47.433	2.738	1.00	31.45	C
ATOM	2192	CG	GLU	A	301	52.592	48.250	1.555	1.00	34.28	C
ATOM	2193	CD	GLU	A	301	51.553	48.517	0.460	1.00	37.15	C
ATOM	2194	OE1	GLU	A	301	50.659	47.668	0.219	1.00	37.47	O
ATOM	2195	OE2	GLU	A	301	51.642	49.589	-0.177	1.00	38.55	O
ATOM	2196	C	GLU	A	301	52.610	46.488	5.042	1.00	31.10	C
ATOM	2197	O	GLU	A	301	52.779	47.211	6.019	1.00	31.18	O
ATOM	2198	N	ILE	A	302	51.989	45.311	5.107	1.00	31.28	N
ATOM	2199	CA	ILE	A	302	51.371	44.823	6.340	1.00	31.59	C
ATOM	2200	CB	ILE	A	302	50.284	43.767	6.019	1.00	31.30	C
ATOM	2201	CG1	ILE	A	302	49.201	44.378	5.115	1.00	31.02	C
ATOM	2202	CD1	ILE	A	302	48.293	43.357	4.435	1.00	29.87	C
ATOM	2203	CG2	ILE	A	302	49.673	43.195	7.311	1.00	30.80	C
ATOM	2204	C	ILE	A	302	52.384	44.286	7.373	1.00	32.02	C
ATOM	2205	O	ILE	A	302	52.263	44.577	8.560	1.00	31.80	O

ATOM	2206	N	HIS	A	303	53.391	43.544	6.909	1.00	32.60	N
ATOM	2207	CA	HIS	A	303	54.253	42.750	7.790	1.00	33.26	C
ATOM	2208	CB	HIS	A	303	54.176	41.282	7.379	1.00	32.20	C
ATOM	2209	CG	HIS	A	303	52.832	40.662	7.606	1.00	29.68	C
ATOM	2210	ND1	HIS	A	303	52.385	40.293	8.857	1.00	27.26	N
ATOM	2211	CE1	HIS	A	303	51.171	39.780	8.755	1.00	27.29	C
ATOM	2212	NE2	HIS	A	303	50.819	39.796	7.481	1.00	26.60	N
ATOM	2213	CD2	HIS	A	303	51.839	40.346	6.743	1.00	26.43	C
ATOM	2214	C	HIS	A	303	55.723	43.174	7.849	1.00	35.09	C
ATOM	2215	O	HIS	A	303	56.435	42.838	8.796	1.00	34.73	O
ATOM	2216	N	LEU	A	304	56.181	43.889	6.827	1.00	37.42	N
ATOM	2217	CA	LEU	A	304	57.588	44.256	6.724	1.00	40.17	C
ATOM	2218	CB	LEU	A	304	58.187	43.707	5.421	1.00	39.43	C
ATOM	2219	CG	LEU	A	304	58.574	42.224	5.234	1.00	38.74	C
ATOM	2220	CD1	LEU	A	304	57.830	41.238	6.125	1.00	34.54	C
ATOM	2221	CD2	LEU	A	304	58.465	41.807	3.760	1.00	35.74	C
ATOM	2222	C	LEU	A	304	57.751	45.774	6.796	1.00	42.83	C
ATOM	2223	O	LEU	A	304	58.861	46.286	6.661	1.00	43.07	O
ATOM	2224	N	HIS	A	305	56.629	46.462	7.033	1.00	46.30	N
ATOM	2225	CA	HIS	A	305	56.516	47.933	7.107	1.00	49.71	C
ATOM	2226	CB	HIS	A	305	56.747	48.459	8.545	1.00	50.37	C
ATOM	2227	CG	HIS	A	305	58.085	48.106	9.125	1.00	53.30	C
ATOM	2228	ND1	HIS	A	305	58.344	46.886	9.716	1.00	56.26	N
ATOM	2229	CE1	HIS	A	305	59.597	46.860	10.138	1.00	57.48	C
ATOM	2230	NE2	HIS	A	305	60.159	48.022	9.847	1.00	57.58	N
ATOM	2231	CD2	HIS	A	305	59.234	48.820	9.216	1.00	56.22	C
ATOM	2232	C	HIS	A	305	57.339	48.707	6.063	1.00	50.97	C
ATOM	2233	O	HIS	A	305	58.423	49.221	6.359	1.00	51.59	O
ATOM	2234	N	SER	A	306	56.795	48.799	4.850	1.00	52.46	N
ATOM	2235	CA	SER	A	306	57.518	49.345	3.693	1.00	53.65	C
ATOM	2236	CB	SER	A	306	56.768	49.009	2.401	1.00	53.75	C
ATOM	2237	OG	SER	A	306	57.340	47.873	1.784	1.00	54.33	O
ATOM	2238	C	SER	A	306	57.820	50.851	3.763	1.00	54.12	C
ATOM	2239	O	SER	A	306	58.964	51.291	3.600	1.00	54.51	O
ATOM	2240	OXT	SER	A	306	56.943	51.696	3.974	1.00	54.48	O
ATOM	2241	O1A	ANP	L	1	74.739	30.562	-0.833	1.00	18.02	O
ATOM	2242	PA	ANP	L	1	74.774	30.444	0.630	1.00	19.01	P
ATOM	2243	O2A	ANP	L	1	73.576	29.828	1.256	1.00	17.67	O
ATOM	2244	O3A	ANP	L	1	76.090	29.652	0.938	1.00	19.50	O
ATOM	2245	PB	ANP	L	1	76.391	28.426	1.887	1.00	21.38	P
ATOM	2246	O1B	ANP	L	1	77.321	27.642	1.069	1.00	18.82	O
ATOM	2247	O2B	ANP	L	1	77.348	29.007	2.991	1.00	24.75	O
ATOM	2248	N3B	ANP	L	1	75.190	27.617	2.664	1.00	20.02	N
ATOM	2249	PG	ANP	L	1	73.526	27.764	2.959	1.00	31.62	P
ATOM	2250	O3G	ANP	L	1	73.022	29.016	3.938	1.00	19.18	O
ATOM	2251	O2G	ANP	L	1	73.054	27.935	1.600	1.00	20.72	O
ATOM	2252	O1G	ANP	L	1	72.907	26.389	3.404	1.00	20.30	O
ATOM	2253	O5*	ANP	L	1	74.945	31.880	1.324	1.00	18.06	O
ATOM	2254	C5*	ANP	L	1	75.248	31.923	2.714	1.00	17.09	C
ATOM	2255	C4*	ANP	L	1	74.482	33.091	3.324	1.00	18.01	C
ATOM	2256	O4*	ANP	L	1	74.771	34.292	2.621	1.00	19.09	O
ATOM	2257	C1*	ANP	L	1	73.660	35.124	2.442	1.00	17.31	C
ATOM	2258	C2*	ANP	L	1	72.535	34.397	3.160	1.00	18.01	C
ATOM	2259	O2*	ANP	L	1	72.451	34.900	4.487	1.00	19.01	O
ATOM	2260	C3*	ANP	L	1	72.983	32.937	3.178	1.00	17.74	C
ATOM	2261	O3*	ANP	L	1	72.429	32.083	4.163	1.00	17.16	O
ATOM	2262	N9	ANP	L	1	73.486	35.319	0.979	1.00	17.49	N
ATOM	2263	C8	ANP	L	1	73.739	34.403	-0.019	1.00	15.85	C
ATOM	2264	N7	ANP	L	1	73.458	34.943	-1.228	1.00	14.30	N
ATOM	2265	C5	ANP	L	1	73.025	36.193	-1.045	1.00	15.53	C
ATOM	2266	C6	ANP	L	1	72.607	37.177	-1.929	1.00	16.13	C
ATOM	2267	N6	ANP	L	1	72.542	36.951	-3.254	1.00	14.38	N
ATOM	2268	C4	ANP	L	1	73.039	36.448	0.334	1.00	15.81	C
ATOM	2269	N3	ANP	L	1	72.632	37.646	0.795	1.00	17.04	N
ATOM	2270	C2	ANP	L	1	72.219	38.650	-0.068	1.00	17.00	C
ATOM	2271	N1	ANP	L	1	72.213	38.406	-1.417	1.00	16.49	N
ATOM	2272	O	HOH	W	1	63.572	15.756	8.058	1.00	26.33	O
ATOM	2273	O	HOH	W	2	61.017	10.214	-2.362	1.00	24.27	O
ATOM	2274	O	HOH	W	3	54.457	23.038	-11.444	1.00	30.92	O

ATOM	2275	O	HOH W	4	63.756	21.549	-5.585	1.00	27.71		O
ATOM	2276	O	HOH W	5	63.196	11.516	-9.068	1.00	26.46		O
ATOM	2277	O	HOH W	6	58.424	12.040	-6.552	1.00	34.61		O
ATOM	2278	O	HOH W	7	54.593	37.425	12.022	1.00	32.21		O
ATOM	2279	O	HOH W	8	71.368	23.298	-3.142	1.00	29.05		O
ATOM	2280	O	HOH W	9	64.911	20.478	-0.663	1.00	26.42		O
ATOM	2281	O	HOH W	10	43.132	26.500	18.254	1.00	34.21		O
ATOM	2282	O	HOH W	11	64.667	17.153	-3.465	1.00	26.68		O
ATOM	2283	O	HOH W	12	75.478	24.941	1.494	1.00	29.16		O
ATOM	2284	O	HOH W	13	63.267	18.804	11.098	1.00	24.60		O
ATOM	2285	O	HOH W	14	47.333	35.497	10.172	1.00	39.07		O
ATOM	2286	O	HOH W	15	41.592	25.798	13.188	1.00	29.60		O
ATOM	2287	O	HOH W	16	46.216	35.678	3.186	1.00	30.38		O
ATOM	2288	O	HOH W	17	73.656	23.760	-0.205	1.00	33.83		O
ATOM	2289	O	HOH W	18	54.975	14.884	-3.637	1.00	27.43		O
ATOM	2290	O	HOH W	19	58.350	33.360	-6.094	1.00	29.01		O
ATOM	2291	O	HOH W	20	58.458	11.832	15.075	1.00	34.06		O
ATOM	2292	O	HOH W	21	48.299	24.286	17.311	1.00	29.81		O
ATOM	2293	O	HOH W	22	67.356	21.562	3.234	1.00	31.16		O
ATOM	2294	O	HOH W	23	84.186	28.990	2.689	1.00	31.81		O
ATOM	2295	O	HOH W	24	43.050	31.228	3.507	1.00	47.48		O
ATOM	2296	O	HOH W	25	88.316	32.615	-4.360	1.00	32.51		O
ATOM	2297	O	HOH W	26	71.447	43.185	-7.672	1.00	43.19		O
ATOM	2298	O	HOH W	27	64.646	19.993	-3.620	1.00	28.98		O
ATOM	2299	O	HOH W	28	71.618	43.781	0.688	1.00	40.30		O
ATOM	2300	O	HOH W	29	70.325	37.710	6.677	1.00	31.97		O
ATOM	2301	O	HOH W	30	71.184	18.590	9.525	1.00	35.40		O
ATOM	2302	O	HOH W	31	53.890	12.402	-3.734	1.00	32.44		O
ATOM	2303	O	HOH W	32	52.246	19.524	-9.419	1.00	35.84		O
ATOM	2304	O	HOH W	33	40.639	26.398	16.837	1.00	35.65		O
ATOM	2305	O	HOH W	34	60.620	13.344	-8.811	1.00	44.92		O
ATOM	2306	O	HOH W	35	75.110	44.117	2.424	1.00	40.04		O
ATOM	2307	O	HOH W	36	74.471	37.990	7.461	1.00	40.83		O
ATOM	2308	O	HOH W	37	59.228	35.799	-5.068	1.00	33.92		O
ATOM	2309	O	HOH W	38	57.123	17.309	16.065	1.00	40.82		O
ATOM	2310	O	HOH W	39	73.994	32.523	-2.675	1.00	33.30		O
ATOM	2311	O	HOH W	40	69.993	44.693	3.957	1.00	50.42		O
ATOM	2312	O	HOH W	41	65.864	18.120	0.377	1.00	37.77		O
ATOM	2313	O	HOH W	42	48.834	35.741	2.440	1.00	31.77		O
ATOM	2314	O	HOH W	43	52.185	7.956	4.576	1.00	38.71		O
ATOM	2315	O	HOH W	44	64.765	11.133	-15.777	1.00	33.65		O
ATOM	2316	O	HOH W	45	48.197	17.129	-9.023	1.00	35.25		O
ATOM	2317	O	HOH W	46	71.559	9.704	-7.782	1.00	42.63		O
ATOM	2318	O	HOH W	47	72.838	31.092	-4.833	1.00	32.07		O
ATOM	2319	O	HOH W	48	54.340	33.741	-9.311	1.00	38.01		O
ATOM	2320	O	HOH W	49	54.223	11.905	9.111	1.00	33.22		O
ATOM	2321	O	HOH W	50	52.887	36.641	-1.776	1.00	38.05		O
ATOM	2322	O	HOH W	51	58.033	32.102	18.276	1.00	41.20		O
ATOM	2323	O	HOH W	52	58.764	11.092	17.987	1.00	35.48		O
ATOM	2324	O	HOH W	53	56.210	29.247	-10.737	1.00	40.52		O
ATOM	2325	O	HOH W	54	75.583	29.566	5.684	1.00	42.12		O
ATOM	2326	O	HOH W	55	82.299	27.704	4.152	1.00	43.41		O
ATOM	2327	O	HOH W	56	61.670	6.087	15.210	1.00	42.46		O
ATOM	2328	O	HOH W	57	41.909	26.005	9.492	1.00	38.52		O
ATOM	2329	O	HOH W	58	72.941	15.417	4.788	1.00	53.05		O
ATOM	2330	O	HOH W	59	56.478	27.573	-12.787	1.00	37.09		O
ATOM	2331	O	HOH W	60	83.158	40.743	6.932	1.00	41.95		O
ATOM	2332	O	HOH W	61	44.574	20.141	-2.416	1.00	38.16		O
ATOM	2333	O	HOH W	62	51.818	13.854	13.409	1.00	36.87		O
ATOM	2334	O	HOH W	63	56.901	22.491	-11.879	1.00	46.71		O
ATOM	2335	O	HOH W	64	46.066	31.890	-3.335	1.00	46.54		O
ATOM	2336	O	HOH W	65	46.390	17.471	11.120	1.00	41.50		O
ATOM	2337	O	HOH W	66	73.021	18.047	7.679	1.00	45.56		O
ATOM	2338	O	HOH W	67	56.272	6.117	-3.207	1.00	47.16		O
ATOM	2339	O	HOH W	68	78.807	46.222	0.194	1.00	43.86		O
ATOM	2340	O	HOH W	69	70.343	14.512	-11.989	1.00	41.06		O
ATOM	2341	O	HOH W	70	43.908	38.440	0.670	1.00	53.02		O
ATOM	2342	O	HOH W	71	40.352	28.430	2.051	1.00	45.97		O
ATOM	2343	O	HOH W	72	44.496	19.095	11.235	1.00	54.47		O

ATOM	2344	O	HOH	W	73	47.165	15.788	6.720	1.00	41.01	O
ATOM	2345	O	HOH	W	74	56.445	43.287	-5.157	1.00	44.15	O
ATOM	2346	O	HOH	W	75	73.363	25.539	-17.736	1.00	50.03	O
ATOM	2347	O	HOH	W	76	67.665	14.838	-15.990	1.00	47.37	O
ATOM	2348	O	HOH	W	77	77.512	31.796	8.477	1.00	43.71	O
ATOM	2349	O	HOH	W	78	64.562	45.570	-0.458	1.00	42.82	O
ATOM	2350	O	HOH	W	79	72.601	12.906	5.087	1.00	41.65	O
ATOM	2351	O	HOH	W	80	64.569	29.017	13.834	1.00	46.57	O
ATOM	2352	O	HOH	W	81	58.851	5.715	-3.038	1.00	36.10	O
ATOM	2353	O	HOH	W	82	66.378	16.370	-1.785	1.00	36.18	O
ATOM	2354	O	HOH	W	83	52.161	13.315	8.870	1.00	38.72	O
ATOM	2355	O	HOH	W	84	84.302	27.201	-0.028	1.00	44.09	O
ATOM	2356	O	HOH	W	85	49.501	13.263	-4.243	1.00	40.50	O
ATOM	2357	O	HOH	W	86	63.118	41.154	-5.640	1.00	44.61	O
ATOM	2358	O	HOH	W	87	75.334	10.847	-0.667	1.00	41.03	O
ATOM	2359	O	HOH	W	88	51.946	9.440	7.089	1.00	44.13	O
ATOM	2360	O	HOH	W	89	46.051	15.476	9.731	1.00	44.74	O
ATOM	2361	O	HOH	W	90	60.662	7.651	-3.345	1.00	33.21	O
ATOM	2362	O	HOH	W	91	78.926	37.602	8.589	1.00	45.81	O
ATOM	2363	O	HOH	W	92	83.687	38.788	8.645	1.00	42.46	O
ATOM	2364	O	HOH	W	93	65.774	37.305	-9.200	1.00	42.61	O
ATOM	2365	O	HOH	W	94	48.890	32.798	13.190	1.00	44.81	O
ATOM	2366	O	HOH	W	95	71.057	6.982	7.124	1.00	46.01	O
ATOM	2367	O	HOH	W	96	73.156	42.259	2.367	1.00	41.64	O
ATOM	2368	O	HOH	W	97	56.031	35.393	16.920	1.00	47.09	O
ATOM	2369	O	HOH	W	98	90.130	23.863	-3.527	1.00	56.29	O
ATOM	2370	O	HOH	W	99	64.199	16.375	1.499	1.00	32.31	O
ATOM	2371	O	HOH	W	100	52.185	30.882	13.804	1.00	45.03	O
ATOM	2372	O	HOH	W	101	78.245	25.957	-3.060	1.00	37.82	O
ATOM	2373	O	HOH	W	102	70.395	32.498	-12.472	1.00	40.91	O
ATOM	2374	O	HOH	W	103	76.497	26.635	-1.230	1.00	45.90	O
ATOM	2375	O	HOH	W	104	53.869	39.933	10.992	1.00	48.40	O
ATOM	2376	O	HOH	W	105	52.957	42.953	-5.317	1.00	43.64	O
ATOM	2377	O	HOH	W	106	81.062	46.768	-1.405	1.00	51.11	O
ATOM	2378	O	HOH	W	107	88.023	38.607	-2.261	1.00	44.62	O
ATOM	2379	O	HOH	W	108	55.351	15.949	-6.982	1.00	56.30	O
ATOM	2380	O	HOH	W	109	72.893	16.276	-11.510	1.00	40.24	O
ATOM	2381	O	HOH	W	110	64.150	29.039	11.361	1.00	44.87	O
ATOM	2382	O	HOH	W	111	70.497	11.613	14.584	1.00	42.70	O
ATOM	2383	O	HOH	W	112	47.743	30.590	14.200	1.00	41.84	O
ATOM	2384	O	HOH	W	113	67.986	19.239	2.487	1.00	45.28	O
ATOM	2385	O	HOH	W	114	66.956	9.523	-15.205	1.00	44.06	O
ATOM	2386	O	HOH	W	115	71.948	39.028	3.510	1.00	48.92	O
ATOM	2387	O	HOH	W	116	73.384	36.583	9.395	1.00	49.46	O
ATOM	2388	O	HOH	W	117	69.213	13.943	11.885	1.00	43.79	O
ATOM	2389	O	HOH	W	118	92.376	29.991	-13.421	1.00	50.66	O
ATOM	2390	O	HOH	W	119	71.748	33.616	8.364	1.00	44.60	O
ATOM	2391	O	HOH	W	120	72.751	30.625	9.138	1.00	54.54	O
ATOM	2392	O	HOH	W	121	44.373	14.896	1.763	1.00	54.90	O
ATOM	2393	O	HOH	W	122	72.331	37.663	5.252	1.00	54.91	O
ATOM	2394	O	HOH	W	123	85.766	37.929	7.966	1.00	45.42	O
ATOM	2395	O	HOH	W	124	82.375	46.624	-12.952	1.00	49.98	O
ATOM	2396	O	HOH	W	125	69.185	5.514	-10.117	1.00	57.15	O
ATOM	2397	O	HOH	W	126	72.843	16.943	-2.415	1.00	48.35	O
ATOM	2398	O	HOH	W	127	58.459	18.549	-11.193	1.00	68.47	O
ATOM	2399	O	HOH	W	128	64.272	33.293	-12.839	1.00	48.86	O
ATOM	2400	O	HOH	W	129	59.782	37.121	-16.253	1.00	59.29	O

TABLE 5

DISEASES ASSOCIATED WITH GENETIC DEFECTS IN KINASES

Serine/Threonine Protein Kinases

CYCLIN-DEPENDENT KINASE 7; CDK7
DYSTROPHIA MYOTONICA; DM
MINIBRAIN (DROSOPHILA) HOMOLOG; MNBH
RAC SERINE/THREONINE PROTEIN KINASE
SERINE-THREONINE PROTEIN KINASE N; PKN
SERINE/THREONINE PROTEIN KINASE 2; STK2
PROTEIN KINASE, DNA-ACTIVATED, CATALYTIC SUBUNIT; PRKDC
ZIPPER PROTEIN KINASE; ZPK
PROTEIN-TYROSINE KINASE STY
BRUTON AGAMMAGLOBULINEMIA TYROSINE KINASE; BTK
MKN28 KINASE
PROTEIN KINASE, X-LINKED; PRKX
ELK-RELATED TYROSINE KINASE; ERK
RIBOSOMAL PROTEIN S6 KINASE, 90 KD, POLYPEPTIDE 3; RPS6KA3
GLYCOGEN STORAGE DISEASE VIII
DEATH-ASSOCIATED PROTEIN KINASE 1; DAPK1
PCTAIRE PROTEIN KINASE 1; PCTK1
PROTEIN KINASE, INTERFERON-INDUCIBLE DOUBLE-STRANDED RNA; PRKR
ACTIVIN A RECEPTOR, TYPE II-LIKE KINASE 1; ACVRLK1
PROTEIN KINASE, cAMP-DEPENDENT, CATALYTIC, ALPHA; PRKACA
PROTEIN KINASE, Y-LINKED; PRKY
G PROTEIN-COUPLED RECEPTOR KINASE 2 (DROSOPHILA)-LIKE; GPRK2L
PROTEIN KINASE C, THETA FORM; PRKCQ
LIM DOMAIN KINASE 1; LIMK1
PHOSPHOGLYCERATE KINASE 1; PGK1
LIM DOMAIN KINASE 2; LIMK2
C-JUN KINASE
ACTIVIN A RECEPTOR, TYPE II-LIKE KINASE 2; ACVRLK2
JANUS KINASE 1; JAK1
ELKL MOTIF KINASE; EMK1
MALE GERM CELL-ASSOCIATED KINASE; MAK
CASEIN KINASE 2, ALPHA-PRIME SUBUNIT; CSNK2A2
CASEIN KINASE 2, BETA POLYPEPTIDE; CSNK2B
CASEIN KINASE 2, ALPHA 1 POLYPEPTIDE; CSNK2A1
LEUKEMIA, CHRONIC MYELOID; CML
RET PROTO-ONCOGENE; RET
HEMATOPOIETIC PROGENITOR KINASE 1
CONSERVED HELIX-LOOP-HELIX UBIQUITOUS KINASE; CHUK
CASEIN KINASE 1, DELTA; CSNK1D
CASEIN KINASE 1, EPSILON; CSNK1E
DEATH-ASSOCIATED PROTEIN; DAP
V-AKT MURINE THYMOMA VIRAL ONCOGENE HOMOLOG 1; AKT1
TUMOR PROTEIN p53; TP53
PROTEIN PHOSPHATASE 1, REGULATORY (INHIBITOR) SUBUNIT 2; PPP1R2
SEVERE COMBINED IMMUNODEFICIENCY DISEASE-1; SCID1
HYPERLIPOPROTEINEMIA, TYPE I
COLLAGEN, TYPE I, ALPHA-1 CHAIN; COL1A1
UBIQUITIN-BINDING PROTEIN P62
TAY-SACHS DISEASE; TSD
CYSTIC FIBROSIS; CF
p160-ROCK

BCL2-ASSOCIATED ATHANOGENE 1; BAG1
HYPOXANTHINE GUANINE PHOSPHORIBOSYLTRANSFERASE 1; HPRT1
ONCOGENE PIM-1; PIM1; PIM
CARTILAGE-DERIVED MORPHOGENETIC PROTEIN 1
GALACTOSEMIA
GRANULOMATOUS DISEASE, CHRONIC, AUTOSOMAL CYTOCHROME-b-POSITIVE FORM I
TRANSFORMING GROWTH FACTOR-BETA RECEPTOR, TYPE II; TGFBR2
RHODOPSIN; RHO
MOTHERS AGAINST DECAPENTAPLEGIC (DROSOPHILA) HOMOLOG 2; MADH2
TRIPLE FUNCTIONAL DOMAIN; TRIO
TRANSFORMING GROWTH FACTOR-BETA RECEPTOR, TYPE I; TGFBR1
GENERAL TRANSCRIPTION FACTOR IIH, POLYPEPTIDE 1; GTF2H1
ANTI-MULLERIAN HORMONE TYPE II RECEPTOR; AMHR2
V-RAF MURINE SARCOMA VIRAL ONCOGENE HOMOLOG B1; BRAF
BONE MORPHOGENETIC RECEPTOR TYPE II; BMPR2
GLYCOGEN STORAGE DISEASE V
COMPLEX IV, CYTOCHROME c OXIDASE SUBUNIT III
V-RAF MURINE SARCOMA 3611 VIRAL ONCOGENE HOMOLOG 1; ARAF1
GAUCHER DISEASE, TYPE I; GD I
V-RAF MURINE SARCOMA 3611 VIRAL ONCOGENE HOMOLOG 2; ARAF2
CYCLIN A; CCNA
ANEMIA, HYPOCHROMIC; ANH1
GRANULOMATOUS DISEASE, CHRONIC; CGD
ACTIVIN A RECEPTOR, TYPE I; ACVR1

Serine Protein Kinases

CYCLIN-DEPENDENT KINASE 7; CDK7
DYSTROPHIA MYOTONICA; DM
MINIBRAIN (DROSOPHILA) HOMOLOG; MNBH
RAC SERINE/THREONINE PROTEIN KINASE
SERINE-THREONINE PROTEIN KINASE N; PKN
PROTEIN KINASE, SERINE/ARGININE-SPECIFIC
PROTEIN SERINE KINASE H1; PSKH1
SERINE/THREONINE PROTEIN KINASE 2; STK2
PROTEIN KINASE, DNA-ACTIVATED, CATALYTIC SUBUNIT; PRKDC
ZIPPER PROTEIN KINASE; ZPK
PROTEIN-TYROSINE KINASE STY
SYK-RELATED TYROSINE KINASE; SRK
BRUTON AGAMMAGLOBULINEMIA TYROSINE KINASE; BTK
MKN28 KINASE
NON-METASTATIC CELLS 1, PROTEIN EXPRESSED IN; NME1
ELK-RELATED TYROSINE KINASE; ERK
PROTEIN KINASE, X-LINKED; PRKX
FIBROBLAST GROWTH FACTOR RECEPTOR-2; FGFR2
RIBOSOMAL PROTEIN S6 KINASE, 90 KD, POLYPEPTIDE 3; RPS6KA3
PCTAIRE PROTEIN KINASE 1; PCTK1
DEATH-ASSOCIATED PROTEIN KINASE 1; DAPK1
ACTIVIN A RECEPTOR, TYPE II-LIKE KINASE 1; ACVRLK1
GLYCOGEN STORAGE DISEASE VIII
PROTEIN KINASE, INTERFERON-INDUCIBLE DOUBLE-STRANDED RNA; PRKR
PROTEIN KINASE, Y-LINKED; PRKY
G PROTEIN-COUPLED RECEPTOR KINASE 2 (DROSOPHILA)-LIKE; GPRK2L
LIM DOMAIN KINASE 1; LIMK1
PROTEIN KINASE, cAMP-DEPENDENT, CATALYTIC, ALPHA; PRKACA
PROTEIN KINASE C, THETA FORM; PRKCQ
C-JUN KINASE
PHOSPHOGLYCERATE KINASE 1; PGK1
LIM DOMAIN KINASE 2; LIMK2

ACTIVIN A RECEPTOR, TYPE II-LIKE KINASE 2; ACVRLK2
JANUS KINASE 1; JAK1
INSULIN RECEPTOR; INSR
CASEIN KINASE 2, ALPHA 1 POLYPEPTIDE; CSNK2A1
CASEIN KINASE 2, BETA POLYPEPTIDE; CSNK2B
CASEIN KINASE 2, ALPHA-PRIME SUBUNIT; CSNK2A2
ATAXIA-TELANGIECTASIA; AT
MALE GERM CELL-ASSOCIATED KINASE; MAK
ELKL MOTIF KINASE; EMK1
LEUKEMIA, CHRONIC MYELOID; CML
HEMATOPOIETIC PROGENITOR KINASE 1
RET PROTO-ONCOGENE; RET
CASEIN KINASE 1, DELTA; CSNK1D
CASEIN KINASE 1, EPSILON; CSNK1E
CONSERVED HELIX-LOOP-HELIX UBIQUITOUS KINASE; CHUK
HYPERCHOLESTEROLEMIA, FAMILIAL; FHC
TUMOR PROTEIN p53; TP53
TAY-SACHS DISEASE; TSD
DEATH-ASSOCIATED PROTEIN; DAP
V-AKT MURINE THYMOMA VIRAL ONCOGENE HOMOLOG 1; AKT1
COLLAGEN, TYPE I, ALPHA-1 CHAIN; COL1A1
SEVERE COMBINED IMMUNODEFICIENCY DISEASE-1; SCID1
ADENOMATOUS POLYPOSIS OF THE COLON; APC
PROTEIN PHOSPHATASE 1, REGULATORY (INHIBITOR) SUBUNIT 2; PPP1R2
UBIQUITIN-BINDING PROTEIN P62
MUSCULAR DYSTROPHY, TARDIVE, DREIFUSS-EMERY TYPE, WITH CONTRACTURES
CAVEOLIN, CAVEOLAE PROTEIN, 22-KD; CAV
FIBROBLAST GROWTH FACTOR RECEPTOR-3; FGFR3
CYSTIC FIBROSIS; CF
HYPOXANTHINE GUANINE PHOSPHORIBOSYLTRANSFERASE 1; HPRT1
GROWTH FACTOR RECEPTOR-BOUND PROTEIN-10; GRB10
HYPERLIPOPROTEINEMIA, TYPE I
CREB-BINDING PROTEIN; CREBBP
THYROID AUTOANTIGEN 70 KD; G22P1
ONCOGENE PIM-1; PIM1; PIM
SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 3; STAT3
CYCLIC-AMP-RESPONSE-ELEMENT-BINDING PROTEIN-1; CREB1
BCL2-ASSOCIATED ATHANOGENE 1; BAG1
P32 SPLICING FACTOR SF2 ASSOCIATED PROTEIN
CARTILAGE-DERIVED MORPHOGENETIC PROTEIN 1
p160-ROCK
GROWTH FACTOR RECEPTOR-BOUND PROTEIN-14; GRB14
THROMBASTHENIA OF GLANZMANN AND NAEGELI
INSULIN RECEPTOR SUBSTRATE 1; IRS1
GRANULOMATOUS DISEASE, CHRONIC, AUTOSOMAL CYTOCHROME-b-POSITIVE FORM I
GUANYLATE CYCLASE 2D, MEMBRANE; GUC2D
GALACTOSEMIA
RHODOPSIN; RHO
TRANSFORMING GROWTH FACTOR-BETA RECEPTOR, TYPE II; TGFBR2
ICHTHYOSIS, X-LINKED
TRIPLE FUNCTIONAL DOMAIN; TRIO
MOTHERS AGAINST DECAPENTAPLEGIC (DROSOPHILA) HOMOLOG 2; MADH2
MCF.2 CELL LINE DERIVED TRANSFORMING SEQUENCE; MCF2
ESTROGEN RECEPTOR; ESR
V-RAF MURINE SARCOMA 3611 VIRAL ONCOGENE HOMOLOG 1; ARAF1
V-RAF MURINE SARCOMA 3611 VIRAL ONCOGENE HOMOLOG 2; ARAF2
BONE MORPHOGENETIC RECEPTOR TYPE II; BMPR2
GAUCHER DISEASE, TYPE I; GD I
TRANSFORMING GROWTH FACTOR-BETA RECEPTOR, TYPE I; TGFBR1
GENERAL TRANSCRIPTION FACTOR IIH, POLYPEPTIDE 1; GTF2H1
CHYMOTRYPSIN-LIKE PROTEASE; CTRL

GLYCOGEN STORAGE DISEASE V
CYCLIN A; CCNA
LETHAL GIANT LARVAE (DROSOPHILA) HOMOLOG 1; LLGL1
GRANULOMATOUS DISEASE, CHRONIC; CGD
CASEIN, BETA; CSN2
DENTIN MATRIX ACIDIC PHOSPHOPROTEIN 1; DMP1
TREACHER COLLINS-FRANCESCHETTI SYNDROME 1; TCOF1
COMPLEX IV, CYTOCHROME c OXIDASE SUBUNIT III
DIABETES MELLITUS, AUTOSOMAL DOMINANT
V-RAF MURINE SARCOMA VIRAL ONCOGENE HOMOLOG B1; BRAF
ANEMIA, HYPOCHROMIC; ANH1
ANTI-MULLERIAN HORMONE TYPE II RECEPTOR; AMHR2
PLASMINOGEN ACTIVATOR INHIBITOR, TYPE 2; PAI2
ACTIVIN A RECEPTOR, TYPE I; ACVR1

Threonine Protein Kinases

CYCLIN-DEPENDENT KINASE 7; CDK7
DYSTROPHIA MYOTONICA; DM
MINIBRAIN (DROSOPHILA) HOMOLOG; MNBH
RAC SERINE/THREONINE PROTEIN KINASE
SERINE-THREONINE PROTEIN KINASE N; PKN
SERINE/THREONINE PROTEIN KINASE 2; STK2
PROTEIN KINASE, DNA-ACTIVATED, CATALYTIC SUBUNIT; PRKDC
ZIPPER PROTEIN KINASE; ZPK
PROTEIN-TYROSINE KINASE STY
PROTEIN KINASE, MITOGEN-ACTIVATED, KINASE 1; PRKMK1
BRUTON AGAMMAGLOBULINEMIA TYROSINE KINASE; BTK
MKN28 KINASE
PROTEIN KINASE, X-LINKED; PRKX
ELK-RELATED TYROSINE KINASE; ERK
GLYCOGEN STORAGE DISEASE VIII
PYRUVATE KINASE DEFICIENCY OF ERYTHROCYTE
RIBOSOMAL PROTEIN S6 KINASE, 90 KD, POLYPEPTIDE 3; RPS6KA3
DEATH-ASSOCIATED PROTEIN KINASE 1; DAPK1
PCTAIRE PROTEIN KINASE 1; PCTK1
PROTEIN KINASE, INTERFERON-INDUCIBLE DOUBLE-STRANDED RNA; PRKR
ACTIVIN A RECEPTOR, TYPE II-LIKE KINASE 1; ACVRLK1
PROTEIN KINASE, Y-LINKED; PRKY
G PROTEIN-COUPLED RECEPTOR KINASE 2 (DROSOPHILA)-LIKE; GPRK2L
PROTEIN KINASE, cAMP-DEPENDENT, CATALYTIC, ALPHA; PRKACA
PROTEIN KINASE C, THETA FORM; PRKCQ
MUSCULAR DYSTROPHY, PSEUDOHYPERTROPHIC PROGRESSIVE, DUCHENNE AND BECKER TYPES; DMD
LIM DOMAIN KINASE 1; LIMK1
PHOSPHOGLYCERATE KINASE 1; PGK1
LIM DOMAIN KINASE 2; LIMK2
C-JUN KINASE
ACTIVIN A RECEPTOR, TYPE II-LIKE KINASE 2; ACVRLK2
JANUS KINASE 1; JAK1
CASEIN KINASE 2, ALPHA 1 POLYPEPTIDE; CSNK2A1
CASEIN KINASE 2, BETA POLYPEPTIDE; CSNK2B
MALE GERM CELL-ASSOCIATED KINASE; MAK
MEVALONICACIDURIA
ELKL MOTIF KINASE; EMK1
CASEIN KINASE 2, ALPHA-PRIME SUBUNIT; CSNK2A2
MAP KINASE KINASE 6
CASEIN KINASE 1, EPSILON; CSNK1E
CASEIN KINASE 1, DELTA; CSNK1D

LEUKEMIA, CHRONIC MYELOID; CML
CONSERVED HELIX-LOOP-HELIX UBIQUITOUS KINASE; CHUK
HEMATOPOIETIC PROGENITOR KINASE 1
RET PROTO-ONCOGENE; RET
PROTEIN PHOSPHATASE 1, REGULATORY (INHIBITOR) SUBUNIT 2; PPP1R2
DUAL SPECIFICITY PHOSPHATASE 1; DUSP1
V-AKT MURINE THYMOMA VIRAL ONCOGENE HOMOLOG 1; AKT1
DEATH-ASSOCIATED PROTEIN; DAP
TUMOR PROTEIN p53; TP53
GLYCOGEN STORAGE DISEASE II
SEVERE COMBINED IMMUNODEFICIENCY DISEASE-1; SCID1
UBIQUITIN-BINDING PROTEIN P62
HYPERLIPOPROTEINEMIA, TYPE I
BCL2-ASSOCIATED ATHANOGENE 1; BAG1
ONCOGENE PIM-1; PIM1; PIM
HYPOXANTHINE GUANINE PHOSPHORIBOSYLTRANSFERASE 1; HPRT1
p160-ROCK
CARTILAGE-DERIVED MORPHOGENETIC PROTEIN 1
CYSTIC FIBROSIS; CF
TAY-SACHS DISEASE; TSD
COLLAGEN, TYPE I, ALPHA-1 CHAIN; COL1A1
GRANULOMATOUS DISEASE, CHRONIC, AUTOSOMAL CYTOCHROME-b-POSITIVE FORM I
NEUROMATA, MUCOSAL, WITH ENDOCRINE TUMORS
TRANSFORMING GROWTH FACTOR-BETA RECEPTOR, TYPE II; TGFBR2
GALACTOSEMIA
MOTHERS AGAINST DECAPENTAPLEGIC (DROSOPHILA) HOMOLOG 2; MADH2
TRIPLE FUNCTIONAL DOMAIN; TRIO
ANTI-MULLERIAN HORMONE TYPE II RECEPTOR; AMHR2
BONE MORPHOGENETIC RECEPTOR TYPE II; BMPR2
V-RAF MURINE SARCOMA VIRAL ONCOGENE HOMOLOG B1; BRAF
CYCLIN A; CCNA
COMPLEX IV, CYTOCHROME c OXIDASE SUBUNIT III
RHODOPSIN; RHO
V-RAF MURINE SARCOMA 3611 VIRAL ONCOGENE HOMOLOG 1; ARAF1
GRANULOMATOUS DISEASE, CHRONIC; CGD
TRANSFORMING GROWTH FACTOR-BETA RECEPTOR, TYPE I; TGFBR1
ANEMIA, HYPOCHROMIC; ANH1
GENERAL TRANSCRIPTION FACTOR IIH, POLYPEPTIDE 1; GTF2H1
GLYCOGEN STORAGE DISEASE V
GAUCHER DISEASE, TYPE I; GD I
ADENINE PHOSPHORIBOSYLTRANSFERASE; APRT
V-RAF MURINE SARCOMA 3611 VIRAL ONCOGENE HOMOLOG 2; ARAF2
ACTIVIN A RECEPTOR, TYPE I; ACVR1

Tyrosine Protein Kinases

NEUROTROPHIC TYROSINE KINASE, RECEPTOR, TYPE 1; NTRK1
PROTEIN-TYROSINE KINASE, CYTOPLASMIC; PTK2
SYK-RELATED TYROSINE KINASE; SRK
PROTEIN TYROSINE KINASE CTK; CTK
TYRO3 PROTEIN TYROSINE KINASE; TYRO3
BRUTON AGAMMAGLOBULINEMIA TYROSINE KINASE; BTK
LEUKOCYTE TYROSINE KINASE; LTK
PROTEIN-TYROSINE KINASE SYK; SYK
PROTEIN-TYROSINE KINASE STY
TEK TYROSINE KINASE, ENDOTHELIAL; TEK
ELK-RELATED TYROSINE KINASE; ERK
TYROSINE KINASE WITH IMMUNOGLOBULIN AND EGF FACTOR HOMOLOGY DOMAINS; TIE
PROTEIN TYROSINE KINASE TKF

NEUROTROPHIC TYROSINE KINASE, RECEPTOR, TYPE 3; NTRK3
MIXED-LINEAGE PROTEIN KINASE-3; MLK3
PROTEIN KINASE, MITOGEN-ACTIVATED 4; PRKM4
PROTEIN KINASE, MITOGEN-ACTIVATED 1; PRKM1
PROTEIN TYROSINE KINASE PTK7; PTK7
PROTEIN TYROSINE KINASE EEK
MINIBRAIN (DROSOPHILA) HOMOLOG; MNBH
BONE MARROW KINASE, X-LINKED; BMX
EPH-LIKE TYROSINE KINASE 1; ETK1
MACROPHAGE STIMULATING 1 RECEPTOR; MST1R
BTK-ASSOCIATED PROTEIN, 135 KD
LYMPHOCYTE-SPECIFIC PROTEIN TYROSINE KINASE; LCK
FIBROBLAST GROWTH FACTOR RECEPTOR-2; FGFR2
PROTEIN TYROSINE KINASE-3; TYK3; FER
PROTEIN TYROSINE KINASE TXK; TXK
TEC PROTEIN TYROSINE KINASE; TEC
PROTEIN TYROSINE KINASE-2; TYK2
EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 1; EPLG1
T-CELL TYROSINE KINASE EMT; EMT
EPH TYROSINE KINASE 1; EPHT1
ZONA PELLUCIDA RECEPTOR TYROSINE KINASE, 95 KD; ZRK
PROTEIN KINASE, MITOGEN-ACTIVATED, KINASE 1; PRKMK1
EPH TYROSINE KINASE 3; EPHT3
GROWTH ARREST-SPECIFIC GENE-6; GAS6
KINASE INSERT DOMAIN RECEPTOR; KDR
AXL RECEPTOR TYROSINE KINASE; AXL
FIBROBLAST GROWTH FACTOR RECEPTOR-1; FGFR1
V-ERB-B2 AVIAN ERYTHROBLASTIC LEUKEMIA VIRAL ONCOGENE HOMOLOG 2; ERBB2
FMS-LIKE TYROSINE KINASE-3; FLT3
NEUROEPITHELIAL TYROSINE KINASE; NEP
NEUROTROPHIC TYROSINE KINASE RECEPTOR-RELATED 3; NTRKR3
EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 5; EPLG5
NEUROTROPHIC TYROSINE KINASE, RECEPTOR, TYPE 2; NTRK2
RYK RECEPTOR-LIKE TYROSINE KINASE
TYROSINE KINASE, B-LYMPHOCYTE SPECIFIC; BLK
EPH TYROSINE KINASE 2; EPHT2
EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 2; EPLG2
GLYCOGEN STORAGE DISEASE VIII
EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 7; EPLG7
JANUS KINASE 1; JAK1
FMS-RELATED TYROSINE KINASE-1; FLT1
PROTEIN KINASE, cAMP-DEPENDENT, REGULATORY, TYPE I, ALPHA; PRKAR1A
WEE-1 TYROSINE KINASE; WEE1
EPH-LIKE TYROSINE KINASE 2; ETK2
RECEPTOR TYROSINE KINASE MuSK
INSULIN RECEPTOR; INSR
JANUS KINASE 3 JAK3
FMS-RELATED TYROSINE KINASE-3 LIGAND
PROTEIN KINASE C, BETA 1; PRKCB1
TYROSINE KINASE-TYPE CELL SURFACE RECEPTOR HER3; HER3
JANUS KINASE 2; JAK2
LIM DOMAIN KINASE 1; LIMK1
DUAL SPECIFICITY PHOSPHATASE 1; DUSP1
MUSCULAR DYSTROPHY, PSEUDOHYPERTROPHIC PROGRESSIVE, DUCHENNE AND BECKER TYPES; DMD
HEMOPOIETIC CELL KINASE; HCK
TYROSINE 3-MONOOXYGENASE/TRYPTOPHAN 5-MONOOXYGENASE ACTIVATION PROTEIN, ETA POLYPEPTIDE; YWHAH
RET PROTO-ONCOGENE; RET
TYROSINE 3-MONOOXYGENASE/TRYPTOPHAN 5-MONOOXYGENASE ACTIVATION PROTEIN, ZETA POLYPEPTIDE; YWHAZ

TYROSINE 3-MONOOXYGENASE/TRYPTOPHAN 5-MONOOXYGENASE ACTIVATION PROTEIN, BETA POLYPEPTIDE; YWHAB
HEPATOMA TRANSMEMBRANE KINASE; HTK
MAP KINASE KINASE 6
PHOSPHATIDYLINOSITOL 3-KINASE, CATALYTIC, ALPHA POLYPEPTIDE; PIK3CA
CYCLIN-DEPENDENT KINASE INHIBITOR 3; CDKN3
DIACYLGLYCEROL KINASE, DELTA, 130 KD
PROTEIN-TYROSINE PHOSPHATASE, NONRECEPTOR TYPE, 13; PTPN13
ABELSON MURINE LEUKEMIA VIRAL ONCOGENE HOMOLOG 1; ABL1
DIACYLGLYCEROL KINASE, ALPHA; DAGK1
FOCAL ADHESION KINASE 2
EPITHELIAL DISCOIDIN DOMAIN RECEPTOR 1; EDDR1
ANAPLASTIC LYMPHOMA KINASE; ALK
PHOSPHATIDYLINOSITOL 3-KINASE, CATALYTIC, GAMMA POLYPEPTIDE; PIK3CG
PHOSPHATIDYLINOSITOL 3-KINASE REGULATORY SUBUNIT; PIK3R1
EPH HOMOLOGY KINASE-1; EHK1
V-KIT HARDY-ZUCKERMAN 4 FELINE SARCOMA VIRAL ONCOGENE HOMOLOG; KIT
FIBROBLAST GROWTH FACTOR RECEPTOR-3; FGFR3
VASCULAR ENDOTHELIAL GROWTH FACTOR C; VEGFC
MACROPHAGE STIMULATING 1; MST1
HYPERCHOLESTEROLEMIA, FAMILIAL; FHC
EPIDERMAL GROWTH FACTOR RECEPTOR; EGFR
S100 CALCIUM-BINDING PROTEIN A10; S100A10
NEUROFIBROMATOSIS, TYPE I; NF1
ONCOGENE TRK
LEUKEMIA, CHRONIC MYELOID; CML
GROWTH FACTOR RECEPTOR-BOUND PROTEIN-7; GRB7
S100 CALCIUM-BINDING PROTEIN A4; S100A4
RAS p21 PROTEIN ACTIVATOR; RASA2
ADENOMATOUS POLYPOSIS OF THE COLON; APC
MET PROTO-ONCOGENE; MET
SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 3; STAT3
smg GDS-ASSOCIATED PROTEIN
UBIQUITIN-BINDING PROTEIN P62
LYMPHOCYTE CYTOSOLIC PROTEIN 2; LCP2
EPIDERMAL GROWTH FACTOR RECEPTOR PATHWAY SUBSTRATE-15; EPS15
GROWTH FACTOR RECEPTOR-BOUND PROTEIN-10; GRB10
GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR-ALPHA; GDNFRA
SHC TRANSFORMING PROTEIN; SHC1
CYSTIC FIBROSIS; CF
TROPOMYOSIN 3; TPM3
CELL DIVISION CYCLE 2, G1 TO S AND G2 TO M; CDC2
MUSCULAR DYSTROPHY, LIMB GIRDLE, TYPE 2C; LGMD2C
ASH PROTEIN
TAY-SACHS DISEASE; TSD
AGRIN; AGRN
S100 CALCIUM-BINDING PROTEIN A6; S100A6
AGRANULOCYTOSIS, INFANTILE GENETIC
TRIPLE FUNCTIONAL DOMAIN; TRIO
HYPOXANTHINE GUANINE PHOSPHORIBOSYLTRANSFERASE 1; HPRT1
CYTOVILLIN
GOLGI APPARATUS PROTEIN 1; GLG1
GROWTH FACTOR RECEPTOR-BOUND PROTEIN-14; GRB14
V-FES FELINE SARCOMA VIRAL/V-FPS FUJINAMI AVIAN SARCOMA VIRAL ONCOGENE HOMOLOG; FES
TRANSLOCATED PROMOTER REGION
P32 SPLICING FACTOR SF2 ASSOCIATED PROTEIN
CARTILAGE-DERIVED MORPHOGENETIC PROTEIN 1
PAIRED BOX HOMEOTIC GENE 5; PAX5
INSULIN RECEPTOR SUBSTRATE 1; IRS1
SON OF SEVENLESS (DROSOPHILA) HOMOLOG 2; SOS2

PHOSPHATIDYLINOSITOL GLYCAN CLASS A; PIGA
ICHTHYOSIS, X-LINKED
RHODOPSIN; RHO
SEVERE COMBINED IMMUNODEFICIENCY DISEASE, AUTOSOMAL RECESSIVE, T-NEGATIVE/B-POSITIVE TYPE
CAS-BR-M (MURINE) ECOTROPIC RETROVIRAL TRANSFORMING SEQUENCE; CBL
TRANSFORMING GROWTH FACTOR-BETA RECEPTOR, TYPE II; TGFBR2
COLONY-STIMULATING FACTOR-1 RECEPTOR; CSF1R
PHOSPHODIESTERASE I/NUCLEOTIDE PYROPHOSPHATASE 1; PDNP1
NUCLEOPHOSMIN; NPM1
ADDUCIN 1; ADD1
NEUROMATA, MUCOSAL, WITH ENDOCRINE TUMORS
HYALURONAN-MEDIATED MOTILITY RECEPTOR; HMMR
ESTROGEN RECEPTOR; ESR
SRC-LIKE ADAPTER; SLA
BECKWITH-WIEDEMANN SYNDROME; BWS
TYLOSIS WITH ESOPHAGEAL CANCER; TOC
PLACENTAL GROWTH FACTOR; PGF
ETS VARIANT GENE 6; ETV6
MEMBRANE COMPONENT, CHROMOSOME 6, POLYPEPTIDE 2; M6P2
INTERLEUKIN-4; IL4
GARDNER-RASHEED FELINE SARCOMA VIRAL (V-FGR) ONCOGENE; FGR
FIBROBLAST GROWTH FACTOR-8; FGF8
SORTING NEXIN-1; SNX1
TRANSCRIPTION FACTOR 1, HEPATIC; TCF1
HEPATOCYTE GROWTH FACTOR; HGF
INTERLEUKIN-6 RECEPTOR; IL6R
V-YES-1 YAMAGUCHI SARCOMA VIRAL ONCOGENE; YES1
ENDOGLIN; ENG
THANATOPHORIC DYSPLASIA WITH KLEEBLATTSCHAEDEL
HEMATOPOIETIC CELL-SPECIFIC LYN SUBSTRATE 1; HCLS1
GENERAL TRANSCRIPTION FACTOR IIH, POLYPEPTIDE 1; GTF2H1
V-SIS PLATELET-DERIVED GROWTH FACTOR BETA POLYPEPTIDE; PDGFB
DIABETES MELLITUS, AUTOSOMAL DOMINANT
PROGRAMMED CELL DEATH 1; PDCD1
TRANSFORMING GROWTH FACTOR-BETA RECEPTOR, TYPE I; TGFBR1
EPIDERMAL GROWTH FACTOR RECEPTOR PATHWAY SUBSTRATE-8; EPS8
VASCULAR ENDOTHELIAL GROWTH FACTOR; VEGF
CELL ADHESION REGULATOR; CAR
ANEMIA, CONGENITAL HYPOPLASTIC, OF BLACKFAN AND DIAMOND
GAUCHER DISEASE, TYPE I; GD I
MAPLE SYRUP URINE DISEASE; MSUD
MCF.2 CELL LINE DERIVED TRANSFORMING SEQUENCE; MCF2
GRANULOMATOUS DISEASE, CHRONIC; CGD
ANGIOPOIETIN 2; ANGPT2
HYPOGAMMAGLOBULINEMIA AND ISOLATED GROWTH HORMONE DEFICIENCY, X-LINKED
GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR-BETA
H4 GENE

CLAIMS

What is claimed is:

1. A kinase scaffold library comprising at least one set of compounds, each set consisting essentially of a plurality of compounds of a chemical structure selected from the group consisting of Formula I, II, III, IV, V, VI, and VII.

2. The library of claim 1, wherein said set comprises at least 50 different compounds.

3. The library of claim 1, wherein said library comprises at least 3 said sets.

4. The library of claim 1, wherein a majority of compounds in said set have been demonstrated to bind to one or more kinases.

5. The library of claim 4, wherein said kinases comprise a plurality of kinases selected from the group consisting of PIM-1, Pyk2, c-Abl, Her2, cMet, VEGFR, EGFR, cKit, Pkcβ, p38, Cdk2, Akt, Gsk3β.

6. The library of claim 1, wherein each said compound is in a separate well in a plate or plurality of plates.

7. A system for fitting compounds in binding sites of one or more protein kinases, comprising

an electronic kinase scaffold library comprising at least one collection of electronic representations of compounds of a chemical structure selected from the group consisting of Formula I, II, III, IV, V, VI, and VII, wherein said kinase scaffold library is embedded in a computer memory device, wherein said electronic representations of said compounds can be selectively retrieved and functionally connected with computer software adapted to fit electronic representations of compounds in an electronic representation of a binding site of a kinase.

8. The system of claim 7, further comprising at least one electronic representation of a kinase binding site embedded in computer memory such that said electronic representation of a kinase binding site can be functionally connected with said computer software.

9. The system of claim 8, where said electronic representation of kinase binding sites comprises electronic representations of binding sites of a plurality of kinases selected from the group consisting of PIM-1, Pyk2, c-Abl, Her2, cMet, VEGFR, EGFR, cKit, Pkcβ, p38, Cdk2, Akt, Gsk3β.

10. A method for obtaining improved ligands binding to a protein kinase, comprising

determining whether a derivative of a compound of Formula I, II, III, IV, V, VI, or VII binds to said kinase with greater affinity or greater specificity or both than said compound, wherein binding with greater affinity or greater specificity or both indicates that said derivative is an improved ligand.

11. The method of claim 10, wherein said derivative has at least 10-fold greater affinity or specificity or both than said compound.

12. The method of claim 10, wherein said derivative has at least 100-fold greater affinity or specificity or both.

13. The method of claim 10, wherein said kinase is selected from the group consisting of PIM-1, Pyk2, c-Abl, Her2, cMet, VEGFR, EGFR, cKit, Pkcβ, p38, Cdk2, Akt, Gsk3β.

14. A method for developing ligands specific for a particular kinase, comprising

determining whether a derivative of a compound of Formula I, II, III, IV, V, VI, or VII that binds to a plurality of kinases has greater specificity for said particular kinase than said compound.

15. The method of claim 14, wherein said compound binds to said kinase with an affinity at least 10-fold greater than for binding to any of said plurality of kinases.

16. The method of claim 15, wherein said compound interacts with at least one of PIM-1 residues 49, 52, 65, 67, 121, 128, and 186.

17. The method of claim 14, wherein said compound binds weakly to said plurality of kinases.

18. The method of claim 14, wherein said kinase is selected from the group consisting of PIM-1, Pyk2, c-Abl, Her2, cMet, VEGFR, EGFR, cKit, Pkcβ, p38, Cdk2, Akt, Gsk3β.

19. A method for developing ligands binding to a kinase, comprising

determining the orientation of at least one molecular scaffold of Formula I, II, III, IV, V, VI, or VII in co-crystals with said kinase; and

identifying chemical structures of said molecular scaffolds, that, when modified, alter the binding affinity or binding specificity or both between the molecular scaffold and said kinase; and

synthesizing a ligand wherein one or more of the chemical structures of the molecular scaffold is modified to provide a ligand that binds to said kinase with altered binding affinity or binding specificity or both.

20. The method of claim 19, wherein said molecular scaffold is a weak binding compound.

21. The method of claim 19, wherein said molecular scaffold binds to a plurality of kinases.

22. The method of claim 19, wherein said molecular scaffold interacts with at least 3 kinases selected from the group consisting of PIM-1, Pyk2, c-Abl, Her2, cMet, VEGFR, EGFR, cKit, Pkcβ, p38, Cdk2, Akt, and Gsk3β.

23. The method of claim 19, wherein said kinase is selected from the group consisting of PIM-1, Pyk2, c-Abl, Her2, cMet, cKit, Pkcβ, Cdk2, and Akt.

24. A method for developing ligands with increased specificity on a kinase, comprising

testing a derivative of a kinase binding compound of Formula I, II, III, IV, V, VI, or VII for increased specificity on said kinase, wherein increased specificity is indicative that said derivative is a ligand with increased specificity.

25. The method of claim 24, wherein said kinase binding compound binds to at least 5 different human kinases.

26. The method of claim 24, wherein said kinase binding compound binds to at least 10 different human kinases.

27. The method of claim 24, wherein said kinase is selected from the group consisting of PIM-1, Pyk2, c-Abl, Her2, cMet, VEGFR, EGFR, cKit, Pkcβ, p38, Cdk2, Akt, Gsk3β..

28. A method for identifying a ligand binding to a kinase, comprising

determining whether a derivative compound that includes a core structure selected from the group consisting of Formula I, II, III, IV, V, VI, and VII binds to said kinase with altered binding affinity or specificity or both as compared to the parent compound.

29. A co-crystal of a kinase and a binding compound of Formula I, II, III, IV, V, VI, or VII.

30. The co-crystal of claim 29, wherein said binding compound interacts with at least one of PIM-1 residues 49, 52, 65, 67, 121, 128, and 186.

31. The co-crystal of claim 29, wherein said kinase is selected from the group consisting of PIM-1, Pyk2, c-Abl, Her2, cMet, VEGFR, EGFR, cKit, Pkcβ, p38, Cdk2, Akt, Gsk3β.

32. The co-crystal of claim 29, wherein said co-crystal is in an X-ray beam.

33. A method for obtaining co-crystals of PIM-1 with a binding compound of Formula I, II, III, IV, V, VI, or VII, comprising subjecting PIM-1 protein at 5-20 mg/ml to crystallization conditions substantially equivalent to Hampton Screen 1 conditions 2, 7, 14, 17, 23, 25, 29, 36, 44, or 49 in the presence of binding compound for a time sufficient for crystal development.

34. The method of claim 33, wherein said binding compound is added to said protein to a final concentration of 0.5 to 1.0 mM.

35. The method of claim 34, wherein said binding compound is in a dimethyl sulfoxide solution.

36. The method of claim 33, wherein said crystallization condition is 0.4-0.9 M sodium acetate trihydrate pH 6.5, 0.1 M imidazole; or 0.2-0.7 M. sodium potassium tartrate, 00.1 M MES buffer pH 6.5.

37. A method for modulating kinase activity, comprising
contacting said kinase with a compound of Formula I, II, III, IV, V, VI, or VII.

38. The method of claim 37, wherein said kinase is selected from the group consisting of PIM-1, Pyk2, c-Abl, Her2, cMet, VEGFR, EGFR, cKit, Pkcβ, p38, Cdk2, Akt, Gsk3β.

39. The method of claim 37, wherein said compound is at a concentration of 200 μM or less.

40. A method for treating a patient suffering from a disease or condition characterized by abnormal kinase activity, comprising
administering to said patient a compound of Formula I, II, III, IV, V, VI, or VII active on said kinase.

41. The method of claim 40, wherein said kinase is selected from the group consisting of PIM-1, Pyk2, c-Abl, Her2, cMet, VEGFR, EGFR, cKit, Pkcβ, p38, Cdk2, Akt, Gsk3β.

42. The method of claim 40 wherein said disease or condition is a cancer.

43. The method of claim 40, wherein said disease or condition is an inflammatory disease or condition.

44. An electronic representation of a binding site of a kinase with a compound of a chemical structure selected from the group consisting of Formula I, II, III, IV, V, VI, and VII bound therein.

45. The electronic representation of claim 44, comprising a binding site surface contour.

46. The electronic representation of claim 44, comprising representations of the binding character of a plurality of conserved amino acid residues.

47. A method for identifying potential kinase binding compounds, comprising

fitting at least one electronic representations of a compound of Formula I, II, III, IV, V, VI, or VII in an electronic representation of a kinase binding site.

48. The method of claim 47, wherein said kinase is selected from the group consisting of PIM-1, Pyk2, c-Abl, Her2, cMet, VEGFR, EGFR, cKit, Pkcβ, p38, Cdk2, Akt, Gsk3β.

49. The method of claim 48, comprising

removing a computer representation of a compound complexed with said kinase and fitting a computer representation of a compound from a computer database with a computer representation of the active site of said kinase; and

identifying compounds that best fit said active site based on favorable geometric fit and energetically favorable complementary interactions as potential binding compounds.

50. The method of claim 48, comprising

modifying a computer representation of a compound complexed with said kinase by the deletion or addition or both of one or more chemical groups;

fitting a computer representation of a compound from a computer database with a computer representation of the active site of said kinase; and

identifying compounds that best fit said active site based on favorable geometric fit and energetically favorable complementary interactions as potential binding compounds.

51. The method of claim 48, comprising

removing a computer representation of a compound complexed with said kinase; and

searching a database for compounds having structural similarity to said compound using a compound searching computer program or replacing portions of said compound with similar chemical structures using a compound construction computer program.

52. A method for attaching a kinase binding compound to an attachment component, comprising

identifying energetically allowed sites for attachment of a said attachment component on a kinase binding compound of Formula I, II, III, IV, V, VI, or VII; and

attaching said compound or derivative thereof to said attachment component at said energetically allowed site.

53. The method of claim 52, wherein said attachment component is a linker for attachment to a solid phase medium, and said method further comprises attaching said compound or derivative to a solid phase medium through a linker attached at a said energetically allowed site.

54. The method of claim 52, wherein said kinase is selected from the group consisting of PIM-1, Pyk2, c-Abl, Her2, cMet, VEGFR, EGFR, cKit, Pkcβ, p38, Cdk2, Akt, Gsk3β.

55. The method of claim 52, wherein said kinase comprises conserved residues matching at least one of PIM-1 residues 49, 52, 65, 67, 121, 128, and 186.

56. The method of claim 53, wherein said linker is a traceless linker.

57. The method of claim 53, wherein said kinase binding compound or derivative thereof is synthesized on a said linker attached to said solid phase medium.

58. The method of claim 57, wherein a plurality of said compounds or derivatives are synthesized in combinatorial synthesis.

59. The method of claim 53, wherein attachment of said compound to said solid phase medium provides an affinity medium.

60. The method of claim 52, wherein said attachment component comprises a label.

61. The method of claim 60, wherein said label comprises a fluorophore.

62. A modified compound, comprising

a compound of Formula I, II, III, IV, V, VI, or VII, with a linker moiety attached thereto.

63. The compound of claim 62, wherein said linker is attached to an energetically allowed site for binding of said modified compound to a kinase selected from the group consisting of PIM-1, Pyk2, c-Abl, Her2, cMet, VEGFR, EGFR, cKit, Pkcβ, p38, Cdk2, Akt, Gsk3β.

64. The compound of claim 62, wherein said linker is attached to a solid phase.

65. The compound of claim 62, wherein said linker comprises or is attached to a label.

66. The compound of claim 62, wherein said linker is a traceless linker.

67. A method for developing a ligand for a kinase comprising conserved residues matching one or more of PIM-1 residues 49, 52, 65, 67, 121, 128, and 186, comprising

determining whether a compound of Formula I, II, III, IV, V, VI, or VII binds to said kinase.

68. The method of claim 67, wherein said kinase is selected from the group consisting of PIM-1, Pyk2, c-Abl, Her2, cMet, VEGFR, EGFR, cKit, Pkcβ, p38, Cdk2, Akt, Gsk3β.

69. The method of claim 67, wherein said kinase comprises conserved residues matching at least 2 of PIM-1 residues 49, 52, 65, 67, 121, 128, and 186.

70. The method of claim 67, wherein said kinase comprises conserved residues matching PIM-1 residues 49, 52, 65, 67, 121, 128, and 186.

71. The method of claim 67, further comprising determining whether said compound modulates said kinase.

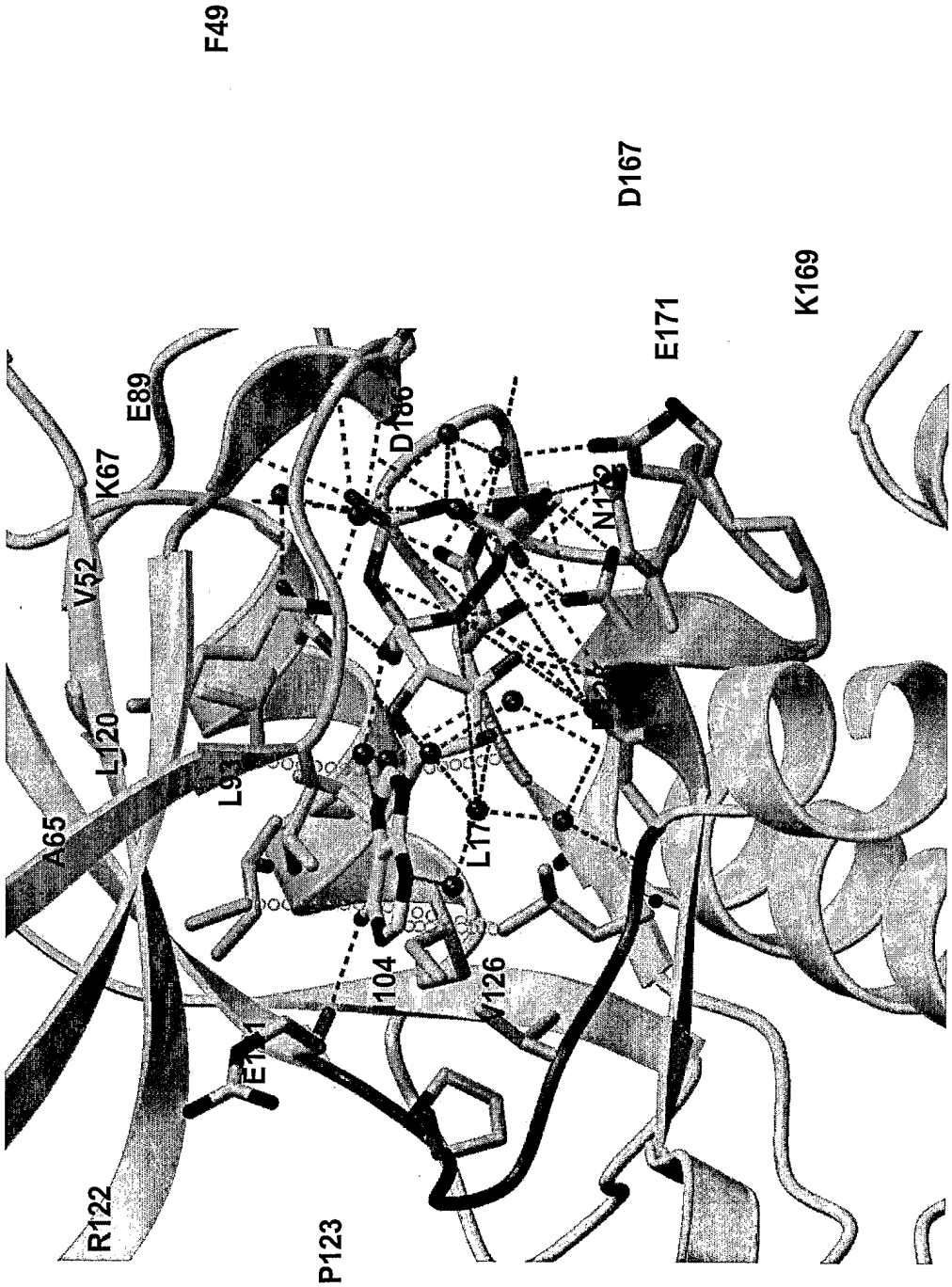
72. The method of claim 67, wherein said determining comprises computer fitting said compound in a binding site of said kinase.

73. The method of claim 67, further comprising forming a co-crystal of said kinase and said compound.

74. The method of claim 73, further comprising determining the binding orientation of said compound with said kinase.

1/1

Fig. 1


F49
D167
K169
E171
E89
K67
D186
V52
L120
A65
L177
104
126
R122
P123